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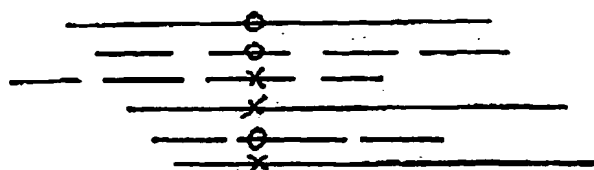
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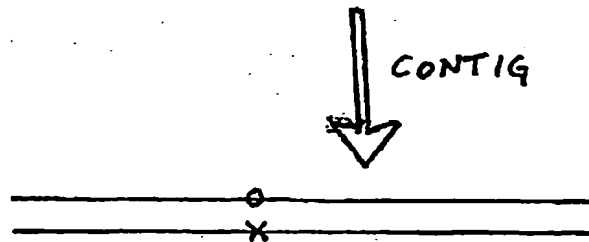
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(54) Title: **NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE
THEREOF**



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X SNP (VARIANT)



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(57) Abstract: The invention provides nucleic acids containing single-nucleotide polymorphisms identified for transcribed human sequences, as well as methods of using the nucleic acids.

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NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE THEREOF

BACKGROUND OF THE INVENTION

5 Sequence polymorphism-based analysis of nucleic acid sequences can augment or replace previously known methods for determining the identity and relatedness of individuals. The approach is generally based on alterations in nucleic acid sequences between related individuals. This analysis has been widely used in a variety of genetic, diagnostic, and forensic applications. For example, polymorphism analyses are used in
10 identity and paternity analysis, and in genetic mapping studies.

One such type of variation is a restriction fragment length polymorphism (RFLP). RFLPS can create or delete a recognition sequence for a restriction endonuclease in one nucleic acid relative to a second nucleic acid. The result of the variation is an alteration in the relative length of restriction enzyme generated DNA fragments in the two nucleic acids.

15 Other polymorphisms take the form of short tandem repeats (STR) sequences, which are also referred to as variable numbers of tandem repeat (VNTR) sequences. STR sequences typically include tandem repeats of 2, 3, or 4 nucleotide sequences that are present in a nucleic acid from one individual but absent from a second, related individual at the corresponding genomic location.

20 Other polymorphisms take the form of single nucleotide variations, termed single nucleotide polymorphisms (SNPs), between individuals. A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA.

SNPs can arise in several ways. A single nucleotide polymorphism may arise due to a
25 substitution of one nucleotide for another at the polymorphic site. Substitutions can be transitions or transversions. A transition is the replacement of one purine nucleotide by another purine nucleotide, or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine, or the converse.

Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an
30 insertion of a nucleotide relative to a reference allele. Thus, the polymorphic site is a site at which one allele bears a gap with respect to a single nucleotide in another allele. Some SNPs



occur within, or near genes. One such class includes SNPs falling within regions of genes encoding for a polypeptide product. These SNPs may result in an alteration of the amino acid sequence of the polypeptide product and give rise to the expression of a defective or other variant protein. Such variant products can, in some cases result in a pathological condition, *e.g.*, genetic disease. Examples of genes in which a polymorphism within a coding sequence gives rise to genetic disease include sickle cell anemia and cystic fibrosis. Other SNPs do not result in alteration of the polypeptide product. Of course, SNPs can also occur in noncoding regions of genes.

SNPs tend to occur with great frequency and are spaced uniformly throughout the genome. The frequency and uniformity of SNPs means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest.

SUMMARY OF THE INVENTION

The invention is based in part on the discovery of novel single nucleotide polymorphisms (SNPs) in regions of human DNA.

Accordingly, in one aspect, the invention provides an isolated polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, *e.g.*, a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 7867) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS: 1-7867), or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

The polynucleotide can be, *e.g.*, DNA or RNA, and can be between about 10 and about 100 nucleotides, *e.g.* 10-90, 10-75, 10-51, 10-40, or 10-30, nucleotides in length.

In some embodiments, the polymorphic site in the polymorphic sequence includes a nucleotide other than the nucleotide listed in Table 1, column 5 for the polymorphic sequence, *e.g.*, the polymorphic site includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

In other embodiments, the complement of the polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of the polymorphic sequence, *e.g.*, the complement of the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

5 In some embodiments, the polymorphic sequence is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated with a polypeptide related to an ATPase associated protein, a cadherin, or any of the other proteins identified in Table 1, column 10.

10 In another aspect, the invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7867), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a
15 fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7867), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in
20 addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

In some embodiments, the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide. The second polynucleotide can be, *e.g.*, (a) a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 -
25 7867), wherein the polymorphic sequence includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence; (b) a nucleotide sequence that is a fragment of any of the polymorphic sequences; (c) a complementary nucleotide sequence including a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7867), wherein the polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5;
30 and (d) a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The invention also provides a method of detecting a polymorphic site in a nucleic acid. The method includes contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the nucleic acid and the oligonucleotide hybridize. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphic site in the nucleic acid.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

In some embodiments, the polymorphic sequence identified by the oligonucleotide is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated polypeptide related to an ATPase associated protein, cadherin, or any of the other protein families identified in Table 1, column 10.

In another aspect, the method includes determining if a sequence polymorphism is present in a subject, such as a human. The method includes providing a nucleic acid from the subject and contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1,

column 5. Hybridization between the nucleic acid and the oligonucleotide is then determined. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphism in said subject.

In a further aspect, the invention provides a method of determining the relatedness of a first and second nucleic acid. The method includes providing a first nucleic acid and a second nucleic acid and contacting the first nucleic acid and the second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the first nucleic acid and the second nucleic acid hybridize to the oligonucleotide, and comparing hybridization of the first and second nucleic acids to the oligonucleotide. Hybridization of first and second nucleic acids to the nucleic acid indicates the first and second subjects are related.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The method can be used in a variety of applications. For example, the first nucleic acid may be isolated from physical evidence gathered at a crime scene, and the second nucleic acid may be obtained from a person suspected of having committed the crime. Matching the two nucleic acids using the method can establish whether the physical evidence originated from the person.

In another example, the first sample may be from a human male suspected of being the father of a child and the second sample may be from the child. Establishing a match using the described method can establish whether the male is the father of the child.

In another aspect, the invention provides an isolated polypeptide comprising a polymorphic site at one or more amino acid residues, and wherein the protein is encoded by a polynucleotide including one of the polymorphic sequences SEQ ID NOS:1-7867, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

The polypeptide can be, *e.g.*, related to one of the protein families disclosed herein. For example, the polypeptide can be related to an ATPase associated protein, cadherin, or any of the other proteins provided in Table 1, column 10.

In some embodiments, the polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.

In some embodiments, the polypeptide encoded by the polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

The invention also provides an antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS:1-7867, or its complement. The polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

In some embodiments, the antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

Preferably, the antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence.

The invention further provides a method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject. The method includes providing a protein sample from the subject and contacting the sample with the above-described antibody under conditions that allow for the formation of antibody-antigen
5 complexes. The antibody-antigen complexes are then detected. The presence of the complexes indicates the presence of the polypeptide.

The invention also provides a method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, *e.g.*, a human, non-human primate, cat, dog, rat, mouse, cow, pig,
10 goat, or rabbit. The method includes providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or its complement, and treating the subject by administering to the subject an effective dose of a therapeutic agent. Aberrant expression can include qualitative alterations in expression of a gene, *e.g.*, expression of a
15 gene encoding a polypeptide having an altered amino acid sequence with respect to its wild-type counterpart. Qualitatively different polypeptides can include, shorter, longer, or altered polypeptides relative to the amino acid sequence of the wild-type polypeptide. Aberrant expression can also include quantitative alterations in expression of a gene. Examples of quantitative alterations in gene expression include lower or higher levels of expression of the
20 gene relative to its wild-type counterpart, or alterations in the temporal or tissue-specific expression pattern of a gene. Finally, aberrant expression may also include a combination of qualitative and quantitative alterations in gene expression.

The therapeutic agent can be administered to a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic
25 sequence. The therapeutic agent can include, *e.g.*, second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele. In some embodiments, the second nucleic acid sequence comprises a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence.

30 Alternatively, the therapeutic agent can be a polypeptide encoded by a polynucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or by a polynucleotide comprising a nucleotide sequence that is complementary to any

one of the polymorphic sequences SEQ ID NOS:1 - 7867, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

The therapeutic agent may further include an antibody as herein described, or an oligonucleotide comprising a polymorphic sequence selected from the group consisting of
5 SEQ ID NOS:1 - 7867, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7867, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for the polymorphic sequence.

In another aspect, the invention provides an oligonucleotide array comprising one or
10 more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein. The first polynucleotide can be, e.g., a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7867); a nucleotide sequence that is a fragment of any of the nucleotide sequences, provided that the fragment includes a polymorphic site in the polymorphic sequence; a complementary nucleotide sequence
15 comprising a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7867); or a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

In preferred embodiments, the array comprises 10; 100; 1,000; 10,000; 100,000 or more oligonucleotides.

The invention also provides a kit comprising one or more of the herein-described
20 nucleic acids. The kit can include, e.g., a polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, e.g., a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 7867) and which includes a polymorphic sequence, or a fragment
25 of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS:1-7867), or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence. The invention provides an isolated allele-specific
30 oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, e.g., a nucleotide sequence comprising one or more polymorphic

sequences (SEQ ID NOS:1 - 7867), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7867), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides human SNPs in sequences which are transcribed, *i.e.*, are cSNPs. Many SNPs have been identified in genes related to polypeptides of known function. If desired, SNPs associated with various polypeptides can be used together. For example, SNPs can be grouped according to whether they are derived from a nucleic acid encoding a polypeptide related to particular protein family or involved in a particular function. Similarly, SNPs can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins which are associated with metabolic pathways, including fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc. Specifically, the present invention

provides a large number of human cSNP's based on at least one gene product that has not been previously identified. In contrast, and as defined specifically in the following paragraph, the cSNP's involve nucleic acid sequences that are assembled from at least one known sequence.

5 The present invention provides a large number of human cSNP's based on at least one gene product that has not been previously identified. In contrast, and as defined specifically in the following paragraph, the cSNP's involve nucleic acid sequences that are assembled from at least one known sequence.

7867 distinct polymorphic sites were identified by the present inventors, using the
10 following procedure. Raw traces underlying sequence data were drawn from public databases and from the proprietary database of the Assignee of the present invention. The sequences were obtained by calling the bases from these traces, and included assigning "Phred" quality scores for each called base. For each allelic set, at the polynucleotide level, four or more nucleotide sequences were identified having at least partial overlap with one
15 another.

As illustrated in FIG. 1, these four or more sequences could be clustered and assembled to make a consensus contig that included an ORF. In this way, the inventors found that the assembled contigs defined associated sets of two, or possibly more than two, alleles defined by an SNP at a particular polymorphic site. In order to be confirmed as a SNP
20 site, the nucleotide change from the consensus sequence had to occur in at least two individual sequences, and had to have a "Phred" score of 23 or higher at the site of the presumed SNP. Furthermore, in a window of 5 bases on either side of the SNP, no more than 50% mismatching with the consensus sequence was allowed. In the assembly leading to each of the contigs defining the allelic set, the SNP alleles occur in polynucleotides found in public
25 databases. Furthermore, it was found that the assembled contigs defined associated sets of two, or possibly more than two, alleles defined by an SNP at a particular polymorphic site. These associations were not previously known. The SNPs are presented in Table 1.

At the level of translation of an ORF contained in the contigs, however, the inventors identified allelic sets in which one allele defines a known polypeptide sequence that includes
30 the polymorphic site and another polypeptide allele is not previously known. Then, various associations of alleles are possible. For example, it is possible that an allelic pair is defined

in a noncoding region of the contig containing an ORF. In such cases the inventors believe that the invention resides in the recognition of the allelic pair; this association has not heretofore been made. Alternatively, sets of allelic contigs may exist in which the polymorphic site is within an ORF, but does not result in an amino acid change among the allelic polypeptides. Here too it is believed that the invention resides in the recognition of the allelic pair; and that this association has not heretofore been made. In yet another alternative, the polymorphic site resides within an ORF and results in an amino acid change, or a frameshift, among the alleles of the allelic set. In the sets of gene products that fall within this group, at least one of the alleles at the polypeptide level is a known protein. At least one of the remaining allele or alleles in the set, carrying a variant amino acid at the polymorphic site, is a novel polypeptide not heretofore known. The invention resides at least in the recognition of the polymorphic allele as being a variant of the known reference polypeptide.

Table 1 provides information concerning the allelic sequences. One of the sequences may be termed a reference polymorphic sequence, and the corresponding second sequence includes the variant SNP at the polymorphic site. Since the reference polypeptide sequence is already known, the Sequence Listing accompanying this application provides only the sequence of the polymorphic allele, while its SEQ ID NO is provided in the Table. A reference to the SEQ ID NO that corresponds to the translated amino acid sequence is also given. The Table includes thirteen columns that provide descriptive information for each cSNP, each of which occupies one row in the Table. The column headings, and a description of each, are given below.

SNPs disclosed in Table 1 were detected by aligning large numbers of sequences from genetically diverse sources of publicly available mRNA libraries (Clontech). Software designed specifically to look for multiple examples of variant bases differing from a consensus sequence was created and deployed. A criteria of a minimum of 2 occurrences of a sequence differing from the consensus in high quality sequence reads was used to identify an SNP.

The SNPs described herein may be useful in diagnostic kits, for DNA arrays on chips and for other uses that involve hybridization of the SNP.

Specific SNPs may have utility where a disease has already been associated with that gene. Examples of possible disease correlations between the claimed SNPs with members of the genes of each classification are listed below:

Amylases

- 5 Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

Amyloid

- 10 The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called amyloidosis, which affects the liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-
- 15 stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. Amyloid deposition is also associated with type II diabetes mellitus.

20 **Angiopoeitin**

- Members of the angiopoietin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an essential step in tumor growth in order for the tumor to get the blood supply it needs
- 25 to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

Apoptosis-related proteins

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of antiaging drugs.

Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

Colony-stimulating factor-related proteins

Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

20 Complement-related proteins

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I

diabetes mellitus, meningitis neurological disorders such as Nemaline myopathy, Neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

Cytochrome

5 The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

Kinesins

10 Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

Cytokines, Interferon, Interleukin

15 Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

20 G-protein coupled receptors

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, 25 dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and dwarfism.

Thioesterases

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The SNPs are shown in Table 1 and the Sequence Listing. Both provide a summary of the polymorphic sequences disclosed herein. In the Table, a "SNP" is a polymorphic site embedded in a polymorphic sequence. The polymorphic site is occupied by a single nucleotide, which is the position of nucleotide variation between the wild type and polymorphic allelic sequences. The site is usually preceded by and followed by relatively highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations). Thus, a polymorphic sequence can include one or more of the following sequences: (1) a sequence having the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence; or (2) a sequence having a nucleotide other than the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence. An example of the latter sequence is a polymorphic sequence having the nucleotide denoted in Table 1, column 6 at the polymorphic site in the polymorphic sequence.

Nucleotide sequences for a referenced-polymorphic pair are presented in Table 1. Each cSNP entry provides information concerning the wild type nucleotide sequence as well as the corresponding sequence that includes the SNP at the polymorphic site. Since the wild type sequence is already known, the Sequence Listing accompanying this application provides only the sequence of the polymorphic allele; its SEQ ID NO: is also cross referenced in the Table 1. A reference to the SEQ ID NO: giving the translated amino acid sequence is also given if appropriate. The Table includes thirteen columns that provide descriptive information for each cSNP, each of which occupies one row in the Table. The column headings, and an explanation for each, are given below.

"SEQ ID" provides the cross-references to the nucleotide SEQ ID NOs: for the polymorphic sequences, which are numbered consecutively, and, as explained below, amino acid SEQ ID NOs: as well, in the Sequence Listing of the application. Conversely, each

sequence entry in the Sequence Listing also includes a cross-reference to the CuraGen sequence ID, under the label "CuraGen sequence ID". The first SEQ ID NO: given in the first column of each row of the Table is the SEQ ID NO: identifying the nucleic acid sequence for the polymorphisms. If a polymorphism carries an entry for an amino acid in a coding region, then a second SEQ ID NO: appears in parentheses in the column "Amino acid after" (see below) for the polymorphic amino acid sequence. The latter SEQ ID NOs: refer to amino acid sequences giving the polymorphic amino acid sequences that are the translation of the nucleotide polymorphism. If a polymorphism carries no entry for the protein portion of the row, only one SEQ ID NO: is provided, in the first column.

10 "Base pos. of SNP" gives the numerical position of the nucleotide in the nucleic acid at which the cSNP is found, as identified in this invention.

 "Polymorphic sequence" provides a 51-base sequence with the polymorphic site at the 26th base in the sequence, as well as 25 bases from the reference sequence on the 5' side and the 3' side of the polymorphic site. The designation at the polymorphic site is enclosed in square brackets, and provides first, the reference nucleotide; second, a "slash (/)"; and third, the polymorphic nucleotide. In certain cases the polymorphism is an insertion or a deletion. In that case, the position which is "unfilled" (i.e., the reference or the polymorphic position) is indicated by the word "gap".

15

 "Base before" provides the nucleotide present in the reference sequence at the position at which the polymorphism is found.

20

 "Base after" provides the altered nucleotide at the position of the polymorphism.

 "Amino acid before" provides the amino acid in the reference protein, if the polymorphism occurs in a coding region.

 "Amino acid after" provides the amino acid in the polymorphic protein, if the polymorphism occurs in a coding region. This column also includes the SEQ ID NO: in parentheses for the translated polymorphic amino acid sequence if the polymorphism occurs in a coding region.

25

 "Type of change" provides information on the nature of the polymorphism.

"SILENT-NONCODING" is used if the polymorphism occurs in a noncoding region of a nucleic acid.

"SILENT-CODING" is used if the polymorphism occurs in a coding region of a nucleic acid and results in no change of amino acid in the translated polymorphic protein.

"CONSERVATIVE" is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in the same class as the reference amino acid. The classes are:

Aliphatic: Gly, Ala, Val, Leu, Ile;

Aromatic: Phe, Tyr, Trp;

Sulfur-containing: Cys, Met;

Aliphatic OH: Ser, Thr;

Basic: Lys, Arg, His;

Acidic: Asp, Glu, Asn, Gln;

Pro falls in none of the other classes; and

End defines a termination codon.

"NONCONSERVATIVE" is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in a different class than the reference amino acid.

"FRAMESHIFT" relates to an insertion or a deletion. If the frameshift occurs in a coding region, the Table provides the translation of the frameshifted codons 3' to the polymorphic site.

"Protein classification of CuraGen gene" provides a generic class into which the protein is classified. During the course of the work leading to the filing of the four applications identified above, approximately 100 classes of proteins were identified.

"Name of protein identified following a BLASTX analysis of the CuraGen sequence" provides the database reference for the protein found to resemble the novel reference-polymorphism cognate pair most closely. (The next paragraph explains how a sequence was determined to be "novel").

5 "Similarity (pvalue) following a BLASTX analysis" provides the pvalue, a statistical measure from the BLASTX analysis that the polymorphic sequence is similar to, and therefore an allele of, the reference, or wild-type, sequence. In the present application, a cutoff of $pvalue > 1 \times 10^{-50}$ (entered, for example, as 1.0E-50 in the Table) is used to establish that the reference-polymorphic cognate pairs are novel.

10 "Map location" provides any information available at the time of filing related to localization of a gene on a chromosome.

The polymorphisms are arranged in the Table in the following order.

SEQ ID NOs: 1-5696 are nucleotide sequences for SNPs that are silent.

15 SEQ ID NOs: 5697-6011 are nucleotide sequences for SNPs that lead to conservative amino acid changes.

SEQ ID NOs: 6012-6740 are nucleotide sequences for SNPs that lead to nonconservative amino acid changes.

20 SEQ ID NOs: 6741-7867 are nucleotide sequences for SNPs that involve a gap. With respect to the reference or wild-type sequence at the position of the polymorphism, the allelic cSNP introduces an additional nucleotide (an insertion) or deletes a nucleotide (a deletion). An SNP that involves a gap generates a frame shift.

25 SEQ ID NOs: 7868-8182 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to conservative amino acid changes. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

SEQ ID NOs: 8183-8911 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to nonconservative

amino acid changes. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

5 SEQ ID NOs: 8912-10038 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to frameshift-induced amino acid changes. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

10 Provided herein are compositions which include, or are capable of detecting, nucleic acid sequences having these polymorphisms, as well as methods of using nucleic acids.

IDENTIFICATION OF INDIVIDUALS CARRYING SNPs

15 Individuals carrying polymorphic alleles of the invention may be detected at either the DNA, the RNA, or the protein level using a variety of techniques that are well known in the art. Strategies for identification and detection are described in *e.g.*, EP 730,663, EP 717,113, and PCT US97/02102. The present methods usually employ pre-characterized polymorphisms. That is, the genotyping location and nature of polymorphic forms present at a site have already been determined. The availability of this information allows sets of probes to be designed for specific identification of the known polymorphic forms.

20 Many of the methods described below require amplification of DNA from target samples. This can be accomplished by *e.g.*, PCR. See generally PCR Technology: Principles and Applications for DNA Amplification (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); PCR Protocols: A Guide to Methods and Applications (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, 25 Oxford); and U.S. Patent 4,683,202.

The phrase "recombinant protein" or "recombinantly produced protein" refers to a peptide or protein produced using non-native cells that do not have an endogenous copy of DNA able to express the protein. In particular, as used herein, a recombinantly produced protein relates to the gene product of a polymorphic allele, *i.e.*, a "polymorphic protein"

30

containing an altered amino acid at the site of translation of the nucleotide polymorphism. The cells produce the protein because they have been genetically altered by the introduction of the appropriate nucleic acid sequence. The recombinant protein will not be found in association with proteins and other subcellular components normally associated with the cells
5 producing the protein. The terms "protein" and "polypeptide" are used interchangeably herein.

The phrase "substantially purified" or "isolated" when referring to a nucleic acid, peptide or protein, means that the chemical composition is in a milieu containing fewer, or preferably, essentially none, of other cellular components with which it is naturally
10 associated. Thus, the phrase "isolated" or "substantially pure" refers to nucleic acid preparations that lack at least one protein or nucleic acid normally associated with the nucleic acid in a host cell. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as gel electrophoresis or high performance liquid chromatography.
15 Generally, a substantially purified or isolated nucleic acid or protein will comprise more than 80% of all macromolecular species present in the preparation. Preferably, the nucleic acid or protein is purified to represent greater than 90% of all macromolecular species present. More preferably the nucleic acid or protein is purified to greater than 95%, and most preferably the nucleic acid or protein is purified to essential homogeneity, wherein other macromolecular
20 species are not detected by conventional analytical procedures.

The genomic DNA used for the diagnosis may be obtained from any nucleated cells of the body, such as those present in peripheral blood, urine, saliva, buccal samples, surgical specimen, and autopsy specimens. The DNA may be used directly or may be amplified enzymatically in vitro through use of PCR (Saiki et al. Science 239:487-491 (1988)) or other
25 in vitro amplification methods such as the ligase chain reaction (LCR) (Wu and Wallace Genomics 4:560-569 (1989)), strand displacement amplification (SDA) (Walker et al. Proc. Natl. Acad. Sci. U.S.A. 89:392-396 (1992)), self-sustained sequence replication (3SR) (Fahy et al. PCR Methods P&J& 1:25-33 (1992)), prior to mutation analysis.

The method for preparing nucleic acids in a form that is suitable for mutation
30 detection is well known in the art. A "nucleic acid" is a deoxyribonucleotide or ribonucleotide polymer in either single or double-stranded form, including known analogs of natural nucleotides unless otherwise indicated. The term "nucleic acids", as used herein,

refers to either DNA or RNA. "Nucleic acid sequence" or "polynucleotide sequence" refers to a single-stranded sequence of deoxyribonucleotide or ribonucleotide bases read from the 5' end to the 3' end. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 5' end of the RNA transcript in the 5' direction are referred to as "upstream sequences"; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 3' end of the RNA transcript in the 3' direction are referred to as "downstream sequences". The term includes both self-replicating plasmids, infectious polymers of DNA or RNA and nonfunctional DNA or RNA. The complement of any nucleic acid sequence of the invention is understood to be included in the definition of that sequence. "Nucleic acid probes" may be DNA or RNA fragments.

The detection of polymorphisms in specific DNA sequences, can be accomplished by a variety of methods including, but not limited to, restriction-fragment-length-polymorphism detection based on allele-specific restriction-endonuclease cleavage (Kan and Dozy Lancet ii:910-912 (1978)), hybridization with allele-specific oligonucleotide probes (Wallace et al. Nucl. Acids Res. 6:3543-3557 (1978)), including immobilized oligonucleotides (Saiki et al. Proc. Natl. Acad. Sci. USA, 86:6230-6234 (1969)) or oligonucleotide arrays (Maskos and Southern Nucl. Acids Res 21:2269-2270 (1993)), allele-specific PCR (Newton et al. Nucl Acids Res 17:2503-2516 (1989)), mismatch-repair detection (MRD) (Faham and Cox. Genome Res 5:474-482 (1995)), binding of MutS protein (Wagner et al. Nucl Acids Res 23:3944-3948 (1995), denaturing-gradient gel electrophoresis (DGGE) (Fisher and Lerman et al. Proc. Natl. Acad. Sci. U.S.A. 80:1579-1583 (1983)), single-strand-conformation-polymorphism detection (Orita et al. Genomics 5:874-879 (1983)), RNAase cleavage at mismatched base-pairs (Myers et al. Science 230:1242 (1985)), chemical (Cotton et al. Proc. Natl. w Sci. U.S.A., 82:4397-4401 (1988)) or enzymatic (Youil et al. Proc. Natl. Acad. Sci. U.S.A. 92:87-91 (1995)) cleavage of heteroduplex DNA, methods based on allele specific primer extension (Syvanen et al. Genomics 8:684-692 (1990)), genetic bit analysis (GBA) (Nikiforov et al. &&I Acids 22:4167-4175 (1994)), the oligonucleotide-ligation assay (OLA) (Landegren et al. Science 241:1077 (1988)), the allele-specific ligation chain reaction (LCR) (Barrany Proc. Natl. Acad. Sci. U.S.A. 88:189-193 (1991)), gap-LCR (Abravaya et al. Nucl Acids Res 23:675-682 (1995)), radioactive and/or fluorescent DNA sequencing using standard procedures well known in the art, and peptide nucleic acid (PNA) assays (Orum et al., Nucl. Acids Res, 21:5332-5356 (1993); Thiede et al., Nucl. Acids Res. 24:983-984

(1996)).

“Specific hybridization” or “selective hybridization” refers to the binding, or duplexing, of a nucleic acid molecule only to a second particular nucleotide sequence to which the nucleic acid is complementary, under suitably stringent conditions when that sequence is present in a complex mixture (e.g., total cellular DNA or RNA). “Stringent conditions” are conditions under which a probe will hybridize to its target subsequence, but to no other sequences. Stringent conditions are sequence-dependent and are different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter ones. Generally, stringent conditions are selected such that the temperature is about 5°C lower than the thermal melting point (T_m) for the specific sequence to which hybridization is intended to occur at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the target sequence hybridizes to the complementary probe at equilibrium. Typically, stringent conditions include a salt concentration of at least about 0.01 to about 1.0 M Na ion concentration (or other salts), at pH 7.0 to 8.3. The temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides). Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C are suitable for allele-specific probe hybridization.

“Complementary” or “target” nucleic acid sequences refer to those nucleic acid sequences which selectively hybridize to a nucleic acid probe. Proper annealing conditions depend, for example, upon a probe’s length, base composition, and the number of mismatches and their position on the probe, and must often be determined empirically. For discussions of nucleic acid probe design and annealing conditions, see, for example, Sambrook et al., or Current Protocols in Molecular Biology, F. Ausubel et al., ed., Greene Publishing and Wiley-Interscience, New York (1987).

A perfectly matched probe has a sequence perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion of the target sequence. A “polymorphic” marker or site is the locus at which a sequence difference occurs with respect to a reference sequence. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple

sequence repeats, and insertion elements such as Alu. The reference allelic form may be, for example, the most abundant form in a population, or the first allelic form to be identified, and other allelic forms are designated as alternative, variant or polymorphic alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the "wild type" form, and herein may also be referred to as the "reference" form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two distinguishable forms (i.e., base sequences), and a triallelic polymorphism has three such forms.

As used herein an "oligonucleotide" is a single-stranded nucleic acid ranging in length from 2 to about 60 bases. Oligonucleotides are often synthetic but can also be produced from naturally occurring polynucleotides. A probe is an oligonucleotide capable of binding to a target nucleic acid of a complementary sequence through one or more types of chemical bonds, usually through complementary base pairing via hydrogen bond formation. Oligonucleotide probes are often between 5 and 60 bases, and, in specific embodiments, may be between 10-40, or 15-30 bases long. An oligonucleotide probe may include natural (i.e. A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in an oligonucleotide probe may be joined by a linkage other than a phosphodiester bond, such as a phosphoramidite linkage or a phosphorothioate linkage, or they may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than by phosphodiester bonds, so long as it does not interfere with hybridization.

As used herein, the term "primer" refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and a polymerization agent, such as DNA polymerase, RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not be perfectly complementary to the exact sequence of the template, but should be sufficiently complementary to hybridize with it. The term "primer site" refers to the sequence of the target DNA to which a primer hybridizes. The term "primer pair" refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

DNA fragments can be prepared, for example, by digesting plasmid DNA, or by use of PCR. Oligonucleotides for use as primers or probes are chemically synthesized by methods known in the field of the chemical synthesis of polynucleotides, including by way of non-limiting example the phosphoramidite method described by Beaucage and Carruthers, Tetrahedron Lett 22:1859-1 862 (1981) and the triester method provided by Matteucci, et al., J. Am. Chem. Soc., 103:3185 (1981) both incorporated herein by reference. These syntheses may employ an automated synthesizer, as described in Needham-VanDevanter, D.R., et al., Nucleic Acids Res. 12:61596168 (1984). Purification of oligonucleotides may be carried out by either native acrylamide-gel electrophoresis or by anion-exchange HPLC as described in Pearson, J.D. and Regnier, F.E., J. Chrom., 255:137-149 (1983). A double stranded fragment may then be obtained, if desired, by annealing appropriate complementary single strands together under suitable conditions or by synthesizing the complementary strand using a DNA polymerase with an appropriate primer sequence. Where a specific sequence for a nucleic acid probe is given, it is understood that the complementary strand is also identified and included. The complementary strand will work equally well in situations where the target is a double-stranded nucleic acid.

The sequence of the synthetic oligonucleotide or of any nucleic acid fragment can be can be obtained using either the dideoxy chain termination method or the Maxam-Gilbert method (see Sambrook et al. Molecular Cloning - a Laboratory Manual (2nd Ed.), Vols. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989), which is incorporated herein by reference. This manual is hereinafter referred to as "Sambrook et al." ; Zyskind et al., (1988)). Recombinant DNA Laboratory Manual, (Acad. Press, New York). Oligonucleotides useful in diagnostic assays are typically at least 8 consecutive nucleotides in length, and may range upwards of 18 nucleotides in length to greater than 100 or more consecutive nucleotides.

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the SNP-containing nucleotide sequences of the invention, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific

aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, about 25, about 50, or about 60 nucleotides or an entire SNP coding strand, or to only a portion thereof.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a polymorphic nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. For example, the antisense nucleic acid molecule can generally be complementary to the entire coding region of an mRNA, but more preferably as embodied herein, it is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of the mRNA. An antisense oligonucleotide can range in length between about 5 and about 60 nucleotides, preferably between about 10 and about 45 nucleotides, more preferably between about 15 and 40 nucleotides, and still more preferably between about 15 and 30 in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine,

7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following section).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a polymorphic protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementary to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site.

Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et*

al. (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing, or may comprise a complete cDNA or gene sequence. Optimal alignment of sequences for aligning a comparison window may, for example, be conducted by the local homology algorithm of Smith and Waterman Adv. Appl. Math. 2482 (1981), by the homology alignment algorithm of Needleman and Wunsch J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson and Lipman Proc. Natl. Acad. Sci. U.S.A. 852444 (1988), or by computerized implementations of these algorithms (for example, GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, WI).

Techniques for nucleic acid manipulation of the nucleic acid sequences harboring the cSNP's of the invention, such as subcloning nucleic acid sequences encoding polypeptides into expression vectors, labeling probes, DNA hybridization, and the like, are described generally in Sambrook *et al.*, The phrase "nucleic acid sequence encoding" refers to a nucleic acid which directs the expression of a specific protein, peptide or amino acid sequence. The nucleic acid sequences include both the DNA strand sequence that is transcribed into RNA and the RNA sequence that is translated into protein, peptide or amino acid sequence. The nucleic acid sequences include both the full length nucleic acid sequences disclosed herein as well as non-full length sequences derived from the full length protein. It being further understood that the sequence includes the degenerate codons of the native sequence or sequences which may be introduced to provide codon preference in a specific host cell. Consequently, the principles of probe selection and array design can readily be extended to analyze more complex polymorphisms (see EP 730,663). For example, to characterize a triallelic SNP polymorphism, three groups of probes can be designed tiled on the three polymorphic forms as described above. As a further example, to analyze a diallelic polymorphism involving a deletion of a nucleotide, one can tile a first group of probes based

on the undeleted polymorphic form as the reference sequence and a second group of probes based on the deleted form as the reference sequence.

For assays of genomic DNA, virtually any biological convenient tissue sample can be used. Suitable samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. Genomic DNA is typically amplified before analysis. Amplification is usually effected by PCR using primers flanking a suitable fragment e.g., of 50-500 nucleotides containing the locus of the polymorphism to be analyzed. Target is usually labeled in the course of amplification. The amplification product can be RNA or DNA, single stranded or double stranded. If double stranded, the amplification product is typically denatured before application to an array. If genomic DNA is analyzed without amplification, it may be desirable to remove RNA from the sample before applying it to the array. Such can be accomplished by digestion with DNase-free RNase.

DETECTION OF POLYMORPHISMS IN A NUCLEIC ACID SAMPLE

The SNPs disclosed herein can be used to determine which forms of a characterized polymorphism are present in individuals under analysis.

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 7, 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in published PCT application WO 95/11995. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be
5 complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference sequence in which multiple mutations are expected to
10 occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

An allele-specific primer hybridizes to a site on a target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, Nucleic Acid Res. 17 2427-2448 (1989). This
15 primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch
20 prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

Amplification products generated using the polymerase chain reaction can be
25 analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., PCR Technology, Principles and Applications for DNA Amplification, (W.H. Freeman and Co New York, 1992, Chapter 7).

Alleles of target sequences can be differentiated using single-strand conformation
30 polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., Proc. Nat. Acad. Sci. 86, 2766-2770 (1989). Amplified PCR products can be generated and heated or

otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

5 The genotype of an individual with respect to a pathology suspected of being caused by a genetic polymorphism may be assessed by association analysis. Phenotypic traits suitable for association analysis include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
10 hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria).

 Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases,
15 inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, oral cavity, ovary, pancreas, prostate, skin, stomach,
20 leukemia, liver, lung, and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

 Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
25 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). Since the polymorphic sites are within a 50,000 bp region in the human genome, the probability of recombination between these polymorphic sites is low. That low probability means the haplotype (the set of all 10 polymorphic sites) set forth in this application should be inherited without change for at least
30 several generations. The more sites that are analyzed the lower the probability that the set of polymorphic forms in one individual is the same as that in an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the

invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are diallelic because the population frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

- 5 The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of polymorphic markers does not match
10 between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the
15 probability that a match of suspect and crime scene sample would occur by chance.

$p(ID)$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In diallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism are (see WO
20 95/12607):

$$\text{Homozygote: } p(AA)=x^2$$

$$\text{Homozygote: } p(BB)=y^2=(1-x)^2$$

$$\text{Single Heterozygote: } p(AB)=p(BA)=xy=x(1-x)$$

$$\text{Both Heterozygotes: } p(AB+BA)=2xy=2x(1-x)$$

- 25 The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID)=(x^2)^2+(2xy)^2+(y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

$$p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

The cumulative probability of identity ($cum p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus:

$$cum p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$cum p(nonID) = 1 - cum p(ID).$$

If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

If the set of polymorphisms in the child attributable to the father does not match the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him incompatible as the father) is given by the equation (see WO 95/12607):

$$p(exc) = xy(1-xy)$$

- 5 where x and y are the population frequencies of alleles A and B of a diallelic polymorphic site. (At a triallelic site $p(exc) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z and the respective population frequencies of alleles A, B and C). The probability of non-exclusion is:

$$p(non-exc) = 1 - p(exc)$$

- 10 The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$cum p(non-exc) = p(non-exc1)p(non-exc2)p(non-exc3) \dots p(non-exc_n)$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded) is:

- 15 $cum p(exc) = 1 - cum p(non-exc)$.

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

- 20 The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous
- 25 sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some

polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components. Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic marker sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the individuals, some of whom exhibit a particular trait, and some of whom exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner might elect to undergo in vitro fertilization to avoid the

possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified.

Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., U.S. Pat. No. 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wild type with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered.

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992) (each of which is incorporated by reference in its entirety for all purposes).

Linkage studies are typically performed on members of a family. Available members of the family are characterized for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic

trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the
5 relative likelihood of obtaining observed segregation data for a marker and a genetic locus
when the two are located at a recombination fraction RF , versus the situation in which the
two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in
Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the
human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter
10 4). A series of likelihood ratios are calculated at various recombination fractions (RF),
ranging from $RF=0.0$ (coincident loci) to $RF=0.50$ (unlinked). Thus, the likelihood at a given
value of RF is: probability of data if loci linked at RF to probability of data if loci unlinked.
The computed likelihood is usually expressed as the \log_{10} of this ratio (i.e., a lod score). For
example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a
15 coincidence. The use of logarithms allows data collected from different families to be
combined by simple addition. Computer programs are available for the calculation of lod
scores for differing values of RF (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci.*
(USA) 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be
determined from mathematical tables. See Smith et al., *Mathematical tables for research
20 workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150
(1968). The value of RF at which the lod score is the highest is considered to be the best
estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values
suggest that linkage is less likely (at that value of RF) than the possibility that the two loci are
25 unlinked. By convention, a combined lod score of + 3 or greater (equivalent to greater than
1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked.
Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence
against linkage of the two loci being compared. Negative linkage data are useful in excluding
a chromosome or a segment thereof from consideration. The search focuses on the remaining
30 non-excluded chromosomal locations.

The invention further provides transgenic nonhuman animals capable of expressing an
exogenous variant gene and/or having one or both alleles of an endogenous variant gene

inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. (1989). Inactivation of endogenous variant genes can be
5 achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, Science 244, 1288-1292 The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

10 The invention further provides methods for assessing the pharmacogenomic susceptibility of a subject harboring a single nucleotide polymorphism to a particular pharmaceutical compound, or to a class of such compounds. Genetic polymorphism in drug-metabolizing enzymes, drug transporters, receptors for pharmaceutical agents, and other drug
15 targets have been correlated with individual differences based on distinction in the efficacy and toxicity of the pharmaceutical agent administered to a subject. Pharmacogenomic characterization of a subjects susceptibility to a drug enhances the ability to tailor a dosing regimen to the particular genetic constitution of the subject, thereby enhancing and optimizing the therapeutic effectiveness of the therapy.

In cases in which a cSNP leads to a polymorphic protein that is ascribed to be the
20 cause of a pathological condition, method of treating such a condition includes administering to a subject experiencing the pathology the wild type cognate of the polymorphic protein. Once administered in an effective dosing regimen, the wild type cognate provides complementation or remediation of the defect due to the polymorphic protein. The subject's condition is ameliorated by this protein therapy.

25 A subject suspected of suffering from a pathology ascribable to a polymorphic protein that arises from a cSNP is to be diagnosed using any of a variety of diagnostic methods capable of identifying the presence of the cSNP in the nucleic acid, or of the cognate polymorphic protein, in a suitable clinical sample taken from the subject. Once the presence of the cSNP has been ascertained, and the pathology is correctable by administering a normal
30 or wild-type gene, the subject is treated with a pharmaceutical composition that includes a nucleic acid that harbors the correcting wild-type gene, or a fragment containing a correcting sequence of the wild-type gene. Non-limiting examples of ways in which such a nucleic acid

may be administered include incorporating the wild-type-gene in a viral vector, such as an adenovirus or adeno associated virus, and administration of a naked DNA in a pharmaceutical composition that promotes intracellular uptake of the administered nucleic acid. Once the nucleic acid that includes the gene coding for the wild-type allele of the polymorphism is
5 incorporated within a cell of the subject, it will initiate *de novo* biosynthesis of the wild-type gene product. If the nucleic acid is further incorporated into the genome of the subject, the treatment will have long-term effects, providing *de novo* synthesis of the wild-type protein for a prolonged duration. The synthesis of the wild-type protein in the cells of the subject will contribute to a therapeutic enhancement of the clinical condition of the subject.

10 A subject suffering from a pathology ascribed to a SNP may be treated so as to correct the genetic defect. (See Kren et al., Proc. Natl. Acad. Sci. USA 96:10349-10354 (1999)). Such a subject is identified by any method that can detect the polymorphism in a sample drawn from the subject. Such a genetic defect may be permanently corrected by administering to such a subject a nucleic acid fragment incorporating a repair sequence that
15 supplies the wild-type nucleotide at the position of the SNP. This site-specific repair sequence encompasses an RNA/DNA oligonucleotide which operates to promote endogenous repair of a subject's genomic DNA. Upon administration in an appropriate vehicle, such as a complex with polyethylenimine or encapsulated in anionic liposomes, a genetic defect leading to an inborn pathology may be overcome, as the chimeric oligonucleotides induces
20 incorporation of the wild-type sequence into the subject's genome. Upon incorporation, the wild-type gene product is expressed, and the replacement is propagated, thereby engendering a permanent repair.

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits,
25 the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10, 100, 1000 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or
30 polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the hybridizing methods.

Several aspects of the present invention rely on having available the polymorphic proteins encoded by the nucleic acids comprising a SNP of the inventions. There are various methods of isolating these nucleic acid sequences. For example, DNA is isolated from a genomic or cDNA library using labeled oligonucleotide probes having sequences
5 complementary to the sequences disclosed herein.

Such probes can be used directly in hybridization assays. Alternatively probes can be designed for use in amplification techniques such as PCR.

To prepare a cDNA library, mRNA is isolated from tissue such as heart or pancreas, preferably a tissue wherein expression of the gene or gene family is likely to occur. cDNA is
10 prepared from the mRNA and ligated into a recombinant vector. The vector is transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening cDNA libraries are well known, See Gubler, U. and Hoffman, B.J. *Gene* 25:263-269 (1983) and Sambrook et al.

For a genomic library, for example, the DNA is extracted from tissue and either
15 mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments are then separated by gradient centrifugation from undesired sizes and are constructed in bacteriophage lambda vectors. These vectors and phage are packaged *in vitro*, as described in Sambrook, et al. Recombinant phage are analyzed by plaque hybridization as described in Benton and Davis, *Science* 196:180-182 (1977). Colony hybridization is carried
20 out as generally described in M. Grunstein et al. *Proc. Natl. Acad. Sci. USA.* 72:3961-3965 (1975). DNA of interest is identified in either cDNA or genomic libraries by its ability to hybridize with nucleic acid probes, for example on Southern blots, and these DNA regions are isolated by standard methods familiar to those of skill in the art. See Sambrook, et al.

In PCR techniques, oligonucleotide primers complementary to the two 3' borders of
25 the DNA region to be amplified are synthesized. The polymerase chain reaction is then carried out using the two primers. See *PCR Protocols: a Guide to Methods and Applications* (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990). Primers can be selected to amplify the entire regions encoding a full-length sequence of interest or to amplify smaller DNA segments as desired. PCR can be used in a variety of
30 protocols to isolate cDNAs encoding a sequence of interest. In these protocols, appropriate primers and probes for amplifying DNA encoding a sequence of interest are generated from

analysis of the DNA sequences listed herein. Once such regions are PCR-amplified, they can be sequenced and oligonucleotide probes can be prepared from the sequence.

Once DNA encoding a sequence comprising a cSNP is isolated and cloned, one can express the encoded polymorphic proteins in a variety of recombinantly engineered cells. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of DNA encoding a sequence of interest. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes is made here.

In brief summary, the expression of natural or synthetic nucleic acids encoding a sequence of interest will typically be achieved by operably linking the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain initiation sequences, transcription and translation terminators, and promoters useful for regulation of the expression of a polynucleotide sequence of interest. To obtain high level expression of a cloned gene, it is desirable to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. The expression vectors may also comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the plasmid in both eukaryotes and prokaryotes, i.e., shuttle vectors, and selection markers for both prokaryotic and eukaryotic systems. See Sambrook et al.

A variety of prokaryotic expression systems may be used to express the polymorphic proteins of the invention. Examples include *E. coli*, *Bacillus*, *Streptomyces*, and the like.

It is preferred to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. Examples of regulatory regions suitable for this purpose in *E. coli* are the promoter and operator region of the *E. coli* tryptophan biosynthetic pathway as described by Yanofsky, C., J. Bacterial. 158:1018-1024 (1984) and the leftward promoter of phage lambda as described by A. I. and Hagen, D., Ann. Rev. Genet. 14:399-445 (1980). The inclusion of selection markers in DNA vectors transformed in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin,

tetracycline, or chloramphenicol. See Sambrook et al. for details concerning selection markers for use in *E. coli*.

To enhance proper folding of the expressed recombinant protein, during purification from *E. coli*, the expressed protein may first be denatured and then renatured. This can be accomplished by solubilizing the bacterially produced proteins in a chaotropic agent such as guanidine HCl and reducing all the cysteine residues with a reducing agent such as beta-mercaptoethanol. The protein is then renatured, either by slow dialysis or by gel filtration. See U.S. Patent No. 4,511,503. Detection of the expressed antigen is achieved by methods known in the art as radioimmunoassay, or Western blotting techniques or immunoprecipitation. Purification from *E. coli* can be achieved following procedures such as those described in U.S. Patent No. 4,511,503.

Any of a variety of eukaryotic expression systems such as yeast, insect cell lines, bird, fish, and mammalian cells, may also be used to express a polymorphic protein of the invention. As explained briefly below, a nucleotide sequence harboring a cSNP may be expressed in these eukaryotic systems. Synthesis of heterologous proteins in yeast is well known. Methods in Yeast Genetics, Sherman, F., et al., Cold Spring Harbor Laboratory, (1982) is a well recognized work describing the various methods available to produce the protein in yeast. Suitable vectors usually have expression control sequences, such as promoters, including 3-phosphoglycerate kinase or other glycolytic enzymes, and an origin of replication, termination sequences and the like as desired. For instance, suitable vectors are described in the literature (Botstein, et al., *Gene* 8:17-24 (1979); Broach, et al., *Gene* 8:121-133 (1979)).

Two procedures are used in transforming yeast cells. In one case, yeast cells are first converted into protoplasts using zymolyase, lyticase or glucylase, followed by addition of DNA and polyethylene glycol (PEG). The PEG-treated protoplasts are then regenerated in a 3% agar medium under selective conditions. Details of this procedure are given in the papers by J.D. Beggs, *Nature* (London) 275:104-109 (1978); and Hinnen, A., et al., *Proc. Natl. Acad. Sci. USA*, 75:1929-1933 (1978). The second procedure does not involve removal of the cell wall. Instead the cells are treated with lithium chloride or acetate and PEG and put on selective plates (Ito, H., et al., *J. Bact.*, 153:163-168 (1983)) cells and applying standard protein isolation techniques to the lysates.

The purification process can be monitored by using Western blot techniques or radioimmunoassay or other standard techniques. The sequences encoding the proteins of the invention can also be ligated to various immunoassay expression vectors for use in transforming cell cultures of, for instance, mammalian, insect, bird or fish origin. Illustrative of cell cultures useful for the production of the polypeptides are mammalian cells. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines, and various human cells such as COS cell lines, HeLa cells, myeloma cell lines, Jurkat cells, etc. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter (e.g., the CMV promoter, a HSV *tk* promoter or *pgk* (phosphoglycerate kinase) promoter), an enhancer (Queen et al. Immunol. Rev. 89:49 (1986)) and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences.

Other animal cells are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, (1992)). Appropriate vectors for expressing the proteins of the invention in insect cells are usually derived from baculovirus. Insect cell lines include mosquito larvae, silkworm, armyworm, moth and *Drosophila* cell lines such as a Schneider cell line (See Schneider *J. Embryol. Exp. Morphol.*, 27:353-365 (1987). As indicated above, the vector, e.g., a plasmid, which is used to transform the host cell, preferably contains DNA sequences to initiate transcription and sequences to control the translation of the protein. These sequences are referred to as expression control sequences. As with yeast, when higher animal host cells are employed, polyadenylation or transcription terminator sequences from known mammalian genes need to be incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 intron from SV40 (Sprague, J. et al., *J. Virol.* 45: 773-781 (1983)). Additionally, gene sequences to control replication in the host cell may be Saveria-Campo, M., 1985, "Bovine Papilloma virus DNA a Eukaryotic Cloning Vector" in DNA Cloning Vol. II a Practical Approach Ed. D.M. Glover, IRL Press, Arlington, Virginia pp. 213-238. The host cells are competent or rendered competent for transformation by various means. There are several well-known

methods of introducing DNA into animal cells. These include: calcium phosphate precipitation, fusion of the recipient cells with bacterial protoplasts containing the DNA, treatment of the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation and micro-injection of the DNA directly into the cells.

5 The transformed cells are cultured by means well known in the art (Biochemical Methods in Cell Culture and Virology, Kuchler, R.J., Dowden, Hutchinson and Ross, Inc., (1977)). The expressed polypeptides are isolated from cells grown as suspensions or as monolayers. The latter are recovered by well known mechanical, chemical or enzymatic means.

10 General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" refers to linkage of a promoter upstream from a DNA sequence such that the promoter mediates transcription of the DNA sequence. Specifically, "operably linked" means that the isolated polynucleotide of the invention and an expression control
15 sequence are situated within a vector or cell in such a way that the gene encoding the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression sequence. The term "vector", refers to viral expression systems, autonomous self-replicating circular DNA (plasmids), and includes both expression and nonexpression plasmids.

20 The term "gene" as used herein is intended to refer to a nucleic acid sequence which encodes a polypeptide. This definition includes various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the gene product. The term "gene" is intended to include not only coding sequences but also regulatory regions such as promoters, enhancers, termination regions and similar untranslated
25 nucleotide sequences. The term further includes all introns and other DNA sequences spliced from the mRNA transcript, along with variants resulting from alternative splice sites.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A43 1 cells, human Co10205 cells,
30 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells,

BHK, HL- 60, U937, HaK or Jurkat cells. Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida* or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein.

10 The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac© kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555
15 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed." The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein.

20 The polymorphic protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein. The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic
25 means are known to those skilled in the art.

The polymorphic proteins produced by recombinant DNA technology may be purified by techniques commonly employed to isolate or purify recombinant proteins. Recombinantly produced proteins can be directly expressed or expressed as a fusion protein. The protein is then purified by a combination of cell lysis (e.g., sonication) and affinity chromatography.
30 For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired polypeptide. The polypeptides of this invention may be purified to substantial purity by standard techniques well known in the art, including

selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. See, for instance, R. Scopes, Protein Purification: Principles and Practice, Springer-Verlag: New York (1982), incorporated herein by reference. For example, in an embodiment, antibodies may be raised to the proteins of the invention as described herein. Cell membranes are isolated from a cell line expressing the recombinant protein, the protein is extracted from the membranes and immunoprecipitated. The proteins may then be further purified by standard protein chemistry techniques as described above.

The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-Toyopearl® or Cibacrom blue 3GA Sepharose B; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography. Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT). Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP- HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as polymorphic. Such antibodies include, but are not limited to, polyclonal, monoclonal,

chimeric, single chain, F_{ab} and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human polymorphic proteins are disclosed.

The phrase "specifically binds to", "immunospecifically binds to" or is "specifically immunoreactive with", an antibody when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biological materials. Thus, for example, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. Of particular interest in the present invention is an antibody that binds immunospecifically to a polymorphic protein but not to its cognate wild type allelic protein, or vice versa. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) *Antibodies, a Laboratory Manual*, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

Polyclonal and/or monoclonal antibodies that immunospecifically bind to polymorphic gene products but not to the corresponding prototypical or "wild-type" gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product.

An isolated polymorphic protein, or a portion or fragment thereof, can be used as an immunogen to generate the antibody that binds the polymorphic protein using standard techniques for polyclonal and monoclonal antibody preparation. The full-length polymorphic protein can be used or, alternatively, the invention provides antigenic peptide fragments of polymorphic for use as immunogens. The antigenic peptide of a polymorphic protein of the

invention comprises at least 8 amino acid residues of the amino acid sequence encompassing the polymorphic amino acid and encompasses an epitope of the polymorphic protein such that an antibody raised against the peptide forms a specific immune complex with the polymorphic protein. Preferably, the antigenic peptide comprises at least 10 amino acid
5 residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of polymorphic that are located on the surface of the protein, e.g., hydrophilic regions.

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit,
10 goat, mouse or other mammal) may be immunized by injection with the polymorphic protein. An appropriate immunogenic preparation can contain, for example, recombinantly expressed polymorphic protein or a chemically synthesized polymorphic polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels
15 (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against polymorphic proteins can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as
20 protein A chromatography, to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that originates from the clone of a singly hybridoma cell, and that contains only one type of antigen binding site capable of immunoreacting with a particular epitope of a polymorphic protein. A monoclonal antibody
25 composition thus typically displays a single binding affinity for a particular polymorphic protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular polymorphic protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the
30 hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp.

77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a polymorphic protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methodologies can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*, 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a polymorphic protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to a polymorphic protein may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab)2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab)2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Additionally, recombinant anti-polymorphic protein antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT

In one embodiment, methodologies for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art.

Anti-polymorphic protein antibodies may be used in methods known within the art relating to the detection, quantitation and/or cellular or tissue localization of a polymorphic protein (*e.g.*, for use in measuring levels of the polymorphic protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for polymorphic proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody-derived CDR, are utilized as pharmacologically-active compounds in therapeutic applications intended to treat a pathology in a subject that arises from the presence of the cSNP allele in the subject.

An anti-polymorphic protein antibody (*e.g.*, monoclonal antibody) can be used to isolate polymorphic proteins by a variety of immunochemical techniques, such as immunoaffinity chromatography or immunoprecipitation. An anti-polymorphic protein antibody can facilitate the purification of natural polymorphic protein from cells and of recombinantly produced polymorphic proteins expressed in host cells. Moreover, an anti-polymorphic protein antibody can be used to detect polymorphic protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the polymorphic protein. Anti-polymorphic antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, - α -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that unique compositions and methods of use thereof in SNPs in known genes have been described. Although particular embodiments have been disclosed herein in
5 detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims which follow. In particular, it is contemplated by the inventor that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims.

Seq ID	CuraGen sequence ID	Base pos. of SNP	Polymorphic pos. of sequence	Base before	Base after	Amino acid before	Amino acid after	Type of change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen sequence	Similarity (pValue) following a BLASTX analysis	Map location
1	cg44131670	631	TTCTCGTTCCTG ACAAAGTGCAAT TTTCTTACACCA GGAGAGGATGG ATGTTT	T	C	Phe	Phe	SILENT- CODING	amyloid	Human Gene SPTREMBL-ID:Q60496 PUTATIVE AMYLOID PRECURSOR PROTEIN - CAVIA PORCELLUS (GUINEA PIG), 695 aa.	0	21
2	cg44131386	1635	AAACATCCATCC TCTCCTGGTGA AAGJAATTGCA CTGTCAGGAAC GAGAA	A	G	Phe	Phe	SILENT- CODING	amyloid	Human Gene SPTREMBL-ID:Q13764 AMYLOID-BETA PROTEIN - HOMO SAPIENS (HUMAN), 547 aa.	1.20E-304	
3	cg43323142	246	GGCAGCCCCAT GGTGGTGGCTG GGG[A/G]CAGCC TCATGGTGGTGG CTGGGGGC	A	G	Gly	Gly	SILENT- CODING	amyloid	Human Gene Similar to SPTREMBL- ID:Q16409 PRP AMYLOID - HOMO SAPIENS (HUMAN), 97 aa (fragment).	4.20E-55	20 (20pter)
4	cg43323142	342	GGCAGCCTCATG GTGGTGGCTGG GG[A/G]CAGCCC CATGGTGGTGG CTGGGGGC	A	G	Gly	Gly	SILENT- CODING	amyloid	Human Gene Similar to SPTREMBL- ID:Q16409 PRP AMYLOID - HOMO SAPIENS (HUMAN), 97 aa (fragment).	4.20E-55	20 (20pter)
5	cg43921977	2720	TATTATCCAATGT TAAGAGAGTATG A/GAAATTATTCA TCCAAGTTTCCA TAT	A	G	Phe	Phe	SILENT- CODING	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0.00E+00	20
6	cg43948568	2108	TCATATGGGGCC TGAACAGCTCGC G[A/G]CTCAGCA GGACGTCCCG AGCTGGT	A	G	Ser	Ser	SILENT- CODING	apoptosis	Human Gene SWISSPROT-ID:P55211 CASPASE-9 PRECURSOR (EC 3.4.22.-) (CASP-9) (ICE-LIKE APOPTOTIC PROTEASE 6) (ICE-LAP6) (APOPTOTIC PROTEASE MCH-6) (APOPTOTIC PROTEASE ACTIVATING FACTOR 3) (APAF-3) - HOMO SAPIENS (HUMAN), 416 aa.	2.00E-222	1

7	cg44001801	1601	AGGAGCCTCTTC CTGGGCTCCTCC A[C/T]GAGTAATA GCCTGGAACCGT GGAAT	C	T	Ser	Ser	SILENT- CODING	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
8	cg42913771	334	TACTGCTCAAAA TTCATGAGGTGT C[G/A]ACTTCCAG CCACGTAGATGC CGATT	G	A	Ser	Ser	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
9	cg42913771	340	TCAAAATTCATG AGGTGTCGACTT C[C/T]AGCCACGT AGATGCCGATTG CTTCC	C	T	Ser	Ser	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
10	cg42913771	364	CCAGCCACGTAGC ATGCCGATTGCT T[C/T]CTGTGTGT CTTCTGAGCCA CGGGG	C	T	Phe	Phe	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
11	cg42913771	397	TCTTCTGAGCC ACGGGGAAGGC AA[C/T]CACATT ACGCATACGATG CCAAA	C	T	Asn	Asn	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
12	cg42913771	406	GCCACGGGGAA GGCAACCACATT TA[C/T]GCATACG ATGCCAAAATTG AAATTC	C	T	Tyr	Tyr	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
13	cg42913771	412	GGGAAGGCAAC CACATTTACGCA TA[C/T]GATGCCA AAATTGAAATTC AGACCT	C	T	Tyr	Tyr	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	

14	cg42913771	418	GCAACACACATTT ACGCATACGATG C/C/TAAATTTGA AATTCAGACCTT GACTG	C	T	Ala	Ala	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
15	cg42913771	424	ACATTTACGCAT ACGATGCCAAA T/T/C/GAAATTCA GACCTTGACTGG CTTGT	T	C	Ile	Ile	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
16	cg42913771	436	ACGATGCCAAA TTGAAATTCAGA C/C/A/TTGACTGG CTTGTTCAAAGG AGACA	C	A	Thr	Thr	SILENT- CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.2E-116	
17	cg43271933	435	GGTTGTGGAGT GCCAGGTCAGC CA/A/G/TGTGTCA GCAGTTCACCCT TCTACT	A	G	Gln	Gln	SILENT- CODING	apoptosis recep	Human Gene Homologous to SWISSPROT-ID:Q93038 WSL-1 PROTEIN PRECURSOR (APOPTOSIS- MEDIATING RECEPTOR DR3) (APOPTOSIS- MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN) (APOPTOSIS INDUCING RECEPTOR AIR) (APO-3) (LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH) (LARD) - HOMO SAPIENS (HUMAN), 417 aa.	6.7E-103	1
18	cg43277632	3985	GTTTAACCATTT CTAGCGATGTCA G/T/C/GACGCTAT GACAGACCACGA GATGA	T	C	Ser	Ser	SILENT- CODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)

19	cg43252813	1690	TCAGCCTTCATC GGAAATGCCGCT TTTCTGACTTCA ACTAATGAATTTT ATAC	C	Leu	Leu	SILENT- CODING	ATPase_ associate d	Human Gene SWISSNEW-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa. pcis:SWISSPROT-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.	0 X (Xq12)
20	cg43839527	1245	AAGATGACCTCT CTGGTGCTGACA TTC/AAGGCAAT CTGTACAGAAGC TGGTC	A	Ile	Ile	SILENT- CODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P49014 26S PROTEASE REGULATORY SUBUNIT 4 (P26S4) - MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT), 440 aa.	14
21	cg43833946	961	ATATGTGGGTCC GACCCCTCTAGAT C[G/A]GGCAAGC TAAATTCAATTTT TCTAT	A	Pro	Pro	SILENT- CODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa.	7
22	cg43833946	826	GTGCTCTGATGG CAACATACCCAG C[C/T]CTGTGCA GACGCTTCTAAT CTCAG	T	Glu	Glu	SILENT- CODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa.	7
23	cg43833946	838	CAACATACCCAG CTCTGTGCGAGA C[G/A]CTTCTAAT CTCAGCACCCAGT GCTAT	A	Ser	Ser	SILENT- CODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa.	7
24	cg43833946	937	TCATTGAACGAG CGTGAATCTTAA ATT/GATGTGGGT CCGACCCTCTAG ATCGG	G	Ile	Ile	SILENT- CODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa.	7

25	cg43916747	445	GCATCAAGGAG GAGACGGAGAT CCTT[C]GAAGG GGAGGTGGTGG AGATCCAGA	T	C	Leu	Leu	SILENT- CODING	ATPase_ associate d	Human Gene SPTREMBL-ID:Q12464 CHROMOSOME XVI READING FRAME ORF YPL235W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 471 aa.	4.00E-163	19
26	cg43284434	2039	AGATGGGCCAC CTGACCTGCTTC GC[T]G[GGGGGC ATGTTCCGCACTC GGGGCTG	T	G	Ala	Ala	SILENT- CODING	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
27	cg43251803	2941	TGAGGTAGCAG GACACTGCCATC TG[A]GATCTGCT CGGTACGCACTC GTTCA	A	G	Ile	Ile	SILENT- CODING	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP- ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment).	3.10E-105	
28	cg43986887	320	CAAACTGCCTGT GATCCACTCGGT C[G/A]AGGAAGG CTTTCCGTTCAA TGTAAC	G	A	Leu	Leu	SILENT- CODING	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:O00393 P97 HOMOLOGOUS PROTEIN - HOMO SAPIENS (HUMAN), 277 aa (fragment).	7.90E-93	16
29	cg44022155	1125	TCCAGTACCTCA TCCTGGCTGCAG C[T/C]GTGTCCAA GGGGGGGCCCT TCCGCC	T	C	Ala	Ala	SILENT- CODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:Q12697 PROBABLE CALCIUM- TRANSPORTING ATPASE 9 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1472 aa.	1.50E-63	1
30	cg44022155	903	GGCCAGCGCTG GTCCTGGGACG GGT[A/G]CGGCC ACCGGGGGCGC TGCTCAGCG	A	G	Val	Val	SILENT- CODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:Q12697 PROBABLE CALCIUM- TRANSPORTING ATPASE 9 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1472 aa.	1.50E-63	1
31	cg43920913	364	GTGCAGATTTTG GAATGGCTGCTG ATT[C]AAGAATAA GTTTCCTGGAGA CAGCG	T	C	Asp	Asp	SILENT- CODING	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)

32	cg41562164	2748	GGCTGGCAATG CTCTCTCCAAAG TG[C/G]GCATTGT AGGCACCATCCC CAGTCA	C	G	Ala	Ala	SILENT- CODING	cadherin	Human Gene SWISSPROT-ID:Q13797 INTEGRIN ALPHA-9 PRECURSOR (INTEGRIN ALPHA-RLC) - HOMO SAPIENS (HUMAN), 1035 aa. lpcis: SPTREMBL-ID:Q13797 INTEGRIN ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 1035 aa.	0.00E+00	3
33	cg43918042	3955	ACAGCCCAAGCA TGGGGCGATACA G[G/A]TCCGTTAA TGGTGGGCCCG GCAGTC	G	A	Arg	Arg	SILENT- CODING	cadherin	Human Gene TREMBLNEW- ID:G2852363 NF-PROTOCOLADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa.	0	4
34	cg42483174	1386	GTTAGAGTTAAA GCGGCTCCATAC NT/GIGATCACAG CCCCTCAAAATC TTGIG	T	G	???	???	SILENT- CODING	cadherin	Human Gene SPTREMBL-ID:P97686 ANKYRIN BINDING CELL ADHESION MOLECULE NRCAM - RATTUS NORVEGICUS (RAT), 1215 aa (fragment).	0	7
35	cg43957225	2759	GGCCTCCGGAT CAGCATTGCTGT T[C/T]CGGCAAG GAGAGAACTCG GCATAGG	C	T	Arg	Arg	SILENT- CODING	cadherin	Human Gene SWISSPROT-ID:P53708 INTEGRIN ALPHA-8 - HOMO SAPIENS (HUMAN), 1025 aa.	0.00E+00	10
36	cg43957225	2783	TCCGGCAAGGA GAGAACTCGGCA TA[G/A]GCGCTG AAGTTCTGAATT GCTACAT	G	A	Ala	Ala	SILENT- CODING	cadherin	Human Gene SWISSPROT-ID:P53708 INTEGRIN ALPHA-8 - HOMO SAPIENS (HUMAN), 1025 aa.	0.00E+00	10
37	cg43312078	1430	TCCTAGCGTGTA CCCCCTTGACCG GT[C/T]GGAGATT GAATTACTTAAG GGGA	T	C	Leu	Leu	SILENT- CODING	cadherin	Human Gene SPTREMBL-ID:Q28260 VASCULAR CELL ADHESION MOLECULE-1 - CANIS FAMILIARIS (DOG), 739 aa.	0.00E+00	1 (1p32)
38	cg44026834	1209	CGGAGGTGAGG GTGGAGTAGTCC CT[G/C]GGCAGT GTGGTCGAGTGT GAGTGT	G	C	Pro	Pro	SILENT- CODING	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0.00E+00	17 (17q11)

39	cg44026834	1221	TGGAGTAGTCCC TGGGCAGTGTG GTCTTGAGTGTG AGTGTTCTGAGC GGGTCA	C	T	Ser	SILENT- CODING	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0.00E+00	17 (17q11)
40	cg42558238	2054	AGAGTGCAACCC TGACCTGTGAGA GCTTGACGCCA ACCCTCCCGTCT CCCACT	C	T	Ser	SILENT- CODING	cadherin	Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.lpcis:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa	0.00E+00	19 (19q13.1)
41	cg42558238	2225	AGGGCCCGTTCC CCTCTCAGCAC CTCTTACCGTCT ACTATAGCCCCG AGACCA	C	T	Leu	SILENT- CODING	cadherin	Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.lpcis:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa	0	19 (19q13.1)

42	cg42558238	2228	GCCGTTGGCCTC TCAGCACCCCTCA C/C/TGTCTACTA TAGCCCGGAGAG CCATCG	C	T	Thr	Thr	SILENT- CODING	cadherin	Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.lpcis:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)
43	cg44923512	657	AGGAAATGGACC CAGTGACTCAGC T[G/C]TATACCAT GAGTTGCACCCT GGAGT	G	C	Leu	Leu	SILENT- CODING	cadherin	Human Gene SWISSNEW-ID:Q13740 CD166 ANTIGEN PRECURSOR (ACTIVATED LEUKOCYTE-CELL ADHESION MOLECULE) (ALCAM) - HOMO SAPIENS (HUMAN), 583 aa.lpcis:SWISSPROT-ID:Q13740 CD166 ANTIGEN PRECURSOR (ACTIVATED LEUKOCYTE-CELL ADHESION MOLECULE) (ALCAM) - HOMO SAPIENS (HUMAN), 583 aa.	1.7e-310	3 (3q13.1)
44	cg43956560	1283	GGCTGGCAAGG AGATTAAAAAA GG[C/T]AAGAAAT CCAAGAGAAGTA TGAATG	C	T	Gly	Gly	SILENT- CODING	cadherin	Human Gene SWISSPROT-ID:P14151 L- SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE- 1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1E-218	1 (1q23)

45	cg43956560	521	CGTGGGTGGGA ACCAACAAATCT CTT/C/ACTGAAG AAGCAGAGAACT GGGGAG	T	C	Leu	Leu	SILENT- CODING	cadherin	Human Gene SWISSPROT-ID:P14151 L- SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE- 1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1E-218	1 (1q23)
46	cg43977366	1646	CCTGGAAAGAA TTCTGAACCTCC TTG/C/TACAAATT GCTGGCTGCTCT CATTC	G	C	Leu	Leu	SILENT- CODING	calcium_ channel	Human Gene TREMBLNEW-ID:G259184 RYANODINE RECEPTOR/CALCIUM RELEASE CHANNEL - ORYCTOLAGUS SP, 4872 aa.	0	15
47	cg43280376	1374	CCTGGGACATGA TGGTGCACTCC G/C/TJTCCACCA GCACGTGAAGAT CACCT	C	T	Arg	Arg	SILENT- CODING	carboxyla se	Human Gene SWISSPROT-ID:P38435 VITAMIN K-DEPENDENT GAMMA- CARBOXYLASE (EC 6.4.-.) (GAMMA- GLUTAMYL CARBOXYLASE) - HOMO SAPIENS (HUMAN), 758 aa.	0	2
48	cg43307396	285	TTGTCCAGGGAA GCCTGGACAGC CT[G/A]CCCCAG GCAGTGAGGGA GTTTCTCG	G	A	Leu	Leu	SILENT- CODING	carboxyla se	Human Gene SWISSPROT-ID:P35558 PHOSPHOENOLPYRUVATE CARBOXYKINASE, CYTOSOLIC (GTP) (EC 4.1.1.32) (PHOSPHOENOLPYRUVATE CARBOXYLASE) (PEPCK-C) - HOMO SAPIENS (HUMAN), 622 aa.	0	20 (20q13.3 1)
49	cg43919581	709	AGCCCTACAGCG GGCGGAGGCCA GA/T/C/GCCATCA GGCTGGGCCTG GGGAACC	T	C	Asp	Asp	SILENT- CODING	cathepsin	Human Gene SWISSPROT-ID:P00750 TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68) (TPA) (T- PLASMINOGEN ACTIVATOR) - HOMO SAPIENS (HUMAN), 562 aa.	0	8 (8p12)
50	cg42094324	835	CTGGGGGTCCA CTTGCTGTGTAAT GGT/G/GTGTCTT CAAGGTATCACA TCATGGG	T	G	Gly	Gly	SILENT- CODING	cathepsin	Human Gene Homologous to SWISSPROT-ID:P20151 GLANDULAR KALLIKREIN 2 PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN) (PROSTATE) (HGK-1) - HOMO SAPIENS (HUMAN), 261 aa.	2.1E-147	19 (19q13.2)

51	cg43980411	1251	GCCACAGTTTG TGGCAGATCATC C/T/GTTTCITTT TCTTATTATGCAT AAGA	T	G	Pro	Pro	SILENT- CODING	cathepsin inhib	Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG-SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa.	3.2E-222	18 (18q21.3)
52	cg43266931	673	GCGTGTCCACC GTGGTGAGGGT GAA/A/GJGGTAC GCCCTTGAGGA GCAGGACCA	A	G	Pro	Pro	SILENT- CODING	chloride_ channel	Human Gene Similar to SWISSNEW- ID:O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) - HOMO SAPIENS (HUMAN), 243 aa. pcis:SWISSPROT- ID:O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) - HOMO SAPIENS (HUMAN), 243 aa.	3.1E-59	9
53	cg43970982	2113	AGGAGAACAAG GCATTTCGGAC CTC/AJGGGGAA GCGGAGGTGCC GCIGGIGC	C	A	Arg	Arg	SILENT- CODING	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
54	cg43970982	2136	CTCGGGGAAGC GGAGGTGCCGC TGGT/CJGCTCCT GGAGAACGAGG CAGAACCG	T	C	Gly	Gly	SILENT- CODING	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
55	cg43970982	2307	GAGGCAAAAAGC GAGAAAGAGGAT T/C/T]CCTGGATA CCCAGGACCAAA GGGTA	C	T	Phe	Phe	SILENT- CODING	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
56	cg43970982	2460	CTGGCTACCCAGC GACCAGCTGGTC C/C/AJAGGGCA ACAGGGGCGAC TCCATCG	C	A	Pro	Pro	SILENT- CODING	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2

57	cg43131198	5627	GCCGGCAGGGA C	T	Phe	Phe	SILENT-CODING	collagen	Human Gene SWISSPROT-ID:P53420 COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1690 aa.	0	2 (2q36)
58	cg43970983	2931	GC GTGAGGCTG AGTGTCCTAGGG CC[G]A[GCTGGA GAAGGGCCCTCT GCAGAGG	A	Pro	Pro	SILENT-CODING	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)
59	cg43970983	9092	GTCCGTTATTTC AGTGACTTGGTC C[C]A[G]TGGGTC TAGCCTTCCCCC CTGTGG	A	Pro	Pro	SILENT-CODING	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)
60	cg40339378	4366	TACCTGGCATCC CCGGTAAAGATG G[C]T]CCCAGTG GGCTCCACAGGC CCACCTG	T	Gly	Gly	SILENT-CODING	collagen	Human Gene SPTREMBL-ID:Q12823 A TYPE IV COLLAGEN - HOMO SAPIENS (HUMAN), 1690 aa (fragment).	0	X (Xq22)
61	cg43011543	391	CGCCAAGAAATGG A GCAAGGAAGCC GT[A]T]CCCCAAGA AAGGCAAAAGAAA TACCAT	T	Val	Val	SILENT-CODING	collagen	Human Gene SWISSPROT-ID:P27658 COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN) - HOMO SAPIENS (HUMAN), 744 aa.	0	
62	cg43991318	3003	CTTCGGGGCCCTT G GCTCTCCTTTGG G[G]C]CCGGGCT GCCACAGGCCGT CCTGCCA	C	Gly	Gly	SILENT-CODING	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.3E-73	1 (1p34)
63	cg43281450	1145	CCATCTTGGCTT G TTTGCCCTCCGA T[G]ATGCGGCTG CCTCTGTTCCAC GGGT	T	Ile	Ile	SILENT-CODING	complement	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0	12 (12p13)

64	cg43084083	4497	TTCTCAGTCCTG CCACTTTCACAG TGTJTACGAATA CCACAGACCAGA TAAAC	G	T	Val	Val	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:P01031 COMPLEMENT C5 PRECURSOR (CONTAINS: C5A ANAPHYLATOXIN) - HOMO SAPIENS (HUMAN), 1676 aa.	0	9 (9q34.1)
65	cg43028279	578	AACGAGGATATG CAACAGCAGATG G/G/AJAATTCCTC AGGATCAATTAC ATGTT	G	A	Gly	Gly	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:Q02985 COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16 PRECURSOR - HOMO SAPIENS (HUMAN), 331 aa.	7.5E-191	
66	cg43029279	659	GCATTAAATCTT CAGAAAAGTGTG G/G/AJCCTCCTC CACCTATTAGCA ATGGTG	G	A	Gly	Gly	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:Q02985 COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16 PRECURSOR - HOMO SAPIENS (HUMAN), 331 aa.	7.5E-191	
67	cg43956185	890	TAGAATCTTTGC ATTGAGGTGGTT C/C/TJGTCCAGTT TCCATTAAACA CATCA	C	T	Thr	Thr	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1
68	cg43956185	538	CCAGTTTCCCAT CCCAACATGTTG TJA/TJCGCAATGT GTGAGAACGTGA TGAAA	A	T	Arg	Arg	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
69	cg43956185	572	GAGAACGTGATG AAAGACGATATC C/A/CJCGTTTACA CACAAATTCAGC TGATT	A	C	Arg	Arg	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
70	cg43956185	809	ATGAAGCTGGAG CATATACTGACA A/C/TJGGGAATGA AGTAATGTCCCC ATTGT	C	T	Pro	Pro	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1

71	cg43956183	345	AGTAATGCCATT GATTCTATTTTC TTC	T	C	Glu	Glu	SILENT- CODING	complem ent	Human Gene SWISSPROT-ID:P36980 COMPLEMENT FACTOR H-LIKE PROTEIN DDESK59 PRECURSOR - HOMO SAPIENS (HUMAN), 270 aa.	9.20E-154	1
72	cg21644442	1753	TGGAGCAACCAG AGGCAGCCCC CTTG/CJACTCAG GATGACAGACAG GTGGAAC	G	C	Leu	Leu	SILENT- CODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	5.00E-304	1 (1p21)
73	cg42542496	942	CAAACTTCACTG CCTCAGCCAGAA CTTAACTGGCTC TGGGCTTCTGAA GTGGC	T	A	Thr	Thr	SILENT- CODING	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)
74	cg43931046	2043	AACAGATTATTG TTCATGCTTTATC IG/CJCCAGAACAT TTGTTGAACACA AGTG	G	C	Ser	Ser	SILENT- CODING	cyclin	Human Gene SPTREMBL-ID:P70413 CYCLIN D-INTERACTING MYB-LIKE PROTEIN - MUS MUSCULUS (MOUSE), 761 aa.	0.00E+00	7
75	cg43927697	992	TAGTTAGTTCCA TCAGGTATTTGG C/CJTAAAGTATG TTGCTCGACATC AACCT	C	T	Leu	Leu	SILENT- CODING	cyclin	Human Gene SWISSPROT-ID:P14635 G2/MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.80E-230	5 (5q12)
76	cg43926592	1705	AGAAGGTGCACT CTTGATCACTGG GTTAIGGGAGC TGCTGAGACTCT CCTCTC	T	A	Pro	Pro	SILENT- CODING	cyclin	Human Gene SPTREMBL-ID:Q16589 CYCLIN G2 - HOMO SAPIENS (HUMAN), 344 aa.	8.50E-183	4
77	cg43957094	2212	GCTTGCCTTGAT AAAAAGCACCA G/CJCGGCGGA GCGCCGCGGA GCGACCA	C	G	Arg	Arg	SILENT- CODING	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6

78	cg43242733	222	CTGCAGTCTCTG TCAAGATGATAG A[A/G]GTACTGAC AACAACTGACTC TCAGA	A	G	Glu	Glu	SILENT- CODING	cyclin	Human Gene SWISSPROT-ID:P51959 G2/MITOTIC-SPECIFIC CYCLIN G1 - HOMO SAPIENS (HUMAN), 295 aa.	1.30E-154	5
79	cg43996855	3862	TGGTCAGGTCCT TGTTGATGAGGC C[G/A]TCCTTGTC CAAGAAATCGAGC TGGAT	G	A	Asp	Asp	SILENT- CODING	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.20E-293	2 (2p22)
80	cg40333008	1612	CTGTAGTCTTGG TGCCCATACGAA C[C/A]GAATAGAT GGGGCCATATTT TTTCT	C	A	Ser	Ser	SILENT- CODING	cyto450	Human Gene SWISSNEW-ID:P05093 CYTOCHROME P450 XVIIA1 (P450- C17) (EC 1.14.99.9) (STEROID 17- ALPHA-HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa. Jcds:SWISSPROT-ID:P05093 CYTOCHROME P450 XVIIA1 (P450- C17) (EC 1.14.99.9) (STEROID 17- ALPHA-HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa.	4.90E-274	10 (10q24.3)
81	cg40333008	1689	TGAAGAAGTTGT TATGCATATGGC C[A/G]TGCTCTGG GGAGGAATGGC AGGCTGC	A	G	His	His	SILENT- CODING	cyto450	Human Gene SWISSNEW-ID:P05093 CYTOCHROME P450 XVIIA1 (P450- C17) (EC 1.14.99.9) (STEROID 17- ALPHA-HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa. Jcds:SWISSPROT-ID:P05093 CYTOCHROME P450 XVIIA1 (P450- C17) (EC 1.14.99.9) (STEROID 17- ALPHA-HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa.	4.90E-274	10 (10q24.3)
82	cg43966704	1243	ACTTGAGGCCAG TGGGGAAGCCA GC[G/A]CCTCCA CGCCCCCTCAAA CCCGATG	G	A	Gly	Gly	SILENT- CODING	cytochrome	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.80E-184	11

83	cg43966704	1279	CCCTCAAAACCCG ATGCTTGATCT C[G/A]CCCAGGA TCCAGTCGGGC CCCTTCA	G	A	Gly	Gly	SILENT- CODING	cytochro me	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.80E-184	11
84	cg43966704	1294	TCTTGATCTCGC CCAGGATCCAGT C[G/C]GGCCCT TCAGCAGGATCT CCTTTG	G	C	Pro	Pro	SILENT- CODING	cytochro me	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.80E-184	11
85	cg43966704	1375	CTTCAGCCTCC AGTCATGGCGG CC[G/A]TACAGGT TGGTGAAATCC GGTCTT	G	A	Tyr	Tyr	SILENT- CODING	cytochro me	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.80E-184	11
86	cg43962888	563	CCTCCATCTCCA ACAAGAAATAG T[A/G]GGCTGCAT CTGTGAAGAGGA CAATA	A	G	Val	Val	SILENT- CODING	cytochro me	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.10E-66	2 (2cen)
87	cg43962888	620	TCGCTGGTTT GGCTGCACAAAG G[C/G]GAGGCCC AGCGATGCCCC CGCTGTG	C	G	Gly	Gly	SILENT- CODING	cytochro me	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.10E-66	2 (2cen)
88	cg39454979	2375	ACTTACTACGCT CCAAGATTACCA A[A/G]CCCAACGT GTACCATGAGTC CAAGC	A	G	Lys	Lys	SILENT- CODING	deaminas e	Human Gene SWISSPROT-ID:P51400 DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1) - RATTUS NORVEGICUS (RAT), 711 aa.	0.00E+00	21
89	cg43275625	1124	GCTTGGACTCAT GGTACACGTTGG G[T/C]TTGGTAAT CTTGAGCGTAG TAAGT	T	C	Lys	Lys	SILENT- CODING	deaminas e	Human Gene SPTREMBL-ID:O00465 DSRNA ADENOSINE DEAMINASE DRADA2C - HOMO SAPIENS (HUMAN), 714 aa.	0.00E+00	21

90	cg42476357	891	ACCGGCGCCTG AAGTTCCTCTCC TCG/CJAAAGTTCC AGGTCCATCAGA TGCTTA	G	C	Ser	Ser	SILENT- CODING	deaminase	Human Gene SWISSPROT-ID:P23109 AMP DEAMINASE 1 (EC 3.5.4.6) (MYOADENYLATE DEAMINASE) (AMP DEAMINASE ISOFORM M) - HOMO SAPIENS (HUMAN), 747 aa.	0.00E+00	1 (1p21)
91	cg39454981	2495	ACTTACTACGCT CCAAGATTACCA A/A/GJCCCAACGT GTACCATGAGTC CAAGC	A	G	Lys	Lys	SILENT- CODING	deaminase	Human Gene SWISSPROT-ID:P78563 DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1) - HOMO SAPIENS (HUMAN), 741 aa.	0.00E+00	
92	cg41626024	635	TGGGCTCTGAG GACCTGCAGAAG AC/T/CJAGTGCAC AGCCAGAGAAATG CCCACT	T	C	Thr	Thr	SILENT- CODING	deaminase	Human Gene Similar to SWISSPROT- ID:P32320 CYTIDINE DEAMINASE (EC 3.5.4.5) (CYTIDINE AMINOHYDROLASE) - HOMO SAPIENS (HUMAN), 146 aa.pcds:TREMBLNEW- ID:E1228801 CYTIDINE DEAMINASE (EC 3.5.4.5) - HOMO SAPIENS (HUMAN), 146 aa.	8.80E-78	1 (1p36.2)
93	cg34396112	3375	CAGTTCTCCTGG TGCCTCTGGACA C/A/TJAGTGTGAC CTTGGCCCCCACT GGCCA	A	T	Leu	Leu	SILENT- CODING	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
94	cg34396112	3660	TCAGCTCAGGGA TCCAGGCTGGG CA/G/AJACAATCA TAGGAAACAGCA TATTC	G	A	Val	Val	SILENT- CODING	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
95	cg34396112	3870	TCAGCAACTCTG GGGAAAAAATG GG/C/TTCCTGG GTTGGATCCAGG GGCGTGA	C	T	Glu	Glu	SILENT- CODING	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
96	cg34396112	3876	ACTCTGGGGGAA AAATGGGCTCCT G/C/CJTGGAT CCAGGGGCGTG AACTCCT	G	C	Thr	Thr	SILENT- CODING	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)

97	cg34396112	4245	TTCTATTCTTCT CACAGTTGTCAC T/A/GCAACATGG TGCAAGGAGCA GATGG	T	A	Ala	Ala	SILENT- CODING	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
98	cg34396112	4254	CTTCCACAGTTG TCACTGCAACAT G/G/A/TGCAAGG AGCAGATGGGG GCCAGGC	G	A	His	His	SILENT- CODING	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
99	cg34396112	4362	TCACGTGTGCAAG CCCCGCAGCCC CC/C/TJTCTCCAC AGCCGAGCTTG GTTCCAC	C	T	Glu	Glu	SILENT- CODING	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
100	cg34396112	609	TCTCCGGGGTG GCAGGGCTGTCT AG/G/C/CGGAAG AGTCCCTTCACG TTATTAC	G	C	Arg	Arg	SILENT- CODING	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
101	cg43314766	1860	CGGAAGCATCCA TAGTACGCCACG G/A/G/GATCCAAT CTGAAAAGCCTG TCTTG	A	G	Ser	Ser	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P00352 ALDEHYDE DEHYDROGENASE, CYTOSOLIC (EC 1.2.1.3) (CLASS 1) (ALDHII) (ALDH-E1) - HOMO SAPIENS (HUMAN), 500 aa.	7.20E-273	9 (9q21)
102	cg4396714	1683	TAGATTCAGTTA ATCTCTTGGCAA T/G/A/ACTCTTCG AATATTGCTGGC GGGGA	G	A	Val	Val	SILENT- CODING	dehydrog enase	Human Gene TREMBLNEW- ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.60E-266	11
103	cg4396714	2433	ATCTCCAATTAG CTCCGCGGCTTA C/A/G/GACCCACC CAAGAGCCCCCT TCACCA	A	G	Ser	Ser	SILENT- CODING	dehydrog enase	Human Gene TREMBLNEW- ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.60E-266	11

104	cg43859104	779	ACAGGATCATTC TTCAGTAATATTC [A/T]GCCCTTGACA AGCACAGCGGC TACAA	A	T	Ala	Ala	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P51648 FATTY ALDEHYDE DEHYDROGENASE (EC 1.2.1.3) (ALDEHYDE DEHYDROGENASE, MICROSOMAL) (CLASS 3) - HOMO SAPIENS (HUMAN), 485 aa.	1.30E-250	17 (17p11.2)
105	cg43259523	654	AGATGTGGATCA GCAGTGTCTGAG CA[C/T]GCAGGG CTCTTTCTGGTG ATGGCAA	C	T	His	His	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/Branched CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2.00E-229	10 (10q25)
106	cg43057018	1242	TCAATCCTAGAG ACTTACATAAAC C[G/T]ATCCAGGA AGTTATCATTTGA ATTGA	G	T	Pro	Pro	SILENT- CODING	dehydrog enase	Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa. pcls:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.30E-209	4 (4q22)
107	cg44917703	1198	AGAAGGTGATCA AAGTTGGCAAGG T[G/T]CGGACTC GAGACATGGGC GGCTACA	G	T	Val	Val	SILENT- CODING	dehydrog enase	Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.80E-205	13
108	cg44917703	1216	GCAAGGTGCGG ACTCGAGACATG GG[C/T]GGCTAC AGCACCACAACC GACTTCA	C	T	Gly	Gly	SILENT- CODING	dehydrog enase	Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.80E-205	13
109	cg44917703	1222	TGCGGACTCGA GACATGGGCGG CTA[C/T]AGCACC ACAACCGACTTC ATCAAGT	C	T	Tyr	Tyr	SILENT- CODING	dehydrog enase	Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.80E-205	13

110	cg44917703	1243	GCTACAGCACCA CAACCGACTTCA TCTAAGTCTGT CATCGGTCACCT GCAGA	C	T	Ile	Ile	SILENT- CODING	dehydrog enase	Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.80E-205	13
111	cg3000385	566	TGGGCACCTGCTGA GAAAAGTTATTA AAGJTGCAAAGC AGCTGTGCTTTG GGAGC	A	G	Lys	Lys	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P40394 ALCOHOL DEHYDROGENASE CLASS IV MU/SIGMA CHAIN (EC 1.1.1.1) (RETINOL DEHYDROGENASE) (GASTRIC ALCOHOL DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 374 aa.	4.40E-202	4 (4q23)
112	cg43923979	863	GAAAATCTTTTG ACTGAGCTTCCG GAGJGGAAATTC AAAAGGAACCCC ATACA	A	G	Pro	Pro	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4.00E-192	3 (3p13)
113	cg43948373	1642	CAAGTGGGGCT GAGATTGGAGGT GCICAJTTTGGAG GAGAAAAGCACA CTGGTG	C	A	Ala	Ala	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE- DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
114	cg43948373	1678	AAAAGCACACTG GTGGTGGCAGG GAGAJTCTGGC AGTGATGCCTGG AAACAGT	G	A	Glu	Glu	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE- DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
115	cg43948373	1741	CTACTTGACTA TCAACTACAGTA AAGJGACCTTCC TCTGGCCCAAGG AATCA	A	G	Lys	Lys	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE- DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5

116	cg43960596	903	CCAACAGGGTG GTGTGGAGCGG GGA/A/G]GAGGC CACCCGCTGCA GGTCCTCGG	A	G	Ser	SILENT- CODING	dehydrog enase	Human Gene SWISSNEW-ID:Q92781 11 CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa.jpcl:SWISSPROT-ID:Q92781 11-CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa.	4.40E-170	12
117	cg43969759	566	CGTCTCGGATGG TGCTGAGTGGTG G[G/A]TAGAGTCT CCCCTGGGACA GATGCT	G	A	Tyr	SILENT- CODING	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa.	1.80E-109	11
118	cg43104003	710	ACCCAGCGCCTA TGCTGGCCCCG AC[G/A]TCACTGA TAGGTAAGATGA AGTCCC	G	A	Asp	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSNEW- ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYL-TETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa.jpcl:SWISSPROT-ID:P11586 C-1- TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYL-TETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934 aa.	7.10E-92	6

119	cg42717491	384	CTGTCTCTTTGG ACTGAACAAAAG A[G/A]CACTCGAT GACTCCTTCCTT CCCAT	G	A	Cys	Cys	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa.	2.40E-52	
120	cg43248620	2294	TCTGTACCCTCA CGTGCAGGCTC CG[C/T]GATGTTT TGCTGGAAGCT GAGCAG	C	T	Ser	Ser	SILENT- CODING	dna_ma_ bind	Human Gene SPTREMBL-ID:Q14550 ZINC-FINGER DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 1482 aa.	0.00E+00	1
121	cg43273880	4271	GCTGTGTGTCAG CAATGCAGGAAT A[C/T]GAAGAGCA GCTGAAAGAAAA TGCCA	C	T	Tyr	Tyr	SILENT- CODING	dna_ma_ bind	Human Gene SWISSPROT-ID:O14647 CHROMODOMAIN-HELICASE-DNA- BINDING PROTEIN 2 (CHD-2) - HOMO SAPIENS (HUMAN), 1739 aa.	0.00E+00	15
122	cg43273880	4952	CTAGAAAAGACA AAGAAGGGGAC AA[A/G]GAAAGAA AGAAAGGAAAG ATAAGA	A	G	Lys	Lys	SILENT- CODING	dna_ma_ bind	Human Gene SWISSPROT-ID:O14647 CHROMODOMAIN-HELICASE-DNA- BINDING PROTEIN 2 (CHD-2) - HOMO SAPIENS (HUMAN), 1739 aa.	0.00E+00	15
123	cg42175288	1364	ACAGAAGTGGG GGTGGCTATGGT GG[A/G]GACAGA AGCAGCGGTGG TGGCTACA	A	G	Gly	Gly	SILENT- CODING	dna_ma_ bind	Human Gene SPTREMBL-ID:Q92804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa.	0.00E+00	17
124	cg43988816	2369	TCCCTTCCCCTC GGGAGTTGCTCC A[C/G]GTACGGA TCTGACTTTTGT GGTAA	C	G	Thr	Thr	SILENT- CODING	dna_ma_ bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA- BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)

125	cg44005808	3412	AGACCACCTCTC AGGCCCACTCG CTG/CJCTCTCT CGCCTGCCTCCA CAAGGC	G	C	Leu	Leu	SILENT- CODING	dna_ma_ bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa. cds:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00
126	cg43276473	311	CATCTGCTCCCA CCGTAACCTCTAG TTAG/CAGCTGC CCAATGGGCAGA CAGTTC	A	G	Val	Val	SILENT- CODING	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q62347 TRANSCRIPTION FACTOR/DNA BINDING PROTEIN - MUS MUSCULUS (MOUSE), 287 aa.	5.30E-142
127	cg44031583	307	CAAACCTGATTG TACATCAGAGAA C/C/TTCATACAGG AGAGAAACCCCTA TGGTT	C	T	Thr	Thr	SILENT- CODING	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	7.10E-125
128	cg43969880	580	AACGGATACACA CGGGAGAGAG CC/C/TTATCAGT GCAAGGAGTGT GGGAAA	C	T	Pro	Pro	SILENT- CODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	9.40E-58
129	cg43946971	1334	TGGCCATGCACA AGCGCAGTGCC CA/T/CJGGCGAG CTGGAGGCCAC GGAGGAGA	T	C	His	His	SILENT- CODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	4.90E-52 (6p21.3)
130	cg43946971	1361	GCGAGCTGGAG GCCACGGAGGA GAGT/CJGAGCA GGCCCTCTATGA GCAGCAGC	T	C	Ser	Ser	SILENT- CODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	4.90E-52 (6p21.3)

131	cg43949306	1784	TGGAGTCTGTCC TCGTCTTCTTCT C[A/G]GTCTCTGC GTAGGCCAGGT CGTCTT	A	G	Thr	Thr	SILENT- CODING	dynein	Human Gene SWISSPROT-ID:P38650 DYNEN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C) - RATTUS NORVEGICUS (RAT), 4644 aa.	0.00E+00	14
132	cg43958656	565	GAACCGGCATG GCCAAAGCCGC GGC[G/A]ATCGG CATCGACCTGGG CACCACCT	G	A	Ala	Ala	SILENT- CODING	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
133	cg43958656	763	AGAACACCGTGT TTGACGCGAAGC G[G/C]CTGATCG GCCGCAAGTTCC GCGACC	G	C	Arg	Arg	SILENT- CODING	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
134	cg43958656	769	CCGTGTTTGACG CGAAGCGGCTG ATC[T/G]GCCGC AAGTTCGGCGAC CCGGTGG	C	T	Ile	Ile	SILENT- CODING	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
135	cg44017749	10249	CCATTAAACCGAG CCCACAAGACCA C[A/G]GGCACCA ACAAACGCTCC TCATCA	A	G	Thr	Thr	SILENT- CODING	eph	Human Gene SWISSPROT-ID:Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2- MACROGLOBULIN RECEPTOR) (A2MR) (APOER) (CD91) - HOMO SAPIENS (HUMAN), 4544 aa.	0.00E+00	12
136	cg43982507	2646	CCAATAAATTC CTGGATCAGAGC T[A/T]GCCACTCT AGTCAACAACCT GAATG	A	T	Leu	Leu	SILENT- CODING	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00 9 (9p24)	
137	cg43982507	636	CCATGGGCACGT CCGCGCTCTGG GC[G/C]CTCTGG CTGCTGCTCGCG CTGTGCT	G	C	Ala	Ala	SILENT- CODING	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00 9 (9p24)	

138	cg43953981	2111	CTTGAACAAGTT TAGCTCCAATGT TTC/TTTGTATT ATCTTTTAAGTCA ATTG	C	T	Lys	Lys	SILENT- CODING	eph	Human Gene SWISSPROT-ID:P10809 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN) (60 KD CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (GROEL PROTEIN) (HUCHA60) - HOMO SAPIENS (HUMAN), 573 aa.	8.30E-295	9
139	cg43945167	1149	AGAGCTTGTCCA GTTCTTCGCCGG A/A/GJAATTCCCC AGAGGCTCTCGC CTTGT	A	G	Phe	Phe	SILENT- CODING	eph	Human Gene SWISSPROT-ID:P30533 ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR- RELATED PROTEIN-ASSOCIATED PROTEIN 1) (RAP) - HOMO SAPIENS (HUMAN), 357 aa.	9.60E-191	4 (4p16.3)
140	cg43918531	1596	GCAAAAAGCAAC AGATATCTCTTG C/A/CJACACAAAT GGTTAGAAATGAT TTTGA	A	C	Ala	Ala	SILENT- CODING	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa. Jpdis:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5
141	cg43918531	1611	TATCTCTTGCAA CACAAATGGTTA G/A/GJATGATTTT GAAGATTGATGA CATTC	A	G	Arg	Arg	SILENT- CODING	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa. Jpdis:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5

142	cg43918531	1618	TGCAACACAAAT GGTTAGAATGAT TT/CJTGAAGATT GATGACATTCGT AAGCC	T	C	Leu	Leu	SILENT- CODING	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa.lpcis:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5
143	cg43944783	1309	TGTTGTAGTCGC CCTTTTCAAAGT A/C/TAACCGCTGC TTGATTGGTAAT GTAAG	C	T	Val	Val	SILENT- CODING	eph	Human Gene Similar to SWISSPROT- ID:P15705 HEAT SHOCK PROTEIN ST11 - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 589 aa.	2.80E-74	11
144	cg42889246	592	TCATTGAGACCT TCGAAAGGCTGG CTA/GJCTGATAA AAGCACAAACACG GAACCA	A	G	Leu	Leu	SILENT- CODING	eph	Human Gene Similar to SPTREMBL- ID:Q12988 HEAT SHOCK PROTEIN 27 - HOMO SAPIENS (HUMAN), 241 aa.	7.50E-73	
145	cg42889246	679	CCCGACAGTACA AACTACCAGATG GT/CJGTGGAAAT CAAAGATTGTC TGCAG	T	C	Gly	Gly	SILENT- CODING	eph	Human Gene Similar to SPTREMBL- ID:Q12988 HEAT SHOCK PROTEIN 27 - HOMO SAPIENS (HUMAN), 241 aa.	7.50E-73	
146	cg43984905	2206	ACCTTGCCCTCA TCCGCTTCTTGG TIG/AJGAAGATTA TGATGCCTCCTC CAAGA	G	A	Val	Val	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3

147	cg43984905	2227	TGGTGGGAAGATT ATGATGCCTCCT C/C/TAAAGAATGA CTTCATTGGCCA GAGTA	C	T	Ser	Ser	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
148	cg43984905	2233	AAGATTATGATG CCTCCTCCAAGA A/T/CjGACTTCAT TGGCCAGAGTAC CATCC	T	C	Asn	Asn	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
149	cg43984905	2239	ATGATGCCTCCT CCAAGAATGACT T/C/TjATTGGCCA GAGTACCATCCC CTTGA	C	T	Phe	Phe	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
150	cg43984905	2254	AGAATGACTTCA TTGGCCAGAGTA C/C/TjATCCCCCT GAACAGCCTCAA GCAAG	C	T	Thr	Thr	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3

151	cg44011461	2428	GGATGAGGGCA TAGATGCTGCTG AA[G/C]GTGAGG TTGTCAGTCAAG TAGTATT	G	C	Thr	Thr	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
152	cg44011461	2432	TGAGGGCATAGA TGCTGCTGAAGG TG[C/J]AGGTTGTC AGTCAAGTAGTA TTTCA	G	C	Leu	Leu	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
153	cg44011461	2750	CATCACTGAAGG ACAGCTTGGCAT C[G/A]GCAATGG CGCAGTAGTGCC GAGTCC	G	A	Ala	Ala	SILENT- CODING	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
154	cg40343531	592	AGGATCACTTAC TCTCACTCCCG CIC/TGCGGGGG TGGTGCTCAGCT GCTTGG	C	T	Ala	Ala	SILENT- CODING	esterase nhib	Human Gene SPTREMBL-ID:Q14432 CGMP-INHIBITED CAMP PHOSPHODIESTERASE - HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	12
155	cg43937658	1406	CATCTGCTGGGG CCACCTTTGCTG C[G/A]TAACTCCA CATCTCAATCCG GTCAT	G	A	Tyr	Tyr	SILENT- CODING	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16

156	cg43320667	1510	CAGGAACGCCA GCCCCGGGCTGA GGC[C/G]GCCAC ATCAGCAATGGA CCTCTTGG	C	G	Ala	Ala	SILENT- CODING	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00	3 (3p25)
157	cg43320667	852	GCTCAGGACCAT TCTCTGGCGGAA C[G/A]ATGCTTC GCTGGGCTGGA CCATGA	G	A	Ile	Ile	SILENT- CODING	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00	3 (3p25)
158	cg43320667	908	ATCGGCTGCTTC AGGGAGCCCTTT A[A/G]GGTGAGG AACATGTAGGCC ATGTAC	A	G	Leu	Leu	SILENT- CODING	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00	3 (3p25)
159	cg44131042	558	ATCTTTATCCCA GATCTCCTCTGT C/T]CCCATAGGT TACAGCCACCCC GCCC	C	T	Val	Val	SILENT- CODING	gaba	Human Gene SWISSPROT-ID:P80404 4-AMINO-BUTYRATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.19) (GAMMA-AMINO-N- BUTYRATE TRANSAMINASE) (GABA TRANSAMINASE) (GABA AMINOTRANSFERASE) - HOMO SAPIENS (HUMAN), 500 aa.	4.20E-268	16
160	cg3001932	230	CAAAACTAAAG GGATGTGGAGA GT[G/C]CGGAAA AGGGGCTACTTT GGGATT	G	C	Val	Val	SILENT- CODING	gaba	Human Gene SWISSPROT-ID:P47870 GAMMA-AMINOBUTYRIC-ACID RECEPTOR BETA-2 SUBUNIT PRECURSOR (GABA(A) RECEPTOR) - HOMO SAPIENS (HUMAN), 474 aa.	1.90E-256	5 (5q34)
161	cg43299024	2993	TGGCTGTGCCC CTGACCAAGGGT GG[G/A]GAGGCC CGAGGGGAGCT GTTCTGGG	G	A	Gly	Gly	SILENT- CODING	glucoamy lase	Human Gene TREMBLNEW- ID:G2826521 MALTASE- GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)

162	cg43992911	1660	GAAAAGAAGTTA AGATCTTGAAGG GTC/TCTGAACCT GAAGGTGCAGA GTGGGC	C	T	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P08183 MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 1280 aa.	0.00E+00	7
163	cg43286488	1436	GGTCAGCTTCAG CCAGATAGCCAC TTG/AIGGGTCAT GGAGCTGGAGG GCAAAGG	G	A	Pro	Pro	SILENT- CODING	glycoprot ein	Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M/ME20S) (ME20- M/ME20-S) (95 KD MELANOCYTE- SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa. pcis:SWISSPROT- ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.	0.00E+00	12

164	cg43286488	1706	GGCCCCCTAGAA CTTGCCAGTATT G[G/A]CCCCAGG TCTTCCAGACAT AAACAA	A	Gly	Gly	SILENT- CODING	glycoprot- ein	Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M/ME20S) (ME20- M/ME20-S) (95 KD MELANOCYTE- SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.[pcis:SWISSPROT- ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.	0.00E+00	12
165	cg43286488	1841	CTGGCTGTCCTC CCCACACCTGGC T[C/A]CCATTGAT GATGGTATTGTT GACCC	A	Gly	Gly	SILENT- CODING	glycoprot- ein	Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M/ME20S) (ME20- M/ME20-S) (95 KD MELANOCYTE- SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.[pcis:SWISSPROT- ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.	0.00E+00	12

166	cg43943531	1102	CTCCCTGGACG GGCGGTTTCTAC TC[G/A]CTGCTG GATCCCTCTTAT GCTAAGA	G	A	Ser	Ser	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	11 (11q23.3)
167	cg43943531	1417	ACATGAAGAATC TGGACATAAGTC G[T/C]CCAGACAA GAAGAGCAAGAA GCAAC	T	C	Arg	Arg	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3)
168	cg43943531	847	CCTACTGTACTG TTTACTGCCCTGG G[C/T]ACTATACT TTCATGCAGAT CTCCT	C	T	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3)
169	cg43943531	916	TCCTTTTCATCAG AGCACATGGCAG C[C/G]TTTGGGG TCCTTGGTCTCT GCCAGA	C	G	Ala	Ala	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3)
170	cg43065490	2042	AAGCAGAGCAGT ATCAACCCCTCA C[G/A]CGTTTCAGT CAGCCTCCAGAA CTCCC	G	A	Thr	Thr	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
171	cg43065549	1597	AGGGTTATGATG GATGGCAGATTTC T[C/G]GACCCAA GTGCTCCTAATG GAGGTG	C	G	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
172	cg43065549	1648	GAGTCCTGGGG TCCTGTGATCTG GT[A/G]CCGGTC AGAGCAGTCAAG GAGGGGA	A	G	Val	Val	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)

173	cg43065549	1675	CGGTCAGAGCA GTCAAGGAGGG GAC[G/C]CTGGG GCTGACCCAG CAGTGTGAG	G	C	Thr	Thr	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
174	cg43018621	507	CGGACAACCTG GAGCTGAAGAAG CT[G/A]GTATACC TCTACTTGATGA ATTACG	G	A	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene SWISSNEW-ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa. pcis:SWISSPROT-ID:Q10567 BETA- ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.	0	22 (22q12)
175	cg43924995	458	CAAAATGGCAGA TGAATTTACAG TIA/TTCGCTATGA AACTACAAATAA AACTT	A	T	Val	Val	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P13473 LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2) (CD107B ANTIGEN) - HOMO SAPIENS (HUMAN), 410 aa.	1.2E-222	X (Xq24)
176	cg43301245	1420	GCCCATCAAAGC CATGGGTGCGC AGI/GIATGCG GGTACTGACTTG ATGAAAG	A	G	Phe	Phe	SILENT- CODING	glycoprot ein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa. pcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	3E-210	1

177	cg43301245	757	GGTCCAGGGCC CATACCATGGCG CC[C/T]GCCAGC TGCCTGTCTTC AGGTACT	T	Ala	Ala	SILENT- CODING	glycoprot ein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa	3E-210	1
178	cg43301245	769	ATACCATGGCGC CGCCAGCTGC CT[G/A]TCCTTCA GGTACTGCACCT TGCTTT	A	Asp	Asp	SILENT- CODING	glycoprot ein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa	3E-210	1
179	cg43059879	580	TTACTTCCCTGC ATTCTGGTAATTT [A/T]GTCCAATTT CCATGTGTCGTG CAGG	T	Thr	Thr	SILENT- CODING	glycoprot ein	Human Gene SWISSNEW-ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C- BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:SWISSPROT-ID:P02749 BETA- 2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:TRMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa	6.6E-199 (17q23)	17

180	cg43932434	1575	TGGGGTGGATC CGGGGAATCAC CAC/A/GTGGCCCT TCTATGAACCCA TACCTGC	A	G	His	His	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.8E-195	11 (11pter)
181	cg43988092	1994	TGAAGTTTCCAG TACTGAAATCCA G/C/T/TCTGATT TTCTGCTCTTGC AAGGC	C	T	Lys	Lys	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4E-192	8
182	cg43918166	2108	AACCATCTTTGC AGTGGTATCTAA TTC/AIAGGGAGTT GATTTCATAACG AGGTT	C	A	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.5E-190	5
183	cg44022653	1149	TCTCAGCCTCGG AACAGTTGTGGG T/A/GJCCCAGTG CACACTCATCCA CGTCCT	A	G	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)

184	cg43076975	1141	TGAATATGCTAA GGGAGTATCTTA GTTCGCTGACG CATTAAAGTG GTATTG	T	C	Ser	Ser	SILENT- CODING	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P15144 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (GP150) (MYELOID PLASMA MEMBRANE GLYCOPROTEIN CD13) - HOMO SAPIENS (HUMAN), 966 aa. pcis:SWISSPROT-ID:P15144 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (GP150) (MYELOID PLASMA MEMBRANE GLYCOPROTEIN CD13) - HOMO SAPIENS (HUMAN), 966 aa	3.40E-120	5
185	cg43051798	1072	AGGTGAACATCG CAAATCGCTTCC CAGCAGCCCT CGTTGCCGCAG CACCCAC	A	G	Cys	Cys	SILENT- CODING	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa. pcis:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL- TMP - HOMO SAPIENS (HUMAN), 202 aa	4.00E-114	3
186	cg43287997	330	TGGGCCTCTGCC TCATTACAGTTG GCTGTGTTGGG GGCAAGATGGTA ATGAAG	C	T	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa. pcis:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa	1.30E-113 (11q23)	11

187	cg43959140	705	TTTCCCTGCGGC TATCACAAAATG G/A/GGTATACCC ATAAGGAGCTCC ATCCA	A	G	Thr	Thr	SILENT- CODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:Q09332 UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	1.30E-108	
188	cg36834323	312	ACCCTGCAGATG CTAAGAAATGCTG C/G/CJAAAGATAT GAATGGAAAGTC TTGC	G	C	Ala	Ala	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P38159 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HNRNP G) (GLYCOPROTEIN P43) - HOMO SAPIENS (HUMAN), 437 aa.	6.40E-91	
189	cg44019280	1508	CCGTGGCCTGG AGGAGGGAGAG GGA/G/CJAGCAG GAGCAGCAGCA GCCACGAGG	G	C	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.50E-80	11
190	cg44924334	508	CCACCTGCCAGT CTATTGCCTTCC C/C/JAGCAAGAC CTCTGCCAGTAT AGGCA	C	T	Pro	Pro	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q13491 NEURONAL MEMBRANE GLYCOPROTEIN M6-B - HOMO SAPIENS (HUMAN), 283 aa (fragment).	5.60E-76	
191	cg44924334	674	ACCTGTTATTG CTGCATTGTGG G/G/TGCTGCAG CTACACTGGTTT CCCTGC	G	T	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q13491 NEURONAL MEMBRANE GLYCOPROTEIN M6-B - HOMO SAPIENS (HUMAN), 283 aa (fragment).	5.60E-76	
192	cg41568631	1548	CTGTGGAGTCCA TCAAGAATGGCC T/G/CJGTCTACAT GAAGTACGACAC GCCCT	G	C	Leu	Leu	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70 (14q11.2)	14
193	cg43918233	1133	CTGCCCTCCAGTG AGAACCCTGAAG G/A/GJACACTTTC GGATTCCACGG GTAGCG	A	G	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.60E-67	2

194	cg43965366	2066	TCACGTCGAACG TCCTCTCTTGA ATCTCTCTGCTT CGGGACCCCGG TGTAAGA	T	C	Glu	Glu	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - MUS MUSCULUS (MOUSE), 690 aa.	8.90E-61	6 (6p25)
195	cg43982558	1326	AGGCTGCAGTG CGCTTCGTGGGT TTCTCTCCAGATA AAAAGCATAAGC TGTATG	C	T	Phe	Phe	SILENT- CODING	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)
196	cg41603916	259	TCACCTGGCGCT ACCAGCCCGAA GG[G/A]GGCAGA GATGCCATTTCG ATCTTCC	G	A	Gly	Gly	SILENT- CODING	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q91406 IP1=CNS MYELIN P0-LIKE GLYCOPROTEIN - UNKNOWN, 202 aa.	3.00E-52	1 (1q22)
197	cg43250682	1520	TTCTGACTCCAA AAATCAACCAGA CIG/CJTCTTAGCG GGATCATGACTA TGTGTA	G	C	Thr	Thr	SILENT- CODING	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0.00E+00	4
198	cg43250682	2120	AGACCATGGCG ATGCCTATTGTG TIG/AJGCTGGG GATTACACAAAG AGAGTG	G	A	Val	Val	SILENT- CODING	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0.00E+00	4
199	cg43956596	1584	GCATTGCTTCA CCAAGCAGCCG GAJAGJCCGGTG ATCCAGTGAAG GATGCCA	A	G	Glu	Glu	SILENT- CODING	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa. pcis:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0.00E+00	16

200	cg43956596	1587	TTGTCCTCACCA AGCAGCCGGAA CC[G/A]GTGATTC CAGTGAAGGATG CCACTT	G	A	Pro	Pro	SILENT- CODING	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.lpcds:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0.00E+00	16
201	cg43956596	718	CAGTCGGCAGA GAGAGCGGGAG CGG[C/A]GGGAA CATGGTGTCTAT GCCTCGTC	C	A	Arg	Arg	SILENT- CODING	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.lpcds:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0	16
202	cg43931167	2037	ATGACTTTGGCT GGGAGTAGTG GT[A/G]AATTTCT CAAAAAAGTCAA ATGTTA	A	G	Val	Val	SILENT- CODING	helicase	Human Gene SWISSPROT-ID:O14232 PUTATIVE HELICASE C6F12.16 IN CHROMOSOME I - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 1117 aa.	3.3E-307	5
203	cg43958815	720	GCTTCTTCGGCT TCTTGTGAGGGC GT[C]ACCCAGGC CACGGAGAGCA GGAGGAA	T	C	Val	Val	SILENT- CODING	helicase	Human Gene Similar to SWISSPROT- ID:Q06218 PROBABLE ATP- DEPENDENT RNA HELICASE DBP9 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 594 aa.	3.9E-100	
204	cg43263560	544	ACAAACCCCTTG CTTTAATTAAAGA [C/T]GGCCGTGTT ATTGGTGGTATC TGT	C	T	Asp	Asp	SILENT- CODING	histone	Human Gene Similar to TREMBLNEW- ID:G2707336 HISTONE ACETYLTRANSFERASE - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 418 aa.	3E-61	3
205	cg43988803	1992	GACATGCTCAGC AGACATCTGCAG TT[C]AACGGGC GTCCCTGCCCC ACACGG	T	C	Val	Val	SILENT- CODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.2E-242 (13q14.1)	13

206	cg43332152	981	ACCTGGGCGCC AAGCGGCGGG ACC[G/C]CGCAC CACCATCAAAGC CAAGCAGC	G	C	Pro	Pro	SILENT- CODING	homeobo x	Human Gene SWISSPROT-ID:P36199 HOMEBOX PROTEIN LIM-1 (HOMEBOX PROTEIN LMX-2) - MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND MESOCRICETUS, 406 aa.	3.4E-227	17
207	cg41637704	1201	AGGAGCTGCTG GGCCCGCCAGC GCC[G/C]CGAGA CAAGGCGAGCG GACCGCCTG	G	C	Pro	Pro	SILENT- CODING	homeobo x	Human Gene SWISSPROT-ID:P50219 HOMEBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.2E-224	7
208	cg43143467	581	CTTCAACCATC TCATTCGCGGG G[G/A]TTCCTCC CACTGCCATGCC GACCT	G	A	Gly	Gly	SILENT- CODING	homeobo x	Human Gene SPTREMBL-ID:Q12777 PAX-3 - HOMO SAPIENS (HUMAN), 332 aa (fragment).	2.1E-179	2 (2q35)
209	cg43971192	625	TGTTGAAAAGAC CACTCTGTGTAT T[G/G]GTACTTGG TCCAGATTTACA AGTGT	C	G	Thr	Thr	SILENT- CODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.9E-144	18
210	cg40291306	693	AGATCAAGATCT GGTCCAGAACCC G[A/C]AGGATGA AGTGGAAAGAAAG ATTCCA	A	C	Arg	Arg	SILENT- CODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q00444 HOMEBOX PROTEIN HOX-C5 (HOX-3D) (CP11) - HOMO SAPIENS (HUMAN), 222 aa.	8.3E-121	12
211	cg40291306	694	GATCAAGATCTG GTTCCAGAACCCG A[A/C]GGATGAA GTGGAAGAAAGA TTCCAA	A	C	Arg	Arg	SILENT- CODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q00444 HOMEBOX PROTEIN HOX-C5 (HOX-3D) (CP11) - HOMO SAPIENS (HUMAN), 222 aa.	8.3E-121	12

212	cg43823497	1741	ACTTCACCTTCT CTGTGGCCAGG CA/C/TTTGATCT TTTCCTCCACCA AGAAGC	C	T	Lys	Lys	SILENT- CODING	hydrolas e	Human Gene SWISSPROT-ID:P45974 UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE T) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T) (DEUBIQUITINATING ENZYME T) (ISOPEPTIDASE T) - HOMO SAPIENS (HUMAN), 858 aa.	0	12
213	cg43822794	2430	TAAATGCCACC GAACCTATCGGC T/C/G/TTTGAGT GGTCTACCATCA CGGCA	C	G	Leu	Leu	SILENT- CODING	hydrolas e	Human Gene SWISSPROT-ID:Q14894 PROBABLE UBIQUITIN CARBOXYL- TERMINAL HYDROLASE (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME) (KIAA0190) - HOMO SAPIENS (HUMAN), 798 aa.	0.00E+00	14
214	cg43285385	616	TTAAGACATTGA AAAACCTCTTTAA [C/T]TTTTTCATTC ATTGTAAATTTCT TCA	C	T	Lys	Lys	SILENT- CODING	hydrolas e	Human Gene TREMBLNEW- ID:G2951931 HUMAN GAMMA- GLUTAMYL HYDROLASE (EC 3.4.22.12) - HOMO SAPIENS (HUMAN), 318 aa.	4.80E-173	8
215	cg43825870	1390	TTTTTCTAAGTC GAAAGCAGAAAA G/T/C/JGGAGCTT ATCTCCTTCTTC ACAGG	T	C	Gln	Gln	SILENT- CODING	Interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0.00E+00	1

216	cg43925670	1720	ATATGATGATGA TTTTCTTTCCATT [A/G]AATTTCTCC TTCAAGCTGGTG TTTA	A	G	Phe	Phe	SILENT- CODING	Interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. cds: SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0.00E+00	1
217	cg43082514	921	CCAGCGATGAAG AGAGTGCCGAG GG[G/A]CGGCCA CACTGGCGGAA GAGGAATA	G	A	Gly	Gly	SILENT- CODING	Interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
218	cg43922672	1212	CTGCTGAAACAT CTGCCCTGGACA C[A/G]GGGTTCT CGCTCAACCTTT CAGAGC	A	G	Thr	Thr	SILENT- CODING	Interleukin	Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0	15
219	cg42887911	402	CCCTGCCACCCC TGGCCATGAGTG C[A/G]GGGGCAC TGGGAGCTCTAC AGCTCC	A	G	Ala	Ala	SILENT- CODING	Interleukin	Human Gene Homologous to SWISSPROT-ID:P20809 INTERLEUKIN- 11 PRECURSOR (IL-11) (ADIPOGENESIS INHIBITORY FACTOR) (AGIF) - HOMO SAPIENS (HUMAN), 199 aa.	2.5E-103	19
220	cg43929155	434	TCCTATGCAAGG CAGTCCATGTCA T[C/T]TACACAGT CAACCTCTACAG CAGTG	C	T	Ile	Ile	SILENT- CODING	Interleukin receptor	Human Gene Similar to SWISSPROT- ID:P21109 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (CXCR-1) - ORYCTOLAGUS CUNICULUS (RABBIT), 355 aa.	4.2E-55	2
221	cg43951261	2559	AACAAGCATTGA TGATGACTATTG T[A/G]AATTTGGC TCAGAACTTTGT GGGAA	A	G	Val	Val	SILENT- CODING	Isomerase	Human Gene SWISSPROT-ID:Q02880 DNA TOPOISOMERASE II, BETA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1626 aa.	0	3 (3p)

222	cg43983971	1428	AGGCAATGATGA ACAGGGAGGAC TCG/CJGGGTTTC AGCTGGGCCAG GGTTTTGG	G	C	Pro	Pro	SILENT- CODING	isomerase	Human Gene SWISSPROT-ID:P06744 GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) (NEUROLEUKIN) (NLK) - HOMO SAPIENS (HUMAN), 558 aa.	3.60E-305	19 (19q13.1)
223	cg43930054	738	TCGTGGTTGTGG GTGTGCTGGCTA TTC/TAAGTGTCCC CTGTACCATCAG GAGGA	C	T	Val	Val	SILENT- CODING	isomerase	Human Gene SWISSPROT-ID:P34949 MANNANOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNANOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa.	2.00E-222	15 (15q22)
224	cg43981450	1141	ACTCTGCCCTTAG TCCTCTTTGCAA A/C/TAACATCTGC AAACTCTCTCTTC ATT	C	T	Val	Val	SILENT- CODING	isomerase	Human Gene Homologous to SWISSPROT-ID:P70473 2- ARYLPYRUVATE-COA EPIMERASE (EC 5.3.1.2) - RATTUS NORVEGICUS (RAT), 361 aa.	1.80E-117	5
225	cg43981450	1237	CAAGTCCAAGTC CTTTAAGCAGCA G/T/CJGGCGTAGA ACTGGGGTTCTA TTGCTC	T	C	Ala	Ala	SILENT- CODING	isomerase	Human Gene Homologous to SWISSPROT-ID:P70473 2- ARYLPYRUVATE-COA EPIMERASE (EC 5.3.1.2) - RATTUS NORVEGICUS (RAT), 361 aa.	1.80E-117	5

226	cg43924460	609	TCATAAAGAGTG TTACACCGTGCG C[AT]CCAAAGTA CCACAAAGCCTG CTCCA	A	T	Ala	Ala	SILENT- CODING	isomerase	Human Gene Similar to SWISSNEW- ID:Q27450 PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) - BRUGIA MALAYI, 843 aa.lpcis:SWISSPROT-ID:Q27450 PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS- TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) - BRUGIA MALAYI, 843 aa.lpcis:SPTREMBL-ID:Q27450 PEPTIDYLPROLYL ISOMERASE (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) - BRUGIA MALAYI, 843 aa.	4.20E-71	8 (8p22)
227	cg43145505	253	ACTTGATGCCCC CAAGAATCCTAG TTA/G]GAATGTTT ACTACCAAATGG AATGA	A	G	Val	Val	SILENT- CODING	kinase	Human Gene SWISSNEW-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.lpcis:SWISSPROT- ID:P42336 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.	0.00E+00	3

228	cg43145505	358	TATTTAAAGAAG CAAGAAAATACC G[C/T]CTCCATCA ACTTCTTCAAGA TGAAT	C	T	Pro	Pro	SILENT- CODING	Kinase	Human Gene SWISSNEW-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa. cds:SWISSPROT- ID:P42336 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.	0.00E+00	3
229	cg43918241	943	TGCTAAAGAGT GTAAAGACCTAA TTC/TACACGGAT GCTACAGAGAGA TCCCA	C	T	Ile	Ile	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q63553 SNF1-RELATED KINASE - RATTUS NORVEGICUS (RAT), 746 aa.	0.00E+00	3
230	cg43252989	2330	ATTTTGAGGTT GGTTTATGATG G[G/T]GTGAACT ACACAAAATAGA AGATT	G	T	Gly	Gly	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:O00444 SERINE/THREONINE PROTEIN KINASE - HOMO SAPIENS (HUMAN), 970 aa.	0.00E+00	4
231	cg43916734	18295	GCAGGCTATTGT TTATCCCTTCAC G[C/A]GAAGCAG CGAAAGCTATTC CTTCAA	C	A	Arg	Arg	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
232	cg43257400	2027	TTGCCTGTACAC AGAGTTCTGCCCC G[G/C]TCCCCTGT AGGATCCAGTCT AGAAAG	G	C	Arg	Arg	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q60680 CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE - MUS MUSCULUS (MOUSE), 745 aa.	0.00E+00	10
233	cg43298663	2266	CTCGAGAGGCC AAGCCAGAGAAA TTT/CJAACAGCC GCTTTCGGAATA AGATGT	T	C	Phe	Phe	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q00542 DIACYLGLYCEROL KINASE ZETA - HOMO SAPIENS (HUMAN), 1117 aa.	0.00E+00	11

234	cg43151490	322	ATCTGACGGTGA GCGTGGACCCAG GT[A/G]CGCGTG GGCCAGACCCAG CACAAAGC	A	G	Val	Val	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P24723 PROTEIN KINASE C, ETA TYPE (EC 2.7.1.-) (NPKC-ETA) (PKC-L) - HOMO SAPIENS (HUMAN), 682 aa.	0.00E+00	14
235	cg44929725	2320	TGGATCTCTTCA TGCACCGGAAAA G[C/T]GATGTCCT TACCACACCCATG GAAAT	C	T	Ser	Ser	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
236	cg44929725	2347	ATGTCCTTACCA CACCATGGAAAT T[T/C]AAAGTTGC CAAACAGCTGGC CAGTG	T	C	Phe	Phe	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
237	cg44929725	2449	AAAACCTCCTCC TGGCCCGTGAG GG[C/A]ATCGAC AGTGAGTGTGGC CCATTCA	C	A	Gly	Gly	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
238	cg44929725	2884	CTGAAGTGGACC CCACACATTTTG A[A/G]AAGCGCTT CCTAAAGAGGAT CCGTG	A	G	Glu	Glu	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
239	cg44929725	3649	CTAACTGTCCAG ATGAGGTTTATC A[A/G]CTTATGAG GAAATGCTGGGA ATTCC	A	G	Gln	Gln	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
240	cg44929725	3658	CAGATGAGGTTT ATCAACTTATGA G[G/A]AAATGCTG GGAATTCCAACC ATCCA	G	A	Arg	Arg	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)

241	cg44818305	1129	TGAGTACTCGCA CAGAAGCATTAG A[A/G]GCCTTACA GAGTGAAAAATC ACGAA	A	G	Glu	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	0.00E+00	10 (10q11.2)
242	cg43940596	1642	TCTTCAGGCACA AGGGGTGGTTCA T[A/C]GAGACTTG AAACCTAGCAAC ATTCT	A	G	Arg	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P51812 RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA) (P90-RSK 2) (INSULIN-STIMULATED PROTEIN KINASE 1) (ISPK-1) - HOMO SAPIENS (HUMAN), 740 aa.	0.00E+00	X
243	cg43931272	2078	GTCTCTTCCCAA CCACAAAACACT C[C/T]GGTGGTAA ATACCAATAAGT ACCAG	C	T	Pro	SILENT- CODING	kinase	Human Gene TREMBLNEW- ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	
244	cg43930294	1630	TAGCTGGTTGAT GAGAAGCATGCC C[T/C]TGATATC ACTTGTTAACTT GGGAG	T	C	Gln	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:O00311 CDC7-RELATED KINASE - HOMO SAPIENS (HUMAN), 574 aa.	2.90E-308	1
245	cg43952792	1125	TCCGCGAGAGT GAAACCACCAAA GGT[G/G]GCCTATT CACATTCTATCC GTGATT	T	G	Gly	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
246	cg43922705	3970	TCTGCTGGTCCA GGGTATGCAGG AA[G/A]GCTGAGT TGGGGTCCAGG GTGCGCT	G	A	Ala	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P27987 1D-MYO-INOSITOL-TRISPHOSPHATE 3 KINASE B (EC 2.7.1.127) (INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE) (IP3K) (IP3 3-KINASE) - HOMO SAPIENS (HUMAN), 505 aa (fragment).	3.80E-279	1 (1q41)
247	cg43241753	1745	CCCTGTGTGTGGCA TTGTTTCAATCAT [A/G]TGTTGGAA ACCAGGTTACCA ACAT	A	G	His	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q16675 PROTEIN-TYROSINE KINASE PRECURSOR - HOMO SAPIENS (HUMAN), 477 aa.	4.20E-268	9

248	cg43985549	625	GCGCCTTTGGAA AGGTATACCTGG C[AT]CAAGATAT AAAGACGAAGAA AAGAA	A	T	Ala	Ala	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)
249	cg43985549	703	AATTTAAGCCAT CTGATGTGGAAA T[C/T]CAGGCTTG CTCCGGCACGA GAACA	C	T	Ile	Ile	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)
250	cg43928820	1479	CATACAGGATGC AACCCAAAGGACC A[G/T]ATGTCAC TTTATTGTTATA GGCA	G	T	Ile	Ile	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P51956 SERINE/THREONINE-PROTEIN KINASE NEK3 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 3) (HSPK 36) - HOMO SAPIENS (HUMAN), 459 aa (fragment).	1.40E-251	13
251	cg43069976	469	TGGCTAGTGTA TTACAAAGGGAA C[C/G]AAGGAAA GGCAATACTTAG ATGAAG	C	G	Thr	Thr	SILENT- CODING	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa. ipcls:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1

252	cg43069976	589	GTCATACCGTAT TGCATCGGGATC TIG/TJAAACCAGC CAATGTTTTCCT GGATG	T	Leu	Leu	SILENT- CODING	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.jpcl:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1
253	cg43069976	667	TGGGCTAGCTA GAATATTAAACC ATT/CJGACACGA GTTTTCGCAAAA CATTG	C	His	His	SILENT- CODING	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.jpcl:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1
254	cg43967889	1159	AATTACGGGACC CAAATGTCAAAC TTAT/CJCAAATGG GCGAGACACAC CTGCAC	T	Leu	Leu	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P49841 GLYCOGEN SYNTHASE KINASE-3 BETA (EC 2.7.1.37) (GSK-3 BETA) - HOMO SAPIENS (HUMAN), 420 aa.	1.90E-226	3

255	cg43966621	451	AGAGGCGGGAA ATGGGGAGCCC ATA[C/A]CCAAAG CCAGCCAGCGG GGTTCCCC	C	A	Gly	Gly	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa. Jcds: SPTREMBL-ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407 aa.	3.80E-219	17
256	cg38438124	346	CGACCCCGCGC AACCTAGGTCC TC[T/C]GTCCTGG CGAGCAAGACCA AGACCA	T	C	Ser	Ser	SILENT- CODING	kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII-ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P-5- KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa. Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.80E-216	10
257	cg43917871	2435	AGTATTCTCGAG GTCTGTGTGTAT TTAGJACATCTGT GTAAACTCTGGC CCTGC	A	G	Val	Val	SILENT- CODING	kinase	MUS MUSCULUS (MOUSE), 405 aa. Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215	11 (20p13)
258	cg43924218	902	TTGCAGCAGTAG AGAAGAATGGTG G[C/A]TACAACCA ACTCTGTGATAT CTGGG	C	A	Gly	Gly	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q12851 GC KINASE - HOMO SAPIENS (HUMAN), 819 aa.	1E-203	
259	cg43982923	940	TTGTAAAGTCAT TCCTCTTCCAGC TTATJCTAAAAGG GCTGGGATTCTG TCATA	A	T	Leu	Leu	SILENT- CODING	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19

260	cg43869473	3923	TCACCTGGCAAG CTCTCGGGGCA CTC/TJTGCCGA TAGTGAAATTGA GACCAA	C	T	Leu	Leu	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q27467 SIMILARITY TO TYROSINE-PROTEIN KINASE - CAENORHABDITIS ELEGANS, 1280 aa.	2.1E-154	11
261	cg43858362	2164	GGCCACCATGC CGCTCCAGCGC GGC/G/CJCGCTC ACTGCTGGTATT GCCCATGA	G	C	Arg	Arg	SILENT- CODING	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP- ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.10E-147	12
262	cg42925992	327	TGCAAGTTGTGC AGCAAGAAATTA T/C/TJATGATGAA AGACTGTAAACA CCCAA	C	T	Ile	Ile	SILENT- CODING	kinase	Human Gene Homologous to SPTREMBL-ID:Q12851 GC KINASE - HOMO SAPIENS (HUMAN), 819 aa.	5.10E-105	
263	cg44033347	719	GGTGGATGCTG CTGTGCTGGCCC CC[G/A]TCTGCC CAGCTCACCAGC TCACTGC	G	A	Asp	Asp	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:O00746 NUCLEOSIDE DIPHOSPHATE KINASE, MITOCHONDRIAL PRECURSOR (EC 2.7.4.6) (NDP KINASE, MITOCHONDRIAL) (NDK) (NM23-H4) - HOMO SAPIENS (HUMAN), 187 aa. Jcds:SPTREMBL-ID:O00746 NUCLEOSIDE-DIPHOSPHATE KINASE (EC 2.7.4.6) (NUCLEOSIDE 5'- DIPHOSPHATE PHOSPHOTRANSFERASE) (NDK) - HOMO SAPIENS (HUMAN), 187 aa.	9.10E-99	16

264	cg43986625	337	CCGACCGAGTG CTGAGCACACCC TC/TGTGTCAGC TGGTGCAGAGCT GGTATG	C	T	Ser	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa. [pcis:SPTREMBL-ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407.aa.	3.20E-89	17
265	cg43918784	1346	CTTCTTCTCTGT CTGCAACACACT G/A/GJTCAAAGAT TTCACCCCCAGC AGCAT	A	G	Asp	SILENT- CODING	kinase	Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	1.80E-57	7
266	cg43933456	286	ATAGTAAGTTT CATCAGTAGCTT CT/CJTGTATAAG GTAATGCACATG TCCTT	T	C	Gln	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:P35169 PHOSPHATIDYLINOSITOL 3- KINASE TOR1 (EC 2.7.1.137) (PI3- KINASE) (PTDINS-3-KINASE) (PI3K) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 2470 aa.	2.10E-57	3
267	cg43105476	550	CCAGGAACTCCA CCACCCGGAGG TG/GA/JCCTTCTT TGGCAGCCCAAGT GCAAGG	G	A	Gly	SILENT- CODING	kinaselnh ibitor	Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
268	cg44931523	926	CCGTCATCTGGG CCACCAGGTCAA A/A/GJGATGCAAA CCCCGCACTGAC GAAGC	A	G	Ser	SILENT- CODING	kinaserec eptor	Human Gene SWISSPROT-ID:P54753 EPHRIN TYPE-B RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR HEK-2) - HOMO SAPIENS (HUMAN), 998.aa.	0.00E+00	3
269	cg43048869	2392	GTAACCTGGTGT GTAAGGTTTCTG A/C/TJTCGGACT CTCGCGGGTACT GGAAG	C	T	Asp	SILENT- CODING	kinaserec eptor	Human Gene SWISSPROT-ID:P29320 EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETK1) (HEK) - HOMO SAPIENS (HUMAN), 983 aa.	0	

270	cg43935828	1884	AGGGCCGCCCC CTGCTCATGGTC TTTC/TGAGTATA TGCGGCACGGG GACCTCA	C	T	Phe	Phe	SILENT- CODING	kinaserec eptor	Human Gene SWISSNEW-ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140- TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.lpcds:SWISSPROT- ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140-TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.	0	0
271	cg43935828	1935	ACCGCTTCCTCC GATCCCATGGAC C/C/TGATGCCAA GCTGCTGGCTG GTGGGG	C	T	Pro	Pro	SILENT- CODING	kinaserec eptor	Human Gene SWISSNEW-ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140- TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.lpcds:SWISSPROT- ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140-TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.	0	0

272	cg43935828	2004	CCCTGGGTCTG GGGCAGCTGCT GGC[C/T]GTGGC TAGCCAGGTCGC TGCGGGGA	C	T	Ala	Ala	SILENT- CODING	kinaserec eptor	Human Gene SWISSNEW-ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140- TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.lpcis:SWISSPROT- ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140-TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.	0	0
273	cg43991478	1342	CGTCAGCAAGAT TGTGGGGCTGC AG[C/G]CGGGTG AGGTCACGCAG GATGGTGC	C	G	Arg	Arg	SILENT- CODING	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	0
274	cg43263845	668	GTAAATGAAAAGT TTTCTTATTTTCC [G/A]GAGATGGA AGTCACACAGCC CACTT	G	A	Pro	Pro	SILENT- CODING	kinaserec eptor	Human Gene TREMBLNEW-ID:G247985 ACTIVIN RECEPTOR, ACTRIIB=TRANSMEMBRANE PROTEIN SERINE KINASE - XENOPUS LAEVIS, 510 aa.	3.30E-204	2
275	cg43999555	1415	GCGGATCGTGG AGAACCTGGGCA TC[C/T]TGACCGG GCCGCAGCTCTT CTCCCT	C	T	Leu	Leu	SILENT- CODING	kinaserec eptor	Human Gene Similar to SWISSPROT- ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 - HOMO SAPIENS (HUMAN), 822 aa.lpcis:SPTREMBL- ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE - HOMO SAPIENS (HUMAN), 822 aa.	1.20E-99	11
276	cg43975720	5392	CCTCTCCTGCCA GACAGCCACAG AC[C/T]GGGTG ACCCCCCAGGG GACGCCCA	C	T	Thr	Thr	SILENT- CODING 103	kinesin	Human Gene SWISSPROT-ID:Q12756 KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES) - HOMO SAPIENS (HUMAN), 1690 aa.	0.00E+00	2

277	cg43987378	967	CAGCCCTGTCAA GCAGCCAAGCA GA[G/A]GTGGCA TCTCTGCCGCGAG GAGACTG	G	A	Glu	Glu	SILENT- CODING	kinesin	Human Gene SPTREMBL-ID:Q14834 KINESIN-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 519 aa (fragment).	1.50E-254	6
278	cg44009224	123	GCTACAGTTCAC AGCAGCAAAGG GT[A/G]CCATTTC TTCAGCCTCCCG GTCAAA	A	G	Val	Val	SILENT- CODING	laminin	Human Gene SWISSPROT-ID:Q16787 LAMININ ALPHA-3 CHAIN PRECURSOR (EPILGRIN 170 KD SUBUNIT) (E170) - HOMO SAPIENS (HUMAN), 1713 aa.	0.00E+00	
279	cg42488873	988	CATGCACGTCCT CAAGGCTGTACC C[C/T]AGCTGCGT CGACAGTGCTTG TATTA	C	T	Leu	Leu	SILENT- CODING	lipase	Human Gene SWISSPROT-ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa.	9.80E-261	
280	cg42488873	202	GATTTATCCAC GTTTGTTCCAGA G[A/G]AATTTAAC TTTCTGTAATTTT CCAA	A	G	Phe	Phe	SILENT- CODING	lipase	Human Gene SWISSPROT-ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa.	9.80E-261	
281	cg42686658	452	ACTTTGCCCGCT TTGACCCGCGAGG G[C/T]GGGCTGG CCGGCATCGCC GCAATCA	C	T	Gly	Gly	SILENT- CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHC DN- ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134 (6p21.3)	6
282	cg42686658	860	CACCAGATGCCA TGGAGACCCCTG GT[C/T]TGTCGCC TGGGCCTGGCC ATCGGCC	C	T	Val	Val	SILENT- CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHC DN- ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.7E-134 (6p21.3)	6
283	cg42628872	389	TGAGCCTAGACC CGCGCGTCTCCA TTC/TACAGCAC GCGCCGCCCGG TGTTGG	C	T	Ile	Ile	SILENT- CODING	misc_cha tnal	Human Gene TREMBLNEW- ID:G2465531 KIDNEY AND CARDIAC VOLTAGE DEPENDENT K+ CHANNEL - HOMO SAPIENS (HUMAN), 676 aa.	0	11

284	cg43311602	5361	CTCGCCCGCC GGCTACCCAG CACIAGGTCAG CACTGTGGAG GCCACGGGC	A	G	Thr	Thr	SILENT- CODING	misc_cha nnel	Human Gene SP TREMBL-ID:Q13930 VOLTAGE-DEPENDENT L-TYPE CA CHANNEL ALPHA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 2173 aa.	0	12 (12p13.3)
285	cg43111577	175	TGGAACAGAGC CAGAGATGGAG GCIAGGAGGTG GAACAGAACCG AATCCTG	A	G	Ala	Ala	SILENT- CODING	misc_cha nnel	Human Gene TREMBLNEW- ID:G1518639 CGMP-GATED CATION CHANNEL BETA SUBUNIT - HOMO SAPIENS (HUMAN), 1251 aa.	0	16 (16q13)
286	cg21657051	5819	AAGCATGAGG GTGGTTGTGAAT GCIC/TCTTGTTA GGAGCAATTCCC TCTATC	C	T	Ala	Ala	SILENT- CODING	misc_cha nnel	Human Gene TREMBLNEW- ID:G2665784 VOLTAGE-GATED SODIUM CHANNEL, SUBTYPE III - HOMO SAPIENS (HUMAN), 1366 aa (fragment).	0	
287	cg42684570	1186	CCGAGTAGCCCA GGAGGAGTGTA TTC/TJTGAAGA GACCCCTCTGCC ACTGT	C	T	Lys	Lys	SILENT- CODING	misc_cha nnel	Human Gene SWISSPROT-ID:P46098 5- HYDROXYTRYPTAMINE 3 RECEPTOR PRECURSOR (5-HT-3) (SEROTONIN- GATED ION CHANNEL RECEPTOR) - HOMO SAPIENS (HUMAN), 478 aa.	1.8E-260	11 (11q23.1)
288	cg44021559	2938	TCCTGTCAATTAG GGATGACGTGG GTIAGJCCATTGT AGATGCCACCTT GCACCA	A	G	Gly	Gly	SILENT- CODING	misc_cha nnel	Human Gene Similar to SP TREMBL- ID:Q61626 GLUTAMATE RECEPTOR CHANNEL SUBUNIT GAMMA 2 PRECURSOR - MUS MUSCULUS (MOUSE), 979 aa.	2E-61	9 (9q34.3)
289	cg44021559	2989	GCTTGCGGTTCT GCAGGTTTCATGA TIA/GJCTATAGTT GGCGAACTCCG GTCCC	A	G	Ser	Ser	SILENT- CODING	misc_cha nnel	Human Gene Similar to SP TREMBL- ID:Q61626 GLUTAMATE RECEPTOR CHANNEL SUBUNIT GAMMA 2 PRECURSOR - MUS MUSCULUS (MOUSE), 979 aa.	2E-61	9 (9q34.3)
290	cg44021559	2982	TGCGGTTCTGCA GGTTCATGATAC TIA/GJTAGTTGGC GAACCTCCGGTC CCCAT	A	G	Tyr	Tyr	SILENT- CODING	misc_cha nnel	Human Gene Similar to SP TREMBL- ID:Q61626 GLUTAMATE RECEPTOR CHANNEL SUBUNIT GAMMA 2 PRECURSOR - MUS MUSCULUS (MOUSE), 979 aa.	2E-61	9 (9q34.3)

291	cg44929972	1029	AAAAGCTTGAGA TGCATTTCCATA A[G/A]CTTCCAAG CCTCCTCTCTTG TGATG	G	A	Lys	Lys	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
292	cg44929972	1044	ATTTCATAAGC TTCCAAGCCTCC T[C/T]TCTTGTA TGATGTAACAT GAGAA	C	T	Leu	Leu	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
293	cg44929972	1071	CTTGTGATGATG TAAACATGAGAA T[A/T]GCTGCTGG TGAATCTTTGGC ACTTC	A	T	Ile	Ile	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
294	cg44929972	1080	ATGTAACATGA GAATAGCTGCTG GT[C/G]AATCTTT GGCAGCTTCTCTT TGAAT	T	C	Gly	Gly	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
295	cg44929972	1098	CTGCTGGTGAAT CTTTGGCACTTC T[C/G]TTTGAATT GCCACAGAGGAA TAGAGA	C	G	Leu	Leu	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
296	cg44929972	1143	TAGAGAGTGACT TTTTTTATGAAGA T[C/T]ATGGAGTCC TTGACGCAGATG CTTA	C	T	Asp	Asp	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
297	cg44929972	1158	TTTATGAAGACA TGGAGTCCCTGA C[G/C]CAGATGC TTAGGGCCCTTGG CAACAG	G	C	Thr	Thr	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7

298	cg44929972	1167	ACATGGAGTCCT TGACGCAGATGC TTTCJAGGGCCTT GGCAACAGATG GAAATA	T	C	Leu	Leu	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
299	cg44929972	1173	AGTCCTTGACGC AGATGCTTAGGG C/C/TJTTGGCAAC AGATGGAAATAA ACACC	C	T	Ala	Ala	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
300	cg44929972	1179	TGACGCAGATGC TTAGGGCCTTGG C/A/TJACAGATGG AAATAAACACCG GGCCA	A	T	Ala	Ala	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
301	cg44929972	1230	AAGTGGACAAGA GAAAGCAGCGG TC/A/TJGTTTCA GAGATGTCCTGA GGGCAG	A	T	Ser	Ser	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
302	cg44929972	1242	GAAAGCAGCGG TCAGTTTTTCAGA GATTCJGTCCTGA GGCAGTGGAG GAACGGG	T	C	Asp	Asp	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
303	cg44929972	1245	AGCAGCGGTCA GTTTTTCAGAGAT GTTC/TJCTGAGG GCAGTGGAGGA ACGGGATT	C	T	Val	Val	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
304	cg43921419	1269	GTGGAGATCCTT TTAGTGCAGATG A/C/TJATACTTTT TCCTGTCCTTCA GTCCC	C	T	Asp	Asp	SILENT- CODING	nucl_rec pt	Human Gene SPTREMBL-ID:Q14452 GLUCOCORTICOID RECEPTOR REPRESSION FACTOR 1 - HOMO SAPIENS (HUMAN), 835 aa.	0	19

305	cg43249083	633	CGCTCTCAGCTG GTGAAGACATGA CIG/CJACCTGG ACTCCAACAACA ACACAG	G	C	Thr	Thr	SILENT- CODING	nucl_rec pt	Human Gene SWISSPROT-ID:P20393 V- ERBA RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa.	0	17 (17q11.2)
308	cg43315956	2680	TCAGGAATGACA GGAACAAGAAAA AIG/AJAAGGAGA CTCGAAGCAAG	G	A	Lys	Lys	SILENT- CODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
307	cg43935583	1416	AATGCA TGGGAGGGGGC ATGCCTGGAATG GCT/CJGGAATG CCTGGACTCAAT	T	C	Ala	Ala	SILENT- CODING	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
308	cg43935583	1563	GAAATTC AGAGCAACCCAA AGGTATGAATC TCT/TATCAGTAA ATTGTCAGCCAA	C	T	Leu	Leu	SILENT- CODING	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.30E-195	22
309	cg42933859	233	ATTG TACTCTGTATTAA CTCTTCCTTTGAI G/AJAGTTTGA GGTGAAGCATTT TGAT	G	A	Leu	Leu	SILENT- CODING	nucl_rec pt	Human Gene Similar to SPTREMBL- ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.20E-51	17
310	cg44925604	827	CTCACAGCTGCT CAAATGGGAACA G/AJGTGGGAAG CTGCTGCTTTCT TTTCCC	A	G	His	His	SILENT- CODING	nuclease	Human Gene SWISSPROT-ID:Q01831 DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN) (P125) HOMO SAPIENS (HUMAN), 939 aa.	0.00E+00	3

311	cg44128653	1448	CGTAGGTACAGG CGCTATGAGGCC A[G]A[CTGTATGC AGCAGAGGAGG CCGGTG	G	A	Ser	Ser	SILENT- CODING	nuclease	Human Gene SWISSNEW-ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa.[pcis:SWISSPROT- ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa.	1.40E-203	19
312	cg43952559	211	GAATGTTAACTG ACTTAAGAGCCA TTT/CJAATTCAGT TATACAACCTAT GGGAG	T	C	Ile	Ile	SILENT- CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.[pcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	
313	cg43952559	235	TTAATTCAGTTAT ACAACCTATGGG [A/G]GCATTACAG CCAGGATTCCT TCTC	A	G	Gly	Gly	SILENT- CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.[pcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	

314	cg43952559	251	ACCTATGGGAGC ATTACAGCCAGG ATTCTGCGCTTCT CCTGCTATGATT CCAAA	T	C	Leu	Leu	SILENT- CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.[pcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	
315	cg43952559	884	TAACAAAGGAGG CGGAGGCAGAG TTTAGTCAACTGA TCGAGAAGCAAG TCCATA	A	G	Leu	Leu	SILENT- CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.[pcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	
316	cg43952559	896	CGGAGGCAGAG TTACAACTGATC GAGTAAAGCAA GTCCATAAAGCT CAAAATAA	G	A	Glu	Glu	SILENT- CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.[pcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	

317	cg43952559	914	TGATCGAGAAGC AAGTCCATAAAG CTTCJCAAAATAAA TAGAATAGATCC AGAGA	T	C	Ala	Ala	SILENT- CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.lpcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	
318	cg43943773	407	TATTGAGTTCAT CATTAAAGTCAT CTTGJATTTCAA CCTGAGTGTCCG GAGGG	T	G	Ile	Ile	SILENT- CODING	nuclease nhlib	Human Gene Similar to SWISSPROT- ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19
319	cg43943851	851	TTGTAACGTGTA ACTGTGCCCCGG CTG/CJCTGAAAG CCGACCACCATG CAACCA	G	C	Leu	Leu	SILENT- CODING	oncogen e	Human Gene SWISSPROT-ID:Q15582 TRANSFORMING GROWTH FACTOR- BETA INDUCED PROTEIN IG-H3 PRECURSOR (BETA IG-H3) (KERATO- EPITHELIN) - HOMO SAPIENS (HUMAN), 683 aa.	0.00E+00	5 (5q31)
320	cg44012758	2265	GGACCAACTGTG ACATCAACAACA ATTCJGAGTGTGA ATCCAACCCCTTG TGTC	T	C	Asn	Asn	SILENT- CODING	oncogen e	Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1984 aa.	0.00E+00	
321	cg42827675	215	CAGCCCCGGGC ATGTTCCGAGAC TTTCJGGGGGAA CCGGCCCCGAGC TCCGGGA	C	T	Phe	Phe	SILENT- CODING	oncogen e	Human Gene Homologous to SWISSPROT-ID:P15407 FOS-RELATED ANTIGEN 1 - HOMO SAPIENS (HUMAN), 271 aa.	6.40E-146	11

322	cg43984295	4723	TATCACAGTACA GGCCTTGCCAG CC[G/A]TACTGG CACCTGCAGTCA CCTGGGA	G	A	Tyr	Tyr	SILENT- CODING	oncogen e	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1984 aa.	4.80E-120	20
323	cg43916615	130	TGACCATCCAGC TGATCCAGAACC A[C/T]TTTGTGGA CGAATACGACCC CACTA	C	T	His	His	SILENT- CODING	oncogen e	Human Gene Similar to TREMBLNEW- ID:G332185 TRANSFORMING PROTEIN (P21 HAS) - HARVEY MURINE SARCOMA VIRUS, 241 aa.	3.10E-98	
324	cg42904626	640	AACATAAAGAAA AGATGAGCAAAG A[C/T]GGTAAAAA GAAGAAAAAGAA GTCAA	C	T	Asp	Asp	SILENT- CODING	oncogen e	Human Gene Similar to SWISSPROT- ID:P01118 TRANSFORMING PROTEIN P21/K-RAS 2B - HOMO SAPIENS (HUMAN), 188 aa.	1.1E-97	12
325	cg44029157	533	GCTTCCTGCTGG TGTTGCCCATTA AT[C/G]ACCGGC AGAGTTTCAACG AGGTGG	T	C	Asn	Asn	SILENT- CODING	oncogen e	Human Gene Similar to SWISSPROT- ID:P17082 RAS-RELATED PROTEIN R- RAS2 (RAS-LIKE PROTEIN TC21) (TERATOCARCINOMA ONCOGENE) - HOMO SAPIENS (HUMAN), 204 aa.	5.1E-66	
326	cg43975131	4247	TCTTCTCTTCA GGCGCTCGATG GC[C/A]CGGCTC TGGCCCTTTGTTG GCTTCT	C	A	Arg	Arg	SILENT- CODING	oncogen e	Human Gene Similar to SPTREMBL- ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.8E-64 (17p13.3)	17
327	cg43307658	1322	CCGGCTTCGAG CAGGCCTACCCCT GA[T/C]CCCGGT CCCGAGGCGGC GCAGGCCCC	T	C	Asp	Asp	SILENT- CODING	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0	15

328	cg43307658	1514	GCGGCGAGCAG GGCGGCCTCAG CGT[G/A]GGCAG CGTGACCGGC CCAACCAGA	G	A	Val	Val	SILENT- CODING	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0	15
329	cg44028217	1031	GCACCAGCACCT GGCCCTTCAGCC C[C/T]GCATAGAA GTTGAAGCCACC TTTAA	C	T	Ala	Ala	SILENT- CODING	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)
330	cg44028217	471	GGTAGATGCTGC TGCTGCACAGCT C[C/T]GACTCCC GGTACTTGGTCA CTGCCA	C	T	Ser	Ser	SILENT- CODING	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)
331	cg44028217	638	GGGGGCTGGTA AAGAGCAGGTAC TTA/GGGCAGCT TCCTTTTGAAGC GGAAGG	A	G	Pro	Pro	SILENT- CODING	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)

332	cg44028217	725	GAGTGGCTGGAT CCACGCGGTGT CTT/CJGGGCTC CAGGGGTTGGT GATGTTTT	C	Pro	Pro	SILENT- CODING	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)
333	cg43271573	1320	GGGCTGTTCTGA GTCCTGAAAGGT GTA/GJAATAAGT TACCACCACCAA GTGTCA	G	Val	Val	SILENT- CODING	oxidase	Human Gene SWISSPROT-ID:Q01740 DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (EC 1.14.13.8) (FETAL HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 1) (FMO 1) (DIMETHYLANILINE OXIDASE 1) - HOMO SAPIENS (HUMAN), 531 aa.	5.30E-293	1 (1q23)
334	cg43051423	618	ATCGCAGGTAGT GATAGCCTGAGG A/T/AJCCCCCAGT GCCAGCCTTGCT GCCTA	A	Gly	Gly	SILENT- CODING	oxygenase	Human Gene SWISSPROT-ID:P48775 TRYPTOPHAN 2,3-DIOXYGENASE (EC 1.13.11.11) (TRYPTOPHAN PYRROLASE) (TRYPTOPHANASE) (TRYPTOPHAN OXYGENASE) (TRYPTAMIN 2,3-DIOXYGENASE) (TRPO) - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	4
335	cg43051423	633	AGCCTGAGGATC CCCCAGTGCCA GC/C/TJTGCTGC CTAGCATCCTGT GCACCA	T	Lys	Lys	SILENT- CODING	oxygenase	Human Gene SWISSPROT-ID:P48775 TRYPTOPHAN 2,3-DIOXYGENASE (EC 1.13.11.11) (TRYPTOPHAN PYRROLASE) (TRYPTOPHANASE) (TRYPTOPHAN OXYGENASE) (TRYPTAMIN 2,3-DIOXYGENASE) (TRPO) - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	4

336	cg43051423	642	ATCCCCCAGTGC CAGCCTTGCTGC CTTCJAGCATCCT GTGCACCATGCA CACAT	T	C	Leu	Leu	SILENT- CODING	oxygenase	Human Gene SWISSPROT-ID:P48775 TRYPTOPHAN 2,3-DIOXYGENASE (EC 1.13.11.11) (TRYPTOPHAN PYRROLASE) (TRYPTOPHANASE) (TRYPTOPHAN OXYGENASE) (TRYPTAMIN 2,3-DIOXYGENASE) (TRPO) - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	4
337	cg43051423	648	CAGTGCCAGCCT TGCTGCCTAGCA TTC/TCTGTGCAC CATGCACACATG GTTAT	C	T	Arg	Arg	SILENT- CODING	oxygenase	Human Gene SWISSPROT-ID:P48775 TRYPTOPHAN 2,3-DIOXYGENASE (EC 1.13.11.11) (TRYPTOPHAN PYRROLASE) (TRYPTOPHANASE) (TRYPTOPHAN OXYGENASE) (TRYPTAMIN 2,3-DIOXYGENASE) (TRPO) - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	4
338	cg43972840	190	ACCAAATGAGAA TGGCTGACCTCT CIG/AIGAGCTCC TGAAGGAAGGG ACCAAGG	G	A	Ser	Ser	SILENT- CODING	oxygenase	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.60E-168 (16p13.3)	16
339	cg43254736	905	AGCAGTTGGTGT GCAGGTAGTTGA AIA/GTCGGACAT GCCTCCCGTGAA GCTGT	A	G	Asp	Asp	SILENT- CODING	peptidase	Human Gene Similar to SPTREMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	1.10E-67	
340	cg41626506	1029	TGCTGTCACAAG ACTCAAAGTCTT CIG/AIGGGAATT GCCGACTTGGAA GGCAT	G	A	Pro	Pro	SILENT- CODING	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00 (3q26.3)	3
341	cg41626506	1176	TGTTCTCCACC AAAACCAAGTCAC CIG/AITCCCGCA GAGCCTTCATCT GCTTCC	G	A	Asp	Asp	SILENT- CODING	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00 (3q26.3)	3

342	cg40084915	1911	GGACGTCCATGCG TGCGGTTCTTGT C[G/A]CGGTTCC GGGGCAACAGG GCGATGC	G	A	Arg	Arg	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q00197 RECEPTOR PROTEIN TYROSINE PHOSPHATASE HPTP-J PRECURSOR - HOMO SAPIENS (HUMAN), 1436 aa.	0.00E+00	1
343	cg43956389	4272	CAGTCTGGGA GGTCCAGCCACT GG[G/A]ACTGCA GGATCAAAATGAT CTTATAC	G	A	Val	Val	SILENT- CODING	phosphatase	Human Gene SWISSNEW-ID:Q15262 PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R- PTP- KAPPA) - HOMO SAPIENS (HUMAN), 1439 aa. [pcis:SWISSPROT- ID:Q15262 PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R-PTP- KAPPA) - HOMO SAPIENS (HUMAN), 1439 aa.	0.00E+00	6
344	cg43917453	3092	CGAGAACCTCCA CGTCAGCGAAC GC[A/G]CTGCTG GGCACCTGCAG GAGGCGGG	A	G	Ser	Ser	SILENT- CODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
345	cg43920534	4834	TTTGTTCCTTT GCAACTCTTCTA G[A/T]ATATCCAA AATGCTCTTCATC TGCT	G	A	Leu	Leu	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
346	cg43920534	4841	TCTTTGCAACT CTTCTAGATATC C[C/T]AAAAATGTC TTCATCTGCTAC ATCAA	C	T	Leu	Leu	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
347	cg43920534	4749	TCCAACATGCTT CTTCTTTACCCC A[G/A]TGAGCTG CAGCATGAAGAG GTGTCC	G	A	His	His	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12

348	cg43920534	4785	CATGAAGAGGTG TCCAGCCATCAT A/GJCTTTTAA ATTAAACATCATA GCCTG	A	G	Asp	Asp	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
349	cg43920534	4836	CCTGTATTAAAA GTTTTAAACCTTC [T/C]GTATACCCCT TTGGCCGCTGCC ACGT	T	C	Thr	Thr	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
350	cg43920534	4842	TAAAAGTTTTAA AACTTCTGTATA C/GJCTTTGGCC GCTGCCACGTG GAGTG	C	G	Gly	Gly	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
351	cg43920534	4851	TAAAACCTTCTGT ATACCCCTTTGGC C/AJGCTGCCACG TGGAGTGCTGTG CCTC	C	A	Ala	Ala	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
352	cg43920534	4857	CTTCTGTATACC CTTTGGCCGCTG C/C/AJACGTGGA GTGCTGTGCCTC CGGATT	C	A	Val	Val	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
353	cg43920534	4863	TATACCCCTTTGG CCGCTGCCACGT G/G/AJAGTGCTG TGCCTCCGGATT TTGCAT	G	A	Leu	Leu	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12

354	cg43920534	4872	TGGCCGCTGCC ACGTGGAGTGCT GTG/AJCCTCCG GATTTGCATGC CGGACAT	G	A	Gly	Gly	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
355	cg43920534	4878	CTGCCACGTGGA GTGCTGTGCCTC CIG/AIGATTTTGC ATGCCGGACATC ATTTA	G	A	Ser	Ser	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
356	cg43321833	2271	CTAACACTGTGG AACCAGAGAAGC A/AJGGGGGAGA ACACCATGAAGA TGACIG	A	G	Gln	Gln	SILENT- CODING	phosphat ase	Human Gene TREMBLNEW- ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment).	0.00E+00	20
357	cg43326080	1070	CATCATCTACAT TGGAGAGCTTCA C/AJTCGGGTGG CATCATAGGGCA ATATAI	A	T	Arg	Arg	SILENT- CODING	phosphat ase	Human Gene SWISSPROT-ID:P23487 PROTEIN-TYROSINE PHOSPHATASE BETA PRECURSOR (EC 3.1.3.48) (R- PTP-BETA) - HOMO SAPIENS (HUMAN), 1997 aa.	0.00E+00	12 (12q15)
358	cg42548845	1611	TGAAAAAGCTCA TCGAAGAGAAGG A/C/TJTTTCAAT GCTGTATGCATA TGATC	C	T	Asp	Asp	SILENT- CODING	phosphat ase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	0.00E+00	
359	cg43918944	997	TCCGGACACTTC CTCCAAGTGATA A/C/TJCCAGACTT TGACCCCGGAAGA GGATG	C	T	Asn	Asn	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
360	cg43918944	1003	CACCTTCCTCCAA GTGATAACCCAG A/C/TJTTTGACCC GGAAGAGGATG AGCCCA	C	T	Asp	Asp	SILENT- CODING	phosphat ase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1

361	cg43918944	1009	CTCCAAGTGATA ACCCAGACTTTG A[C/T]CCGGAAG AGGATGAGCCCA CACTTG	C	T	Asp	Asp	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
362	cg43918944	1012	CAAGTGATAACC CAGACTTTGACC C[G/A]GAAGAGG ATGAGCCACAC TTGAGG	G	A	Pro	Pro	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
363	cg43918944	1024	CAGACTTTGACC CGGAAGAGGAT GA[G/A]CCACACA CTTGAGGCCTCT TGGCCTC	G	A	Glu	Glu	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
364	cg43918944	1030	TTGACCCGGAAG AGGATGAGCCCA C[A/G]CTTGAGG CCTCTTGGCCTC ACATAC	A	G	Thr	Thr	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
365	cg43918944	1084	TGGTGATGAAT TCTTCTTGAGAT T[C/T]TTGGAGAG TCCTGATTTCCA GCCCA	C	T	Phe	Phe	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
366	cg43918944	1108	TCTTGGAGAGTC CTGATTTCCAGC C[C/T]AGCATTGC AAAGCGATACAT TGACC	C	T	Pro	Pro	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
367	cg43918944	976	AAATGATCAGTG CTAACATCTTCC G[G/T]ACACTTCC TCCAAAGTGATAA CCCAG	G	T	Arg	Arg	SILENT- CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1

368	cg43988504	819	CTTCTGTCTGGC TGATACCTGCCT C[T/C]TGCTGATG GACAAGAGGAAA GACCC	T	C	Leu	Leu	SILENT- CODING	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.lpcis:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
369	cg43988504	900	AGAAATGAGGAA GTTTCGGATGGG G[C/T]TGATCCAG ACAGCCGACCA GCTGCG	C	T	Leu	Leu	SILENT- CODING	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.lpcis:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
370	cg43933809	446	CAAATAATCTCA GTAAATCTGTAT AT[C/T]GTCCATG AATATCTCCACA AATTT	T	C	Gln	Gln	SILENT- CODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS.MUSCULUS (MOUSE), 327 aa.	1.60E-181	2 (2p23)
371	cg43269274	1510	CAGCCTCACAGT GGACCAGGACC TT[G/T]CCTCCCT TTCCCTGACAC AGTCAA	G	T	Gly	Gly	SILENT- CODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.20E-151	10
372	cg43269274	1674	ACATTTCAGCAGG GCTGTGATGTGC A[A/G]GTTGGCG AGGAACTCGCAC TTGGAT	A	G	Leu	Leu	SILENT- CODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.20E-151	10

373	cg42688448	2412	TTTAAAGTAAAGT AGTGGACAGCCT [G/A]GCCCCATC CATTACTAATGTT TTAG	G	A	Leu	Leu	SILENT- CODING	phosphor ylase	Human Gene SWISSNEW-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa. pcds:SWISSPROT-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa.	0.00E+00	16
374	cg42688448	1787	GAGGAGCACCT GTGGGGTTGC AGG[A/G]CGAGG CGCCATGGTAGT CTGAGGCT	A	G	Arg	Arg	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
375	cg42688448	1790	GAGCACCTGTG GGGGTTGCAGG ACG[A/G]GGCGC CATGGTAGTCTG AGGCTGGG	A	G	Pro	Pro	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
376	cg42688448	1793	CACCTGTGGGG GTTGCAGGACGA GG[C/T]GCCATG GTAGTCTGAGGC TGGGCAT	C	T	Ala	Ala	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
377	cg42688448	1826	TAGTCTGAGGCT GGGCATGGGCA TG[G/C]GCCTGC ATCTGGGCCAAG GCCTGCT	G	C	Ala	Ala	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
378	cg42688448	1856	GCATCTGGGCCA AGGCTGCTGA GG[A/G]ATCATT ACAACTGCCCAT TCTCAC	A	G	Ile	Ile	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20

379	cg42688448	1940	AGTTCTGGATGT TGGTCGGTTCT G[A/C]GGCGGCT GCGGCAAGCGC GGGGCCA	A	C	Pro	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
380	cg42688448	1954	GTCGGGTTCTGA GGCGGCTGCGG CA[A/G]GCGCGG GGCCAGCACGG TGGGCGTC	A	G	Leu	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
381	cg43988623	801	TCTTGAAGATG AACTGCAGCGTA T[A/C]AAACTAAA AGGCACCAATTGA AGTGT	A	C	Ile	SILENT- CODING	polymera se	Human Gene SWISSNEW-ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa. Ipcis:SWISSPROT- ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.	7.00E-199	
382	cg43311989	248	ACTTCGAATAAA GTTGTTCCAATG A[G/A]GACTGCAT AGTTTCCAAATA ACCAAG	G	A	Ser	SILENT- CODING	polymera se	Human Gene SPTREMBL-ID:O00419 MITOCHONDRIAL DNA POLYMERASE ACCESSORY SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 372 aa.	1.90E-197	
383	cg43993893	502	ACTCATTTGATTG TGAAACCCCTTTT CTTCJAGGGCAT GAGCCCTCATAT TCTTAT	T	C	Leu	SILENT- CODING	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa. Ipcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5.00E-178 (8p11.2)	8
384	cg43993893	679	CCATGAACCTTG TCTCACCCCTTTG A[C/A]AGGGTATC TGTGATAAAATG AACCT	C	A	Leu	SILENT- CODING	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa. Ipcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5.00E-178 (8p11.2)	8

385	cg43993893	877	AATCCACATTTTT AACTTCATTAGI T/AACAATATCTT GCATTTGTAACA TCT	T	A	Val	Val	SILENT- CODING	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa. pcls:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5.00E-178	8 (8p11.2)
386	cg43916712	4150	TGTGAGCAATGA ATTCATCATGAA G[G/A]ACTGAGG AATTGGCATCAA TCTGAA	G	A	Val	Val	SILENT- CODING	polymera se	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.20E-148	
387	cg42876552	418	CTTTCTGCAAAAT CAATAGGCACAG A[T/G]ATGCGACC TGTTTAGGATG AACAC	T	G	Ile	Ile	SILENT- CODING	polymera se	Human Gene Similar to SWISSPROT- ID:Q24317 DNA PRIMASE SMALL SUBUNIT (EC 2.7.7.-) (DNA PRIMASE 50 KD SUBUNIT) (DNA POLYMERASE SUBUNIT A) (DPR150) - DROSOPHILA MELANOGASTER (FRUIT FLY), 438 aa.	2.20E-88	12 (12q13)
388	cg43948227	366	TCGAATTTTACA GTTTTCTTACTG C[A/G]TCATCAAT GTCAGAAATCTG TTCCT	A	G	Asp	Asp	SILENT- CODING	polymera se	Human Gene Similar to SWISSNEW- ID:P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) - HOMO SAPIENS (HUMAN), 126 aa. pcls:SWISSPROT-ID:P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) - HOMO SAPIENS (HUMAN), 126 aa.	5.40E-62	5
389	cg42534568	612	AGCGGTCCACA TCAACATCTCCG G[G/C]CTGCGCT TTGAGACGCAGC TGGGCA	G	C	Gly	Gly	SILENT- CODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)

390	cg42837321	1388	ATATGCACCCAG TGACCATAGGGG G/C/GAAGATTGT GGGATCTCTCTG TGCCA	C	G	Gly	Gly	SILENT- CODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
391	cg42837321	353	AGCGCGTGGTC ATCAACATCTCC GG/G/C/CTGCGC TTCGAGACGCAG CTGAAGA	G	C	Gly	Gly	SILENT- CODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
392	cg43331104	878	CCTTCTTCATCG TGGAAACGCTGT G/T/C/ATCATCTG GTTCTCCTTCGA GCTGG	T	C	Cys	Cys	SILENT- CODING	potassiu m_chann el	Human Gene SWISSPROT-ID:Q09470 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUKI) (HBK1) - HOMO SAPIENS (HUMAN), 495 aa.	5.60E-266	12
393	cg43992375	3210	GATTCACCTGGAT TTTGGCAGACCC A/G/C/TTGGGG CTCGGGATGTCT GCACAG	A	G	Leu	Leu	SILENT- CODING	potassiu m_chann el	Human Gene SPTREMBL-ID:Q16547 POTASSIUM CHANNEL BETA3 SUBUNIT - HOMO SAPIENS (HUMAN), 408 aa.	1.30E-218	3
394	cg43951366	505	TTCGAAATGCAA TTATGAGTTATG T/G/C/TTGACATC CAGATCACATTT GATTG	G	C	Val	Val	SILENT- CODING	prostagla ndin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa. pcis:SPTREMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa.	0.00E+00	1 (1q25.2)

395	cg43986296	1743	ACTCATCCCCGA CATCCCTGATGA C/A/CAGCCTGTA GGTCCCTCGGG CTCTCT	A	C	Leu	Leu	SILENT- CODING	protease	Human Gene SPTREMBL-ID:Q62849 SERINE PROTEINASE RPC7 PRECURSOR - RATTUS NORVEGICUS (RAT), 783 aa.	4.60E-223	
396	cg43982119	1306	GCTTGGTTTTTT CTTTTGA CTGG TTCGATCCACG CAGATGGTATTT TCAA	T	C	Arg	Arg	SILENT- CODING	protease	Human Gene SWISSPROT-ID:P20807 CALPAIN P94, LARGE (CATALYTIC) SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (P94 PROTEIN) (MUSCLE- SPECIFIC CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE SUBUNIT) - HOMO SAPIENS (HUMAN), 821 aa.	5.70E-161	15
397	cg43306871	1105	GCTCGCCCTGAA GAAGCAGCAGG TG[G]ATCATCCC CTACTCGAGCCC ACAGTG	G	A	Asp	Asp	SILENT- CODING	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.lpcis:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19
398	cg43923853	2273	CAGACCGAGATG TCATTCCAGTGC TTTCTTATGAAA ATTCTTATTATTA ATTA	T	C	Lys	Lys	SILENT- CODING	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA- 1) - HOMO SAPIENS (HUMAN), 277 aa.lpcis:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4

399	cg43074055	916	CCCTCTACGTGGC ACTGGATCCGTT C/C/TACGCTGC GCCGTGTGGAG GCCAAGG	T	Ser	SILENT- CODING	protease	Human Gene Homologous to SWISSPROT-ID:P24158 MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3) (PR3) (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN) - HOMO SAPIENS (HUMAN), 256 aa.	5.70E-138	19 (19p13.3)
400	cg43967243	387	TCTCTGCTTCTG TAAGAATCCTGA A/T/CJT TAGGATT TTCAACTGTCAC TACTC	C	Lys	SILENT- CODING	protease	Human Gene Homologous to SWISSNEW-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) (P27K) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa. pcds:SWISSPROT-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa	6.40E-130	

401	cg43967243	489	ATGTAATTGCAG TTTCCACTGTCT GTT/CJTCAAATGT CCAATCAAATTT CTTCT	T	C	Glu	Glu	SILENT- CODING	protease	Human Gene Homologous to SWISSNEW-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) (P27K) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.lpcis:SWISSPROT-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa	6.40E-130	
402	cg43930253	972	CCACATATATAA ACCATGTCGTTT C/C/TJGTGGCTG GGTGGGGCATC AGTGATG	C	T	Ser	Ser	SILENT- CODING	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20
403	cg42914280	589	GCAAGCCCAGG TGTGGAGTTCTT GA/C/TJGTGGTC ACTTCAGAACCT TTCCTG	C	T	Asp	Asp	SILENT- CODING	protease	Human Gene Similar to SWISSNEW- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.lpcis:SWISSPROT- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.30E-63	11 (11q23)

404	cg43920929	1459	GATTGTCAATCA TATCCCTGGTTT C/G/TTTTTTAAC CCATGCATTGAT GGAAT	A	G	Asn	Asn	SILENT- CODING	protease nhib	Human Gene SWISSPROT-ID:P07093 GLIA DERIVED NEXIN PRECURSOR (GDN) (PROTEASE NEXIN I) (PN-1) (PROTEASE INHIBITOR 7) - HOMO SAPIENS (HUMAN), 398 aa.	1.20E-208	2
405	cg43920929	1705	TTACGCCGTATC TCATCACCATGG C/G/AJAGCTGCTT CTTGGTCTCGCC GTCCG	G	A	Leu	Leu	SILENT- CODING	protease nhib	Human Gene SWISSPROT-ID:P07093 GLIA DERIVED NEXIN PRECURSOR (GDN) (PROTEASE NEXIN I) (PN-1) (PROTEASE INHIBITOR 7) - HOMO SAPIENS (HUMAN), 398 aa.	1.20E-208	2
406	cg43268468	512	GCAGGGACTTG GTGACTTCGCCT TC[G/A]TAACTCA GCTTCAGCTTGG GGACAG	G	A	Tyr	Tyr	SILENT- CODING	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.60E-188 (17p13.3)	17
407	cg43059041	1182	TCACCATCTCTG GAGTCTATGACC TT[C/G]GGAGATGT GCTGGAGGAAAT GGGCA	T	C	Leu	Leu	SILENT- CODING	protease nhib	Human Gene Similar to SWISSPROT- ID:P17475 ALPHA-1-ANTIPROTEINASE PRECURSOR (ALPHA-1-ANTITRYPSIN) (ALPHA-1- PROTEINASE INHIBITOR) - RATTUS NORVEGICUS (RAT), 411 aa.	4.40E-83 (14q32.1)	14
408	cg43059041	1440	ACTTCACCTGGA GCAGCCTTTTCC T[G/A]GCGAGGG TTATGAACCCAG TGTAAG	G	A	Leu	Leu	SILENT- CODING	protease nhib	Human Gene Similar to SWISSPROT- ID:P17475 ALPHA-1-ANTIPROTEINASE PRECURSOR (ALPHA-1-ANTITRYPSIN) (ALPHA-1- PROTEINASE INHIBITOR) - RATTUS NORVEGICUS (RAT), 411 aa.	4.40E-83 (14q32.1)	14
409	cg43969711	1750	AGAGAAATTCCT TTCTTTGGGAT C[C/T]TTTATGTA AGTGTCATAAG AAGAC	C	T	Lys	Lys	SILENT- CODING	reductas e	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208 2 (2p25)	
410	cg43969711	1884	AGTGCTGAATGT CCTTGGAGAGGT C[C/A]ACCTCCTC GGCGGTCCAAAA GGAAG	C	A	Val	Val	SILENT- CODING	reductas e	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208 2 (2p25)	

411	cg43969711	2158	GCTCCGTGGGC TCCTGGAAGATC CTT/CJCTCGCG GTCCTGCTGGCC AGGACGC	T	C	Arg	Arg	SILENT- CODING	reductas e	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208	2 (2p25)
412	cg43941472	701	TCATTGAGTGTG CCGACTCTGCCC ATT/CJGGCCTGAA GGCCACATCAT CTCTG	T	C	His	His	SILENT- CODING	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
413	cg43987538	1820	CTGATCGCAATT TCAGGACTTCTG GTC/TCCACCAAA TTCAAAACTCT AACAG	C	T	Gly	Gly	SILENT- CODING	reductas e	Human Gene SWISSPROT-ID:Q08257 QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN) - HOMO SAPIENS (HUMAN), 329 aa.	1.1E-171	1 (1p31)
414	cg43286949	355	AATATCTGTTTC GTTTTAGACCAG GTC/TCCCTTTTC TTCAATCCATGA CAGTG	C	T	Gly	Gly	SILENT- CODING	reductas e	Human Gene SWISSNEW-ID:P53004 BILVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILVERDIN-X ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa. pcls: SWISSPROT-ID:P53004 BILVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILVERDIN-X ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.	1.3E-152	7
415	cg43336298	1175	CCATCTCTACAT ATAACAGAACCG GTC/CJCCACTTCC CCCAGGCCAC CCCCAG	T	C	Gly	Gly	SILENT- CODING	reductas e	Human Gene Homologous to TREMBLINW-ID:G2947100 15- OXOPROSTAGLANDIN 13- REDUCTASE - SUS SCROFA (PIG), 329 aa.	6.70E-146	
416	cg43948290	715	TAATAGGTTTGG GCTTGTTGTTAA C/A/GGGCATGTT GATAAACATCCA TTCAG	A	G	Thr	Thr	SILENT- CODING	reductas e	Human Gene Homologous to SWISSPROT-ID:P18405 3-OXO-5- ALPHA-STEROID 4-DEHYDROGENASE 1 (EC 1.3.99.5) (STEROID 5-ALPHA- REDUCTASE 1) (SR TYPE 1) - HOMO SAPIENS (HUMAN), 259 aa.	2.90E-141	5 (5p15)

417	cg42717608	109	CGCAGCTTAATG TGGCCTTTTCCC G[G/T]GAGCAGG CCCACAAGGTCT ATGTCC	G	T	Arg	Arg	SILENT- CODING	reductase	Human Gene Similar to SWISSNEW- ID:P37040 NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) - MUS MUSCULUS (MOUSE), 677 aa. pcis:SWISSPROT-ID:P37040 NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) - MUS MUSCULUS (MOUSE), 677 aa.	1.80E-51	
418	cg43257152	622	CTACCAAGACTT TGAGAAATCACTA C[A/G]AGAAAAAC TCCTTGTGGTGA AGTT	A	G	Thr	Thr	SILENT- CODING	ribosomal prot	Human Gene Similar to SWISSPROT- ID:P17075 40S RIBOSOMAL PROTEIN S20 - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 119 aa.	8.2E-59	3
419	cg44937448	365	TCCTGTTACCA ACCGCACAAAGG A[G/A]GAGGTGA ATGAGTGGTTCA CGAAAT	G	A	Glu	Glu	SILENT- CODING	ribosomal prot	Human Gene Similar to SPTREMBL- ID:Q19302 SIMILAR TO 60S ACIDIC RIBOSOMAL PROTEIN PO - CAENORHABDITIS ELEGANS, 220 aa.	5.3E-55	7
420	cg43255045	5515	GCGAGGAGGAA CAGCTACGCCAG GA[A/G]AGGGAA GAACAGCAGCTG CGCCCC	A	G	Glu	Glu	SILENT- CODING	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0	1
421	cg43927378	843	TCCTGGGTGCTG GCCCTGTGCTG GA[G/A]GCTTTTG GAAATGCCAAGA CAGCCC	G	A	Glu	Glu	SILENT- CODING	struct	Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa.	0	2
422	cg44033566	3341	AGGCCTGGCTCT CCATCACCCAGA A[A/G]GCTGTGG CCTCTGAGGACA TGCCCC	A	G	Lys	Lys	SILENT- CODING	struct	Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa. pcis:SWISSPROT- ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.	0	14 (14q22)

423	cg43131005	8940	ACAGATATCTCT TTAAGGAAGTTG C[A/G]GGGCCAA CAGAAATGTGTG ACCAGA	A	G	Ala	Ala	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P46939 UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP) - HOMO SAPIENS (HUMAN), 3433 aa.	0	
424	cg43131005	8946	ATCTCTTTAAGG AAGTTGCAGGGC C[A/G]ACAGAAAT GTGTGACCAGAG GCAGC	A	G	Pro	Pro	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P46939 UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP) - HOMO SAPIENS (HUMAN), 3433 aa.	0	
425	cg43249606	108	ACACACCTGGAA GCCATTGAGAGC A[G/A]CTGGAGAT GGAGTGGCAGC TGGAGT	G	A	Ser	Ser	SILENT- CODING	struct	Human Gene SWISSNEW-ID:Q01082 SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1) - HOMO SAPIENS (HUMAN), 2364 aa. pcds:SWISSPROT-ID:Q01082 SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1) - HOMO SAPIENS (HUMAN), 2364 aa.	0	
426	cg44918439	1208	AAAAGGAAAAGG AAAGAATAGAAC G[C/T]GTGAAGG AAGAGCTAATGG AACGTC	C	T	Arg	Arg	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P35241 RADIXIN - HOMO SAPIENS (HUMAN), 583 aa.	9.3e-312	11 (11q23)
427	cg44918439	1508	CCAAGAAGAAAA AGGAAGAGGAA GC[T/A]ACTGAGT GGCAACACAAAG CTTTG	T	A	Ala	Ala	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P35241 RADIXIN - HOMO SAPIENS (HUMAN), 583 aa.	9.3e-312	11 (11q23)
428	cg43980812	870	GAAGCTGGGCC CGGCATGTAGAA CA[C/T]ACAAAGC AGCCACACGTGAA AGACGC	C	T	Val	Val	SILENT- CODING	struct	Human Gene SWISSNEW-ID:Q15654 THYROID RECEPTOR INTERACTING PROTEIN 6 (TRIP6) (OPA- INTERACTING PROTEIN 1) (ZYXIN RELATED PROTEIN 1) (ZRP-1) - HOMO SAPIENS (HUMAN), 476 aa.	2.9E-272	7

429	cg43987609	1752	CAGTCTTTTCA AATCTCTTTGCA A[G/A]CGACGTC CAAAGTCCCTGA ACATGG	G	A	Arg	Arg	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P32391 ACTIN-LIKE PROTEIN 3 (ACTIN-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 418 aa.	1.1E-226	2
430	cg43987609	1785	CAAAGTCCCTGA ACATGGTTGAAC CTTATCCAGAGA GGACAATATTCT TGTAGA	T	A	Gly	Gly	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P32391 ACTIN-LIKE PROTEIN 3 (ACTIN-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 418 aa.	1.1E-226	2
431	cg11751474	312	ACGACACCCATC AGCACCACCACC A[C/T]GGTGACC CCAAACCCCAACA CCCACT	C	T	His	His	SILENT- CODING	struct	Human Gene SPTREMBL-ID:Q99322 MUCIN CORE POLYPEPTIDE, TRACHEAL - HOMO SAPIENS (HUMAN), 295 aa (fragment).	3.6E-189	
432	cg43916919	421	CAGATATCAGCA GTTCAAGGGCAA AT[G/G]GGCTGG AGTCAGCCACCT TGGTCA	T	G	Pro	Pro	SILENT- CODING	struct	Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa. [pcis:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa.	4.30E-188 2 (2cen)	
433	cg43304066	2468	TTTGCTTCCGAG CTTCTTCCCCCG C[G/A]GAGCTGA GGTTCCTTAGGC AACCTG	G	A	Ser	Ser	SILENT- CODING	struct	Human Gene SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.20E-186	2
434	cg43304066	2495	AGCTGAGGTTCC TTAGGCAACCTG T[C/T]GTGTTACG CAGAACTAGTGA AGTCT	C	T	Thr	Thr	SILENT- CODING	struct	Human Gene SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.20E-186	2
435	cg43948677	478	TCATGAGTAACC AGCAGTACTACC A[A/G]GCCCTGA GCAGCAGCTCCA TCATGA	A	G	Gln	Gln	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P28289 TROPOMODULIN - HOMO SAPIENS (HUMAN), 359 aa.	2.40E-185 (9q22.2)	9

436	cg43949677	802	TCAAGGAGAAACA AGGTGTTGAAGA C/C/A]CTGAATGT GGAATCCAACCTT CATT	C	A	Thr	Thr	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P28289 TROPOMODULIN - HOMO SAPIENS (HUMAN), 359 aa.	2.40E-185	9 (9q22.2)
437	cg43949677	865	TTCTGCGCCTGG TAGAAGCCCTCC C/C/A]CACACAC TTCTCTGGTCGA GCTGA	C	A	Pro	Pro	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P28289 TROPOMODULIN - HOMO SAPIENS (HUMAN), 359 aa.	2.40E-185	9 (9q22.2)
438	cg43962437	1215	ACGGCGATGCA GGCTACGGGCA GGG[G/C]CCCCGG CGGTACGGGC CCCAGGATT	G	C	Gly	Gly	SILENT- CODING	struct	Human Gene SWISSNEW-ID:P08247 SYNAPTOPHYISIN (MAJOR SYNAPTIC VESICLE PROTEIN P38) - HOMO SAPIENS (HUMAN), 313 aa.lpcds:SWISSPROT-ID:P08247 SYNAPTOPHYISIN (MAJOR SYNAPTIC VESICLE PROTEIN P38) - HOMO SAPIENS (HUMAN), 313 aa.lpcds:TREMBLNEW-ID:G2707601 SYNAPTOPHYISIN - HOMO SAPIENS (HUMAN), 313 aa.	4.80E-173	X (Xp11.2 3)
439	cg43956325	1173	CCTTAACAATCA GCTGCCGCTGT GC/A/G]TTTGACC TCTCAGTCAGAA TGCTGA	A	G	Asn	Asn	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
440	cg43956325	1181	ATCAGCTGCCGC TGTCATTTGAC C/T/G]CTCAGTCA GAATGCTGATGA GCATT	T	G	Arg	Arg	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)

441	cg43956325	1185	GCTGCCGCTGT GCATTTGACCTC TCACJGTCAGAA TGCTGATGAGCA TTTTCT	A	C	Thr	Thr	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
442	cg43956325	1212	TCAGAATGCTGA TGAGCATTTTCT C[A/G]TCAGTTCC AATTCCTCTGAT TGCTT	A	G	Asp	Asp	SILENT- CODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
443	cg43985529	889	GCTCCATGGCC GTCTGCAAGGG CGC[C/G]GGCTC CTGGGCTGGGC TTACGAGAC	C	G	Pro	Pro	SILENT- CODING	struct	Human Gene SPTREMBL-ID:Q95264 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA- E - SUS SCROFA (PIG), 334 aa (fragment).	1.00E-163	
444	cg43985529	895	TGGCCGCTGCA AGGGCCCGGC TC[C/T]TGGGCTG GGCTTACGAGAC TGTTT	C	T	Gln	Gln	SILENT- CODING	struct	Human Gene SPTREMBL-ID:Q95264 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA- E - SUS SCROFA (PIG), 334 aa (fragment).	1.00E-163	
445	cg43274709	941	GAAGATTAGAAG TGAGATTCCAAG G[G/A]GAATGGG GGACAATATGTG ATGACG	G	A	Gly	Gly	SILENT- CODING	struct	Human Gene Homologous to SPTREMBL-ID:Q28910 MUCIN - BOS TAURUS (BOVINE), 600 aa (fragment).	3.90E-106	12
446	cg43051155	1016	CGTGCCGAAGCT CAGCACCCATGA C[A/C]GTGCCATT GCCCTCCTTGTC AAAGA	A	C	Thr	Thr	SILENT- CODING	struct	Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 196 aa.	5.30E-103	17

447	cg42731508	1386	ACGGCTTCGTCA GCGCCGCCGAG CT[G]CGACAC GTCATGACCCGG CTGGGGG	G	A	Leu	Leu	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P27482 CALMODULIN-RELATED PROTEIN NB-1 (CALMODULIN-LIKE PROTEIN) (CLP) - HOMO SAPIENS (HUMAN), 148 aa.	8.10E-75	2
448	cg44014373	559	ATTCATTGTTCT GCCGCTCCAGTT C[G]ATGGCGTA GCTGCGTCAGTT CCTCCT	G	A	His	His	SILENT- CODING	struct	Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa.	6.10E-70	17
449	cg43936426	1293	GCTCCAGGTTCC GGGGCAGGGCC GA[G]GGGACC TCTTCCAACTGG TTCTTCT	G	A	Pro	Pro	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
450	cg43933305	1781	ACACCTGGTTCC TGTGGCCCTTCA C[G]ACGGAAGG AGTCGTTCTCCC CCGTCT	G	A	Arg	Arg	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P46880 ACTIN INTERACTING PROTEIN 1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 615 aa.	3.50E-66	4
451	cg42522566	256	TAGCAGGGGGT CGGTTTGGCCAG GT[G]CACAGG TGTACAGAGAGG TCTACAG	G	C	Val	Val	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6.00E-55	
452	cg42522566	286	GGGTACAGAGA GGTCTACAGGCC TT[C]GCACTGGC AGCCAAGATCAT CAAAG	T	C	Leu	Leu	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6.00E-55	
453	cg42522566	295	AGAGGTCTACAG GCCTTGCACTGG C[A/T]GCCAAGAT CATCAAAGTGAA GAACG	A	T	Ala	Ala	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6.00E-55	

454	cg43977322	2051	CCACATCGATGC A TCTCGGCAAAGG C/A/GCTCGCCT CGGCCCGGAGG CCTGGCT	G	Ser	Ser	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa.	1.50E-52	16
455	cg43918310	227	TGAGTTCCAGC C AGCAGAAGCAG CC/C/TTGCAATCC CACCCCTCAGC TTCAGC	T	Pro	Pro	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P22528 CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) - HOMO SAPIENS (HUMAN), 89 aa.	4.00E-50	1 (1q21)
456	cg43918310	362	CTGAGCCCTGCC T ACCCCAAAGTGC CT/C/GAGCCCT GCCAGCCCAAG GTTCAG	C	Pro	Pro	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P22528 CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) - HOMO SAPIENS (HUMAN), 89 aa.	4.00E-50	1 (1q21)
457	cg43248320	2084	TGGTGGGCTTCC C TGCACTCCTGGA C/C/G/AACCTCC GGCTGCAGACA CTGCCCC	G	Thr	Thr	SILENT- CODING	sulfotran- sferase	Human Gene SWISSPROT-ID:P52848 HEPARAN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARAN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N-DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 882 aa.	0.00E+00	5 (5q32)
458	cg4399876	538	TGGGTATACAG G CACTCAGTGAAA C/G/C/GAGAGTC CACGTTATTCT CCTCCC	C	Thr	Thr	SILENT- CODING	sulfotran- sferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157	2 (2q12)
459	cg43987111	1817	AGGAGTCTGAGA G ACTTCGTGTATT T/G/C/CCCCACAA GGCAATAGAG CAGGTCT	C	Gly	Gly	SILENT- CODING	synthase	Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP-- AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa.	0.00E+00	18 (1p34.1)

460	cg43971304	1192	TCTCCAACAAGG GTGCTGACGTCT T[C/T]CTGGAGG CATTGGCTCGGC TCAACT	C	T	Phe	Phe	SILENT- CODING	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
461	cg43971304	385	TGGGGCCGTAC ACGGAGCAGGG CGT[G/C]AGGAC CCAGGTGGAAC GCTGGAGG	G	C	Val	Val	SILENT- CODING	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
462	cg43948262	1222	GTCTTCCTGCT GCAACCATGAGA A[G/A]ACCCCTGG GGATCCTCCAGG TCTGGG	G	A	Val	Val	SILENT- CODING	synthase	Human Gene SWISSPROT-ID:P22102 PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (EC 6.3.4.13) (GARS) (GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE) / PHOSPHORIBOSYLFORMYLGLYCINA MINE CYCLO-LIGASE (EC 6.3.3.1) (AIRS) (PHOSPHORIBOSYL- AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) / PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2) (GART) (GAR TRANSFORMYLASE) (5- PHOSPHORIBOSYLGLYCINAMIDE TRANSFORMYLASE) - HOMO SAPIENS (HUMAN), 1010 aa.	0.00E+00	21 (21q22.1)
463	cg43918661	587	CTCTTTCTGGTC TTTGCTTTTGCAT [G/A]ATGTCCTGG AAGTTCTTCAGC AGTC	G	A	Ile	Ile	SILENT- CODING	synthase	Human Gene SWISSPROT-ID:P13196 5- AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA- AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-H) - HOMO SAPIENS (HUMAN), 640 aa.	7.50E-173	3 (3p21.1)

464	cg43953338	1430	ATACTTTGATGG GTCTTCGTTACT GCTTAAAGGAGA GAGGAGCTTTAA CTGTGG	C	T	Cys	Cys	SILENT- CODING	synthase	Human Gene Homologous to SWISSPROT-ID:P44708 GLUCOSAMINE-FRUCTOSE-6- PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE- 6- PHOSPHATE AMIDOTRANSFERASE) (GFAT) (L- GLUTAMINE-D-FRUCTOSE-6- PHOSPHATE AMIDOTRANSFERASE) (GLUCOSAMINE-6-PHOSPHATE SYNTHASE) - HAEMOPHILUS INFLUENZAE_609.aa.	3.10E-107	2 (2p13)
465	cg42721903	326	ACATCACGAAAA GGGAAGAAATCT CTTCGCGCTGA CGGCCAACCTCA TGAATT	T	C	Ser	Ser	SILENT- CODING	synthase	Human Gene Similar to SWISSPROT- ID:Q06847 ATP SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN PRECURSOR, MITOCHONDRIAL (EC 3.6.1.34) (OSCP) - RATTUS NORVEGICUS (RAT), 213 aa.	7.40E-79	
466	cg42721903	389	ATGGTCGCCCTAG GCAACACCCAG GGCTTGTCTCT CTGCCCTTCTCCA CCATCA	C	T	Gly	Gly	SILENT- CODING	synthase	Human Gene Similar to SWISSPROT- ID:Q06847 ATP SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN PRECURSOR, MITOCHONDRIAL (EC 3.6.1.34) (OSCP) - RATTUS NORVEGICUS (RAT), 213 aa.	7.40E-79	
467	cg43933068	695	ATTGATCAGAT GACCATTGAGGA CTTCGTAATGAA GCTTCCCGAGAA ACCAA	T	C	Leu	Leu	SILENT- CODING	synthase	Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa.	1.90E-75	12

468	cg43968419	606	AGCATCGGCTGCT GCCTGGTGGCC ACITC/GATGGG GCCTTTCCATG GATGGCG	C	Thr	Thr	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P53556 8-AMINO-7- OXONANOATE SYNTHASE (EC 2.3.1.47) (7-KETO-8-AMINO- PELARGONIC ACID SYNTHETASE) (7- KAP SYNTHETASE) (L-ALANINE-- PIMELYL COA LIGASE) - BACILLUS SUBTILIS, 389 aa. pcis:SWISSPROT- ID:P53556 8-AMINO-7- OXONANOATE SYNTHASE (EC 2.3.1.47) (7-KETO-8-AMINO- PELARGONIC ACID SYNTHETASE) (7- KAP SYNTHETASE) (L-ALANINE-- PIMELYL COA LIGASE) - BACILLUS SUBTILIS, 389 aa.	9.90E-70	
469	cg43064068	1466	GAGAGGTGGTG AAGGCATTTGTG GTIC/AICTGGCCT CGCAGTTCCTGT CCCATG	A	Val	Val	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. pcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.40E-65	
470	cg44017251	1301	ACACACAGCGG CTGGAGTGCATC GAC/TJAATGACG AGTGGCGCCGAT GAGGAAC	C	Asp	Asp	SILENT- CODING	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
471	cg43925970	1694	CTATGCACAGAG CACATAAGGTGA A/GA/GTGGTGA CTCCCAGAGAAG CGACCT	G	Thr	Thr	SILENT- CODING	tm7	Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	9

472	cg43925970	1937	TGATGCCGGTCC CGAAGATCACCA C/A/GJGACAGAC ACATGACAGCAT AGGCTC	A	G	Ser	Silent- Coding	tm7	Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	9
473	cg43925970	1952	AGATCACACAG ACAGACACATGA C/A/CJGCATAGG CTCCATAGGACT CCTGGG	A	C	Ala	Silent- Coding	tm7	Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	9
474	cg43925970	1955	TCACCACAGACA GACACATGACAG C/A/GJTAGGCTC CATAGGACTCCT GGGTCA	A	G	Tyr	Silent- Coding	tm7	Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	9
475	cg36988276	638	TTCAACAAGATTC ATTCTCTCCAAA A/A/GJGTTTACT TGACATTCAAGA TAACA	A	G	Lys	Silent- Coding	tm7	Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa.	0.00E+00	2 (2p21)
476	cg43275892	1359	GAACACAGCAGCT ACTAGGGAGAAG T/C/TJTGCAAGAT GTCAAGGGCCAA GAAGT	C	T	Leu	Silent- Coding	tm7	Human Gene SWISSPROT-ID:Q99572 P2X PURINOCEPTOR 7 (ATP RECEPTOR) (P2X7) (PURINERGIC RECEPTOR) (P2Z RECEPTOR) - HOMO SAPIENS (HUMAN), 595 aa.	0.00E+00	
477	cg40358719	1284	TGGCCGTCCTCT ACTGCTTCCTCA A/C/TJGGGAGG TGCAGCTGGAG GTTCAGA	C	T	Asn	Silent- Coding	tm7	Human Gene SWISSPROT-ID:P47872 SECRETIN RECEPTOR PRECURSOR (SCT-R) - HOMO SAPIENS (HUMAN), 440 aa.	3.00E-242 (2q14.1)	2
478	cg41084824	1298	CCCACCACGGTC TCCACAGCACTC C/C/TJGACAGCC CCGCCAAACCAG AGAAGA	C	T	Pro	Silent- Coding	tm7	Human Gene SWISSPROT-ID:P14416 D(2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.70E-241	11

479	cg41084924	1422	CCTCCCTCAAGA CCATGAGCCGTA G[G]A[A]AGCTCTC CCAGCAGAAAGG AGAAGA	G	A	Arg	Arg	SILENT- CODING	tm7	Human Gene SWISSPROT-ID:P14416 D(2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.70E-241	11
480	cg43264978	1175	CCAAGCTCATCG ATGCCTCCAGAG T[C]G[TC]CAGAGAC GGAGTACTCTGC CTTG	C	G	Val	Val	SILENT- CODING	tm7	Human Gene TREMBLNEW- ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
481	cg43264978	1193	CCAGAGTCTCAG AGACGGAGTACT C[T]C[GCCTT]GGA GCAGAACACCAA ATGAT	T	C	Ser	Ser	SILENT- CODING	tm7	Human Gene TREMBLNEW- ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
482	cg43264978	140	CCCGCCTCAGAA CGATGGATCTGC A[C]T[CTCTT]CGA CTACTCAGAGCC AGGA	C	T	His	His	SILENT- CODING	tm7	Human Gene TREMBLNEW- ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
483	cg43264978	164	ACCTCTTCGACT ACTCAGAGCCAG G[G]C[AACTT]CTC GGACATCAGCTG GCCAT	G	C	Gly	Gly	SILENT- CODING	tm7	Human Gene TREMBLNEW- ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
484	cg3001696	1274	GCCAGACCCC AGCAGCTTCAGC CG[G]C[CCCCG] GAAGCCACGGC CCGCGAGC	G	C	Arg	Arg	SILENT- CODING	tm7	Human Gene SWISSPROT-ID:P41143 DELTA-TYPE OPIOID RECEPTOR (DOR-1) - HOMO SAPIENS (HUMAN), 372 aa.	2.10E-195	1 (1p36.1)
485	cg43967090	790	GGGCTAAATATT TTATGGTTTTATT [C]TATTTACTGT GTTCTCATGCTG TGTT	C	T	Phe	Phe	SILENT- CODING	tm7	Human Gene SWISSNEW-ID:O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39 - HOMO SAPIENS (HUMAN), 453 aa.	5.10E-195	2

486	cg43326635	770	ACTTCAACTCTT TGTTGGTGCT [G/C]CCCCGCT TCTCCTCATGGT CCTCA	G	C	Leu	Leu	SILENT- CODING	tm7	Human Gene SWISSPROT-ID:P30542 ADENOSINE A1 RECEPTOR - HOMO SAPIENS (HUMAN), 326 aa.	1.10E-173	1
487	cg40245117	1286	CATGCCAATTG TTTCCGTCATGA G[A/G]ATGGACTA CATGGTATACCT CAGCT	A	G	Arg	Arg	SILENT- CODING	tm7	Human Gene SWISSPROT-ID:P33765 ADENOSINE A3 RECEPTOR - HOMO SAPIENS (HUMAN), 318 aa.	1.50E-167	1 (1p21)
488	cg21411454	920	TCTACTGCAAGT TCCACAACCTCT TTC/TCCCACATCGC CGCTGTCTTCGC CAGTA	C	T	Phe	Phe	SILENT- CODING	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
489	cg42666032	1372	TGCTGGCGTGC CACGAAGTGGTC TT[C/T]GCCTTCG TGACGGACGAG CACGCCCC	C	T	Phe	Phe	SILENT- CODING	tm7	Human Gene Similar to SWISSPROT- ID:P30083 VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR) (PACAP TYPE II RECEPTOR) (PACAP- R-2) - RATTUS NORVEGICUS (RAT), 459 aa.	2.40E-75	17 (17q25)
490	cg38841806	111	CCAGCTGGCAG CTGGCACTGTGG GC[A/C]CCAGCC TACCTGGCCCTG GTGCTGG	A	C	Ala	Ala	SILENT- CODING	tm7	Human Gene Similar to SWISSPROT- ID:P30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 99D (DTKR) - DRSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	2.10E-67	
491	cg1408914	683	AGGGGAAGTTTC TCTCAGTGTCTT A[C/T]ACAAATGA GGTACCCATGCT GAACC	C	T	Tyr	Tyr	SILENT- CODING	tm7	Human Gene Similar to SPTREMBL- ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa.	2.00E-62	
492	cg1408914	675	TCTCAGTGTCTT ACACAAATGAGG T[A/T]CCCATGCT GAACCCCTTCAT CTACT	A	T	Val	Val	SILENT- CODING	tm7	Human Gene Similar to SPTREMBL- ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa.	2.00E-62	

493	cg1408914	87	CCCCCAAAATGC TGATGAGCTTTA TTC/TTCAGAGAG GAACATCATCTC CTTTC	C	T	Ile	Ile	SILENT- CODING	tm7	Human Gene Similar to SPTREMBL- ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa.	2.00E-62	
494	cg43336100	168	CGGATGATTATG ATCTCATGTATG TAA/GAATTTGGA CAACGAAATAGA CAATG	A	G	Val	Val	SILENT- CODING	tnf	Human Gene SWISSPROT-ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG- 14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	3 (3q25)
495	cg21138682	220	TTTTGCTGTGTA TCTTCATAGAAG GTT/CJTGGACAA GATAGAAGATGA AAGGAA	T	C	Leu	Leu	SILENT- CODING	tnf	Human Gene Homologous to SWISSNEW-ID:P29965 CD40 LIGAND (CD40-L) (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN GP39) (CD154 ANTIGEN) - HOMO SAPIENS (HUMAN), 261 aa. pcis: SWISSPROT-ID:P29965 CD40 LIGAND (CD40-L) (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN GP39) (CD154 ANTIGEN) - HOMO SAPIENS (HUMAN), 261 aa.	3.60E-136	X (Xq26)
496	cg43335558	1143	TGCTGGTCCAG CAAATGAAGGTG A/C/TCCCACTGA GACTCTGAGACA GTGCT	C	T	Asp	Asp	SILENT- CODING	tnfrceptor or	Human Gene Similar to TREMBLNEW- ID:G2653845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	5.50E-89	8
497	cg44027791	1440	TCTTGCCACAGT CGGGGATGTGG CA/A/CACGTGCT TCTTCTTGCCCT GCTCTC	A	C	Val	Val	SILENT- CODING	transcript factor	Human Gene SWISSPROT-ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17

498	cg43934374	1459	TAGGAGCCCATGA AAGGCTTGTCCTC C/A/GJACACCTTT CATGAACCTCAA TCTGA	G	Pro	SILENT- CODING	transcript factor	Human Gene SWISSNEW-ID:Q99081 TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX- BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.lpcis:SWISSPROT-ID:Q99081 TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX- BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.	0.00E+00	15 (15q21)
499	cg43921342	2556	TGGGATTCAGGT TCCGCTCTCGCA C/C/TJTGCTGCTC CAGCCCCAGGAT GACCT	T	Gln	SILENT- CODING	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.lpcis:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.	0.00E+00	
500	cg44130800	1140	ATTTCCTGACATT TGATCCTATAGC T/CJAAAATGGCA AAAACGTGTTAAG TAGG	C	Ala	SILENT- CODING	transcript factor	HOMO SAPIENS (HUMAN), 654 aa. Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment).	7.5e-310	2
501	cg43321351	580	GCTCTGTCAGGC TCTCGGGGGTG GC/A/GJATGGTG ATGGTGTCGGC GGCAGCCG	G	Ile	SILENT- CODING	transcript factor	Human Gene SPTREMBL-ID:O00146 P120E4F TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 783 aa.	1.00E-290	
502	cg43336856	861	CCTGGTAAGGG GGCACCATTGGC GGT/CJCCCTGC CCATACGGGG CATAGCAC	C	Gly	SILENT- CODING	transcript factor	Human Gene TREMBLNEW- ID:G2895870 ZINC FINGER TRANSCRIPTION FACTOR (ZNF207) - HOMO SAPIENS (HUMAN), 478 aa.	1.90E-265	

503	cg43129605	399	GGCCCGCGCTC GGCCGCGCGCC GGTGAAGCG GAGGCTGGACC TGGAAACTG	G	A	Val	Val	SILENT- CODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
504	cg43984259	1159	TGTTTCCGGACG AACTGCTGCTGC TAAJCTGTTGCT GCTGCTGCTGCT GCTGC	A	G	Ser	Ser	SILENT- CODING	transcript factor	Human Gene SWISSPROT-ID:Q16254 TRANSCRIPTION FACTOR E2F4 (E2F- 4) - HOMO SAPIENS (HUMAN), 413 aa.	5.50E-211 (16q22.1)	16
505	cg43984259	1693	CTCCAGCAAAGC ATCTGCAGATGT CAGTTCATGAGT GACGTAGGCCAA ACAGC	C	T	Glu	Glu	SILENT- CODING	transcript factor	Human Gene SWISSPROT-ID:Q16254 TRANSCRIPTION FACTOR E2F4 (E2F- 4) - HOMO SAPIENS (HUMAN), 413 aa.	5.50E-211 (16q22.1)	16
506	cg44028769	343	CCTTCTTGTCCTC CCGAGCCTGTCA CAGATATGATTT GTTATTTCTGGA GATGT	G	A	Ile	Ile	SILENT- CODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q02482 TRANSCRIPTION FACTOR UNC-37 - CAENORHABDITIS ELEGANS, 612 aa.	4.60E-119	1
507	cg43918209	1288	GGTTGGGAAAG GCGCCCTCCGC TTGCG/GGCCGG AGGGGGCTGCA GGCGATCGG	C	G	Ala	Ala	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
508	cg43918942	2589	CTGATGACCTCC TTCACAGTCCCTC CAGTGAAGTCAT GCATTCTGGCTG CAACC	G	T	Arg	Arg	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
509	cg43918942	2617	AGTCATGCATTC TGCTGCAACCA GAGGAGCGCTG CTCCACAGAGGC CAGAGG	A	G	Leu	Leu	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14

510	cg43918942	2629	TGGCTGCAACCA GAAGCGCTGCTC C/A/GCAGAGGC CAGAGGGGCGC CGGCGTG	A	G	Cys	Cys	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
511	cg43918942	2638	CCAGAAGCGCT GCTCCACAGAG GCC/A/CJGAGGG GCGCCGGCCTG TGTGCATCC	A	C	Ser	Ser	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
512	cg43918942	2665	AGGGGCGCCGG CCTGTGTGCATC CA/A/GJTCCCGCT TCATCCTCTGCA GAAGCC	A	G	Asp	Asp	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
513	cg43918942	2683	GCATCCAATCCC GCTTCATCCTCT G/C/TJAGAAAGCCT CAGGCGCAGTCAT GGATA	C	T	Leu	Leu	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
514	cg43918942	2686	TCCAATCCCGCT TCATCCTCTGCA G/A/GJAGCCTCA GGCAGTCATG GATACCT	A	G	Leu	Leu	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
515	cg43918942	2707	GCAGAAGCCTCA GGGCAGTCATG GAT/CJACCTCAT GGTTCTTCTCCC CAAAAT	T	C	Val	Val	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
516	cg43918942	2713	GCCTCAGGGCA GTCATGGATACC TC/A/GJTGTTCT TCTCCCAAAAT CCAGTA	A	G	His	His	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14

517	cg43918942	2728	TGATACCTCAT GGTTCTTCTCCC C/A/GJAATTCCAG TAGATGCGCAAA TCGTG	A	G	Phe	Phe	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
518	cg43918942	2749	CCCCAAATCCCA GTAGATGCGCAA ATTGJCGTGGAAT ATACAGGCACGG GICTA	T	G	Arg	Arg	SILENT- CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
519	cg43051067	1325	CAACCTGCACA TCCACCAGCGAG TATJCACACAGG AGAGAGGCCCTA CAAGT	A	T	Val	Val	SILENT- CODING	transcript factor	Human Gene Similar to SWISSNEW- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa. pcis:SWISSPROT- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.30E-91	
520	cg43129841	1228	AAATGGTGGCAG CAACAGGTTCAA C/C/TJGGTGGCTT TTTGGAAAGTGT CGTGA	C	T	Pro	Pro	SILENT- CODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	2.10E-83	1 (1q32)
521	cg43255753	1095	CCGAGGCCGAG AGCAAAGAGGA GCAIT/CJGGCCC CGAGGCCTGCG ACGCGGCCA	T	C	His	His	SILENT- CODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	4.70E-63	
522	cg42532030	319	ATAAATGTGATG AGTGTTGGGAAAG C/C/TJTCAGTCA GAGCTCAGATCT TATTA	C	T	Ala	Ala	SILENT- CODING	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	1.90E-57	

523	cg439486772	1709	ATCAATATTTAAT ATACTGGCTACCT ACGTTCTAATC AGGAAAAAAT CTTG	A	C	Thr	Thr	SILENT- CODING	transferra se	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAc:POLYPEPTIDE ALFA-1,0 N-ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0.00E+00	18
524	cg43948635	2125	CTATTTGTAGC CCAGCTCCGTCA G/GTGCCTCAG ACAGAGCCCTGC AGTTGG	G	T	Ala	Ala	SILENT- CODING	transferra se	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
525	cg43948635	2164	CCCTGCAGTTGG CCACCACCTGGT G/TCTGATAAAC TTTAAATTCCAG AGTCA	T	C	Gln	Gln	SILENT- CODING	transferra se	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
526	cg43948635	2203	ATCCAGAGTCA TAGCTTGCTTCA G/TG/GCCACAG CAACCCCGAGCA TGCGGT	T	G	Ala	Ala	SILENT- CODING	transferra se	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
527	cg43948635	2248	TGGCGTGGTTGT GGGGACCTCCC TG/C/AJAGGCCA GGGAACACACAG AGAAATGA	C	A	Leu	Leu	SILENT- CODING	transferra se	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
528	cg43948635	2269	CCTGCAGGCCA GGGAACACACAG AGA/A/GTTGATA AGAGACTCCAGG TTGTACA	A	G	Asn	Asn	SILENT- CODING	transferra se	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
529	cg43948635	2275	GGCCAGGGAAC ACAGCAGAATTG ATAGJAGAGACT CCAGGTTGTACA GAATCT	A	G	Leu	Leu	SILENT- CODING	transferra se	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17

530	cg43948635	2370	AAGATCATGCCA GCTCGGCAGCC TC[G/T]CAGGGT CTTGTGAGTGGT GGTGGTC	G	T	Arg	Arg	SILENT- CODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
531	cg43948635	2986	CCAAACTGCTC GGCTGGCGAAAT TTT/CJTCCGAGGC AATCAGCTCCAA TCCAA	T	C	Glu	Glu	SILENT- CODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
532	cg43995237	830	TTACTTGATGCA ACTGACTTGTA T[A/T]GCCAGAAA TCCTGTGCAACA ATAGA	A	T	Ala	Ala	SILENT- CODING	transferase	Human Gene SWISSPROT-ID:P53611 GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (EC 2.5.1.-) (RAB GERANYLGERANYL TRANSFERASE BETA SUBUNIT) (RAB GERANYL- GERANYL TRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) - HOMO SAPIENS (HUMAN), 331 aa.	1.40E-182	1
533	cg42879858	531	CACACGCTGTGGC CTATTTTGTTTTA [C/T]ACATTGAAC AGCAATGTTTCAT TCTG	C	T	Tyr	Tyr	SILENT- CODING	transferase	Human Gene Homologous to SWISSPROT-ID:Q93070 ECTO-ADP- RIBOSYLTRANSFERASE 4 (EC 2.4.2.31) (NAD(P)(+)-ARGININE ADP- RIBOSYLTRANSFERASE 4) (MONO(ADP-RIBOSYL) TRANSFERASE 4) - HOMO SAPIENS (HUMAN), 267 aa (fragment).	4.60E-143	
534	cg43933127	2359	GATTTCTGCAA TTTGTCCTGTAA G[G/A]AATGGAA CATTGGCTGAAT TGTGAA	G	A	Phe	Phe	SILENT- CODING	transport	Human Gene SWISSPROT-ID:P41541 GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP) - BOS TAURUS (BOVINE), 961 aa.	0.00E+00	4

535	cg43919796	1566	CAGAATTGCTAA AGCGCATCCTGG A/C/TJAGCAACAA GAGAGTACAAGA AGCTG	C	T	Asp	Asp	SILENT- CODING	transport	Human Gene SWISSNEW-ID:Q92873 IMPORTIN BETA-2 SUBUNIT (KARYOPHERIN BETA-2 SUBUNIT) (TRANSPORTIN) (M9 REGION INTERACTION PROTEIN) (MIP) - HOMO SAPIENS (HUMAN), 890 aa.lpcis:SWISSPROT-ID:Q92873 IMPORTIN BETA-2 SUBUNIT (KARYOPHERIN BETA-2 SUBUNIT) (TRANSPORTIN) (M9 REGION INTERACTION PROTEIN) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	5
536	cg43053829	1294	TGCTCAGGTTGC CACCAGCCTCTG TTC/AJACTTCGTG GGATAACCCAAG TTGCA	C	A	Val	Val	SILENT- CODING	transport	Human Gene SWISSPROT-ID:Q92887 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - HOMO SAPIENS (HUMAN), 1545 aa.lpcis:SPTRMBL-ID:Q92887 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	10
537	cg4398978	1880	GGTCTGCACGC CCTTCTGGTGG CC/C/TJGTGCAC ATTGCCCGTCTA CGTGAC	C	T	Leu	Leu	SILENT- CODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16

538	cg42719351	1242	CAGGATCCCTGG TGCTGCTGTGCA CTT/CITGTCTTAT CCTCCTCGTCAA GATGC	T	C	Thr	Thr	SILENT- CODING	transport	Human Gene SPTREMBL-ID:Q06495 RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2) - HOMO SAPIENS (HUMAN), 639 aa.	0.00E+00	5 (5q35)
539	cg43935986	1447	TCGTAAGGAGG GTGCTGCACTTG GG[G/T]GTGCAG ATGCTGATGCTG AGCTGTG	G	T	Gly	Gly	SILENT- CODING	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0.00E+00	6 (6p21.3)
540	cg43935986	2101	TATACACAGATG TAGGGAGAGAAG GGI/GIAGCCAG CTGGCTGCGGG ACAGAAAC	A	G	Gly	Gly	SILENT- CODING	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0.00E+00	6 (6p21.3)
541	cg43935986	2380	GACAGGACCTCT ATCCCGCCTGG TIG/TICAGCAGC GGCTGATGGACT GAGGCC	G	T	Val	Val	SILENT- CODING	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0.00E+00	6 (6p21.3)
542	cg44008864	597	CAATGAGGTTGG CTGGAGAATCAA AT/CJTAGCTAC TACTCCTTTGTC CAGGA	T	C	Lys	Lys	SILENT- CODING	transport	Human Gene SPTREMBL-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa. pcds:SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa.	0.00E+00	

543	cg43300953	371	TGGCGGGGACC CCGAGACACCG CTGTCGAGT GCCGACGCCG CGAACCTGA	T	C	Cys	SILENT- CODING	transport	Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.60E-261	5
544	cg43300953	425	GCGCCTGGCGC AACACACAGTGC CCGAGCTGCGG CTGCGGACGG CCGCGAGG	G	A	Pro	SILENT- CODING	transport	Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.60E-261	5
545	cg43864039	3102	GGGAGCCAAGC ACTGCTCCTCCC ACGAGGCCAGC ATGAGGCGACC CGTCAGCT	G	A	Ala	SILENT- CODING	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
546	cg44011204	825	TGCTTCTCGACT CCGTACGGTCCA C[G/A]TAATTTG GAGGAGTCCTG CCCCCA	G	A	Tyr	SILENT- CODING	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa. pcis:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa. pcis:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
547	cg43924839	1431	CCCACTGTAATT TGCTGAGTGTC G[G/A]TTTAACAT TAAACACAGTGCA TAAAG	G	A	Asn	SILENT- CODING	transport	Human Gene SWISSPROT-ID:P78382 CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR) - HOMO SAPIENS (HUMAN), 337 aa.	1.60E-172	6
548	cg43298674	600	AAACAAAGTAGG GGGCAATGATGC TTGCTCCCACTCT GGAGGCCGTGG ATGTGA	G	C	Gly	SILENT- CODING	transport	Human Gene Similar to TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	5.2E-64	5

549	cg42726186	827	CAGTTGGTTCAT CCAACAGGAAAA TTC/TGTGAGGATC TCCTAAATGGC AATCC	C	T	Gln	Gln	SILENT- CODING	transport	Human Gene Similar to SPTREMBL- ID:Q92473 ABC-C TRANSPORTER - HOMO SAPIENS (HUMAN), 1704 aa.	2.5E-60	17
550	cg43269525	3119	TATGAGCTCTTG GCAGCTTTTCAG G/A/CjGTACCCC ACTGTTCAACTG TAAATG	A	C	Thr	Thr	SILENT- CODING	ubiquitin	Human Gene SWISSNEW-ID:Q92462 UBIQUITIN-PROTEIN LIGASE PUB1 (EC 6.3.2.-) - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 767 aa.	6.5E-163	15
551	cg43261895	321	ATCTATACAACT GGGAGGTGGCC ATC/TJTCGGGC CCCCCAACACCT ACTACG	C	T	Ile	Ile	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.5E-129	
552	cg43120117	1162	TTGTAGATCATA ATAACCGAACAA C/G/CjCAGTTGA CAGACCCAAGGT TACACC	G	C	Thr	Thr	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P39940 UBIQUITIN- PROTEIN LIGASE RSP5 (EC 6.3.2.-) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 809 aa.	7.00E-121	
553	cg44005525	795	TCCACTGTCTGG CCATTCTGTCT G/C/TjTCTGCTCT GTTGGTCATATA CTGAG	C	T	Glu	Glu	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
554	cg43921266	1300	CCCCCGAGCTG CTGCAGTGGGA GCCjG/AjTGGTG GTGATGGAGCA GGTCATCTC	G	A	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0.00E+00	1

555	cg43929067	1982	CTCCGGGGT GAGGAATCTGAA GA[G/C]GACTGG GTTGGAGGCAG CACAAAGAC	G	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0.00E+00	1
556	cg43944666	1082	TTCTAGGGGTTT CTAAACCAAAAG A[G/A]TCTACAAC TGGGTTGCTGAA AGCCA	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O15228 DIHYDROXYACETONE PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.42) (DAP-AT) (GLYCERONE-PHOSPHATE O-ACYLTRANSFERASE) - Homo sapiens (Human), 680 aa.	0.00E+00	1
557	cg43947011	1749	TCTTCTCCAATG TGGCCAGGAGAT CT[C/T]CCACCTG GTCCCGTACAGA CTCAT	T	C	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIAA0253 - Homo sapiens (Human), 708 aa (fragment).	0.00E+00	1
558	cg43948542	3513	ATCCTGCATATG CAAAATGGGTAC A[G/A]TCACACAG AGACCTGCCCAT CAAGC	G	A	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE-TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE-TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0.00E+00	1
559	cg43969426	2856	AGAAGATCTTCG ATGGGTCCCTAC A[G/A]CCACAAGA TGTTATGTGTAG CATAG	G	A	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15463 PTPL1-ASSOCIATED RHOGAP - HOMO SAPIENS (HUMAN), 1261 aa.	0.00E+00	1
560	cg43273361	1765	TCAAGAGCAGCT CCTGAGCCCTTC C[A/G]AGAGCAA AGACAGGAATGA GACCCC	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P79101 CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR PROTEIN - BOS TAURUS (BOVINE), 684 aa.	0.00E+00	2

561	cg43961763	550	CCCTTCCCTTTT CTGCCCTTTCTT G/GAJTTGAGGTA TTCAGCACTTT CATTAA	G	A	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P13521 SECRETOGNANIN II PRECURSOR (SGII) (CHROMOGNANIN C) - Homo sapiens (Human), 617 aa.	0.00E+00	2
562	cg44911887	797	CAAGATCTGGAA AAAAGCAAAAA A/GAJAAACCTT AGCTGAAATCAA CCAAA	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99728 BRCA1-ASSOCIATED RING DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 777 aa.	0.00E+00	2
563	cg43925942	2262	ACATATTTGATAA ACTTAAAGAGGC [T/C]GTTAAGGAA GAAAGTATTAAA CGAC	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0.00E+00	3
564	cg43931104	1483	AGGATGAAGAG GACACTTGTCTG GAT/CJTGACATAC TGCACACAGGAT CCATCG	T	C	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75329 ATAXIN-7 - HOMO SAPIENS (HUMAN), 892 aa.	0.00E+00	3
565	cg43939697	947	GATACCAAGGTC CTACCAAGATGA C/GAJAAAGAAGA GTTAAATGCCCT CAAGT	A	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75766 TRIP PROTEIN - HOMO SAPIENS (HUMAN), 784 aa.	0.00E+00	3
566	cg43940975	304	CCTGATGGCTGT CTGGATCCACGG A/GAJAAATATCC AAGACGCTCAAA CTGGA	G	A	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE-TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0.00E+00	3
567	cg43948629	1640	TGCCTGTGACCC TGCCCAACATCG C/GAJTCTTTTAC TGGCAAGGGAG GCCCC	A	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15031 PROBABLE LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.4) (LEUCINE- TRNA LIGASE) (LEURS) (KIAA0028) - Homo sapiens (Human), 903 aa.	0.00E+00	3

568	cg43948629	3577	CCTGTCCTCCCC AACCCAGCTGG A/C/TGTGCTCC CAGGCCTGCTGT GGTTC	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15031 PROBABLE LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.4) (LEUCINE- TRNA LIGASE) (LEURS) (KIAA0028) - Homo sapiens (Human), 903 aa.	0.00E+00	3
569	cg43978862	955	AGTCCTTGACAG TGAACCTTCATCA T/A/G/CAGCTGAA TGTGCATGCCAC AGCTG	A	G	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43020 COAT PROTEIN GAMMA-COP - HOMO SAPIENS (HUMAN), 874 aa.	0.00E+00	3
570	cg43930961	2098	CGGTGGAACCG CTTGGGACTGAT A/G/A/GGGCGA GGCGCGGGTCA GACTCGT	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0.00E+00	4
571	cg43935402	9617	CTCCTCCGGATC CCCAACTTTTGG TT/C/TCAGAATC CAGCCAGAGGA CAGACC	T	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa.	0.00E+00	4
572	cg43994452	954	CGATCTTCACGT GCCGCCTGGTG GG/C/T/GAGAGC TGGCCCATGCA GTTGAGGC	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0.00E+00	4
573	cg43933355	1161	TGATGAGCGCA GCATAGACCTGG G/A/G/CGGCCCA CTCTCCTGTCGT CAAGT	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment).	0.00E+00	5
574	cg43964609	678	TGACCACGTAGA AGCTGGAGCTCT C/C/T/TGGTAGCC AAAGATAAAGCC TGCAT	C	T	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35443 THROMBOSPONDIN 4 PRECURSOR - Homo sapiens (Human), 961 aa.	0.00E+00	5

575	cg43981461	3634	TGATCTGAAA TGCTAATTACCT G[A/C]GAACACC AAGAACTCTTGT GGAACA	A	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q43314 KIAA0433 - HOMO SAPIENS (HUMAN), 1243 aa.	0.00E+00	5
576	cg43999670	3571	AAGTGGAATGG CTCAGAGGAGTG A[A/G]GAGAAATGT GCTAGCACTGAA GAGCG	A	G	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q12766 HYPOTHETICAL PROTEIN KIAA0194 - Homo sapiens (Human), 1435 aa (fragment).	0.00E+00	5
577	cg43918386	304	GACTGGAAGGAT GGTGGCTGTGCT C[A/G]TTACACGG TCGGCAAGGCAT TGTC	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14511 ENHANCER OF FILMENTATION 1 - HOMO SAPIENS (HUMAN), 834 aa.	0.00E+00	6
578	cg43925091	2303	CTAGAACAGAGG TGGAGGAGGCG CC[G/T]GCGGTC CTCTGCCATGTC CCGGCTC	G	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14999 HYPOTHETICAL PROTEIN KIAA0076 (HIA0936) - Homo sapiens (Human), 1698 aa.	0.00E+00	6
579	cg43932558	1823	TCACCCCTGATGG GATTCATGTCGG G[C/T]CGACTAG GCTTGAAACGG CTTICA	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14670 MRNA (KIAA0082) FOR ORF (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 607 aa (fragment).	0.00E+00	6
580	cg43988933	1726	AGAAACTGCTA AATCAAAAAAAA A[A/G]AAAACTTT AAAAAAAACCC TACAC	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46275 SEC63 PROTEIN - HOMO SAPIENS (HUMAN), 759 aa.	0.00E+00	6
581	cg43971946	4582	CTCCTCTTCTT CATCGATCTCAA A[T/C]GTGGGTTG TAATCTTGGCAT TGGCC	T	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92794 MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN - Homo sapiens (Human), 2004 aa.	0.00E+00	8

582	cg43818922	5946	AGTCTGTCAGCA GACGAGCTTCCC G[A/G]AATTGTA CTCCTTGATGTC ATCCC	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75181 KIAA0689 PROTEIN - HOMO SAPIENS (HUMAN), 847 aa (fragment).	0.00E+00	9
583	cg43921541	1233	CATGGTAGGCAT CCAGGAGCCCTT G[C/T]CGGTCTC CAGAGTCGTAAA TTGCAT	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA10753 TIP ASSOCIATING PROTEIN - HOMO SAPIENS (HUMAN), 619 aa.	0.00E+00	11
584	cg43966987	2002	CTGCCGGCCCA GCCTCCTTCTGC TG[C/T]CACATGT TCTGGTGGCAGC CCAATG	C	T	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00213 STAT-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 710 aa.	0.00E+00	11
585	cg43329920	1900	AGAGCCGGGCC CTCGGGGGTCC TCC[A/T]GAATAC CTGGGACAAAGA CACAGGC	A	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0.00E+00	12
586	cg43329920	1903	GCCGGGGCCCTC GGGGGTCTCTCC AGA[A/G]TACCTG GGACAAAGACAC AGGCTGG	A	G	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0.00E+00	12
587	cg43329920	1925	AGAATACCTGGG ACAAAGACACAG G[C/T]TGGAGGA CGAGGAGGACG AGGAAGA	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0.00E+00	12
588	cg43334182	5043	GAGGCAAGACTT GTGGAGCTTGAG G[T/C]TGACTCAC TGGCTGTGCAGT AGTGG	T	C	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15052 KIAA0344 - HOMO SAPIENS (HUMAN), 1246 aa.	0.00E+00	12

589	cg43918356	404	GCTGATGATGGT CCTTAGGTTTCA G[G/A]GTGGCCT GAGTCTTGGATG GGGATA	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0.00E+00	12
590	cg43918356	2336	CGCTACGTCCTA TATTTTGCAAAAT [T/C]AGTTTATCA AACTCAACAGTC AAAT	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment).	0.00E+00	12
591	cg43918566	1480	AGGCTGGCATG GAGCGGGAACT GGA[G/A]AACATC ATCCAGGAGACA GAGAAAG	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0.00E+00	12
592	cg43918566	808	TCCGGCCCCCA CCCAGTGCTGCA CC[G/A]CAGGCC ATCCTCTGTAC CCTTCCC	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0.00E+00	12
593	cg43950437	955	GCTTGGCCCCAC GTGCGAGCTTGC C[C/T]ACAACTGA CAAAAAAGCACT GAAGA	C	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15021 ORF - HOMO SAPIENS (HUMAN), 1401 aa.	0.00E+00	12
594	cg43969319	1996	GATTACAGATT TAATTGAAGAAA A[C/T]CATGTTGT AAATAAGACAGA CTTGA	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15398 HYPOTHETICAL PROTEIN KIAA0008 - Homo sapiens (Human), 765 aa.	0.00E+00	14
595	cg44018598	1379	ATTTACTTGAATT GTCTAGGACAGG [A/G]AGATCTTCA CTATCACTGCTT TGTC	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0.00E+00	14

596	cg44018598	953	AAGGTAGAGAAA ATGTTATCACC T/G/CATCTCTAC AGCAAGTACATT TTGTG	A	G	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0.00E+00	14
597	cg44018598	986	CAGCAAGTACAT TTTGTGGGGAG A/C/TGATGATGA GGGACTCATCC AGTGT	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0.00E+00	14
598	cg44022133	3081	AATGGCCCCAGT CCAATCCCAAAT TT/C/CTTTGTGC TGACTATGCCGA GCAAG	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75158 KIAA0670 PROTEIN - HOMO SAPIENS (HUMAN), 1280 aa (fragment).	0.00E+00	14
599	cg43981471	3033	CCAGCCTCCTG AGGGCCCTGGC CTC/T/CCGAGG AGATCACCCCTC ATTCGTA	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15082 KIAA0377 - HOMO SAPIENS (HUMAN), 1406 aa.	0.00E+00	15
600	cg43926221	5853	GCACCGAGAAA GTCGGTTGTATC TG/C/TTGAAATT GTCTGTTTATT AGTAC	C	T	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15025 KIAA0308 - HOMO SAPIENS (HUMAN), 1297 aa (fragment).	0.00E+00	16
601	cg43945577	1886	TCACCTCCTCTG AATACCTTCCTA C/G/A/TATGGGT CAAGCTTTACAA AAGCG	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0.00E+00	16
602	cg43945577	1988	TCCATTTCCTCC CACTGCTCAGAG ATT/C/GGCGAGA ACTATGTTGTGC TTCTGG	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0.00E+00	16

603	cg43955093	2884	GGGGCTGTGGG GGCATCCGCC AGGT/CJGTCCCT CCATCAGAGG GCTATCAT	T	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0.00E+00	16
604	cg43983241	362	AGTGTGACACAA TATTCACTTTGT [G/C]GAAAAAAT GTTGCTACTTGG AAAT	G	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15219 PROTEIN P84 - HOMO SAPIENS (HUMAN), 657 aa.	0.00E+00	18
605	cg43983241	395	ATGTTGCTACTT GGAAATCAAATA C/A/CJTTCATTTC TGCTGGGAAAAA TTACT	A	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15219 PROTEIN P84 - HOMO SAPIENS (HUMAN), 657 aa.	0.00E+00	18
606	cg42702030	2347	TACAGTGCGGG CACAAAGAAGCTG CA[G/A]GGCCGC CTGCAGCTGTTC GGCCAGG	G	A	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92819 MYELOBLAST KIAA0223 - HOMO SAPIENS (HUMAN), 1165 aa (fragment).	0.00E+00	19
607	cg43297500	1921	GGGCTTCCAGA CAGTCGTGCTGG ATT/CJCCCTGAAGG GGATGCCCCAGAT CGATC	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49747 CARTILAGE OLIGOMERIC MATRIX PROTEIN PRECURSOR (COMP) - Homo sapiens (Human), 757 aa.	0.00E+00	19
608	cg43927434	3540	AGCAGGCCTCCT GTAGCTCGCTAA TIG/TJACCCGTGA CTTACCATCCA CTGCA	G	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92797 SYMPLEKIN - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	19
609	cg43927434	606	GAGGGGGCCGG GGTGTGGGGC CGG[C/G]GCCAA GGTCAGGGGCT CCAGATCAT	C	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92797 SYMPLEKIN - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	19

610	cg43991657	193	CCAGGGCAGCC GCTGCAGCAGC AGA[C/G]GAGCG GGAAGGTGTGG CCACAGCTT	C	G	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0.00E+00	19
611	cg43991657	208	CAGCAGCAGAC GAGCGGGAAGG TGT[G/A]GCCACA GCTTGGCTCAAG GGCGTGG	G	A	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0.00E+00	19
612	cg43919691	1039	TCITCATTTCACT CAACTGCTGCCT [G/A]ACCAGGGC AAGCTCATCGCT GIGTI	G	A	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0.00E+00	20
613	cg43936220	1966	TCTGCGTGCTCA TCTCCCGGCTCG C[A/G]GCTCGA AGGCTTTAGCG CACGGC	A	G	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75132 KIAA0637 PROTEIN - HOMO SAPIENS (HUMAN), 1171 aa.	0.00E+00	22
614	cg43973809	1170	TCGTGGCTGTGG TCTCCAGGATG A[G/A]AACACTCC TTTCGTGCCCGA CATGA	G	A	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47736 RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP) - Homo sapiens (Human), 663 aa.	0.00E+00	1 (1p36.1)
615	cg17663981	207	AAGATGGCTCTG GGGATCCCGAG AA[C/T]CCGGC ACAGCGAGAGC CTGGTGCC	C	T	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
616	cg17663981	210	ATGGCTCTGGG GATCCCGAGAAC CC[G/C]GGCACA GCGAGAGCCTG GTGCCAAG	G	C	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)

617	cg17663981	220	GGATCCCGAGAA CCCGGGCACAG CGA/CJGAGCCT GGTGCCCAAGTG GCCCCAAA	A	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
618	cg17663981	240	CAGCGAGAGCC TGGTGCCCAAGTG GC/C/TJCAAAAGT TCACGGGCGGC ATCGGAA	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
619	cg17663981	243	CGAGAGCCTGG TGCCCAAGTGGCC CA/A/GJAAAGTTCA CGGGCGGCATC GGAAACA	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
620	cg17663981	372	GGAAGGCCGCC TGACACCTGCGAC CA/A/GJAAACCCT GCAGCTGCCCC AAAGGGG	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
621	cg17663981	375	AGGCCGCCCTGC ACCTGGCGACCAA AA/A/GJCCCTGCA GCTGCCCCCAAAG GGGATG	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
622	cg43968854	6834	TATGCACTGACA AGCCACGACTC A/T/CJGAGAAAAC TACCAAAATAGC CTGCA	T	C	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0.00E+00	10 (10q25)

623	cg4398854	9441	AAGAGGAACACA AATTACAAGACT C/GA/GTCCCTG AAAATAAGGGAA TATCCC	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0.00E+00	10 (10q25)
624	cg43979900	2597	TGGCAAAATTGTT GTGACACATTGA A/A/GJTAAGGAAG AAATGGCCGTAT GCACT	A	G	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0.00E+00	14 (14q24.3)
625	cg43979900	2816	CCACGTAAGTCC CACTCCATGGCT C/T/CJTGGGCCG TCATCAACCCCG ATCTCC	T	C	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0.00E+00	14 (14q24.3)
626	cg44014448	3469	TCCAGAAAGATT TGGTGAAGGAAG C/C/TATCAACTC CTATATCAGAGG GGACG	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53675 CLATHRIN HEAVY CHAIN 2 (CLH-22) - Homo sapiens (Human), 1640 aa.	0.00E+00	17 (17q11)
627	cg44928323	3760	CAAGAGCTACAT TTATGGAAGTTC T/G/CJACAAAAT CCTTCAACAAGG CACAG	G	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0.00E+00	17 (17q11.2)

628	cg43973129	1228	AGCGCTATAGGG GCAGAGGAAGT GA[G/A]GAATACA GGGCTCCAAGA CCTCAGA	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P05060 SECRETOGNANIN I PRECURSOR (SGI) (CHROMOGRANIN B) - Homo sapiens (Human), 677 aa.	0.00E+00	20 (20pter)
629	cg43955813	1995	GTCATGATGAAA TTTCCAGATGTT C[G/A]CTGAGTG AGCCATTGGAAA GTGATG	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q03188 CENTROMERE PROTEIN C (CENP-C) (CENTROMERE AUTOANTIGEN C) - Homo sapiens (Human), 943 aa.	0.00E+00	4 (4q12)
630	cg44923983	576	GGAATTACAATT TTGGTGGAGAAT TTC/TGTAGAAGC CATGATTCTGCA ACTTA	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q09161 80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80) - Homo sapiens (Human), 790 aa.	0.00E+00	9 (9q22.3)
631	cg25268354	1419	TCATCACCTCCT GCACGTACAACA C[G/A]GAAGACC GGGAGCTGGCC ACAGTGG	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P09172 DOPAMINE BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-HYDROXYLASE) (DBH) - Homo sapiens (Human), 603 aa.	0.00E+00	9 (9q34)
632	cg43921948	1765	AAGATCCAGAG AGAGAAACCCAG T[A/T]ACTCCAGC ATCCGAGCCCC GGTTTT	A	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08942 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STERIOD SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0.00E+00	X
633	cg43032555	677	GCTTCTCGGCT TCTGACTGGTCC A[A/G]GATCTTCT GCCGCTCAAGC CGACCG	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
634	cg43032555	699	CCAAGATCTTCT GCCGCTCAAGC CG[A/G]CCGCGG GCTTCCTGTTCC AGTCTCT	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	

635	cg43032555	714	GCTCAAGCCGAC CGCGGGCTTCCT GTTCTCCAGTCT CTGAGCCTCATG CTTG	T	C	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
636	cg43032555	765	CGCCGCTTCCT GGGAGTTGGT GTA/GATCTCGA TGCCAGCTGAA CGCTGC	A	G	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
637	cg43032555	783	TGGTGGTAATCT CGATGGCCAGCT GTA/GACGCTGC GCTGAAGGGCAT CCCGGG	A	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
638	cg43032555	792	TCTCGATGGCCA GCTGAACGCTGC GCT/TGAAGG CATCCCGGGTCC TCTGAT	C	T	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
639	cg43032555	795	CGATGGCCAGCT GAACGCTGCGCT GTA/GAGGGCAT CCCGGGTCTCT GATCCA	A	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
640	cg43032555	801	CCAGCTGAACGC TGCGCTGAAG GTA/GTCCCGG GTCCTCTGATCC ACAGGCT	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
641	cg43032555	840	GATCCACAGGCT CCACTGACTGCA CTA/GTCCACACT GCTGACTACCCAG CCCCGT	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	

642	cg43032555	855	CTGACTGCACAT CCACACTGCTGA CT/CJACCAGCC CGTTTGGGGAA AGACAG	T	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
643	cg43032555	873	TGCTGACTACCA GCCCGTTTGGG G/A/GJAGACAG CCTGGTCCCGG GGCCTGG	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
644	cg43054046	2616	TACTGGGTGTGA AAGCTGTTTGG CT/CJGAAAGTTA TGAAAAAATACA CAAAG	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48200 IRON-RESPONSIVE ELEMENT BINDING PROTEIN 2 (IRE-BP 2) (IRON REGULATORY PROTEIN 2) (IRP2) - Homo sapiens (Human), 963 aa.	0.00E+00	
645	cg43277456	832	ACTTCGAGGCCT ATGTGCAGTACC G/C/TJGAGTACAT GGGCTTCATCCA GGCCA	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa.	0.00E+00	
646	cg43303383	232	TGCCCGAATTC CTCCGCTCGTG G/A/TJGCTGGGG CTGCTCCTGACC TTGGCG	A	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa.	0.00E+00	
647	cg43926470	2502	AGAGCCTCTTCT CCACAGCCTTCT C/C/TJGAGTCCCT GGCTGCAGAGAT CAGCT	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75154 KIAA0665 PROTEIN - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	
648	cg43971555	583	AGGTGAACCTCGT GGCGCCCCCGTG TC[G/A]GCAGTA GCGTCCGGGGC TTAGGCG	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC00190 ALPHA MANNOSIDASE 6A8B - HOMO SAPIENS (HUMAN), 679 aa.	0.00E+00	

649	cg43971555	904	GGAAGCGGACA TAGGGGCAGCC AAC[G/A]TCCAGC ACAACCTCCTGG CTAAGCC	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC00190 ALPHA MANNOSIDASE 6A8B - HOMO SAPIENS (HUMAN), 679 aa.	0.00E+00	
650	cg43972478	2073	CTATGTTAGGCT GGCTTTCTATCA AIC/A]GCGTGAA GGGATGGGCAA GATGCCA	C	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43264 H2W10 - HOMO SAPIENS (HUMAN), 779 aa.	0.00E+00	
651	cg43988766	1862	GCACCTCCATGG TGTAGGCCGCC CC[A/G]CAGATGT CACAGCCGTACA TGGGCT	A	G	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O08961 ZINC FINGER PROTEIN 104 (ROAZ) - RATTUS NORVEGICUS (RAT), 1186 aa.	0	
652	cg44932392	840	TGCTAAAGTTCA TATTTAATGAAAA IC/T]GAAGATTCT GCATCAATATCT TCCT	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0	
653	cg43956210	1507	ATAAAGTGAAC CTCTTGATTTTG GIC/A]GGTACTCA GAAACAGAAACA ACTTT	C	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA- GLUCOSAMINIDASE) (BETA-N- ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa.	3E-307	5 (5q13)
654	cg43982721	1732	CGTCCTGCCCAG GCAAGATCTCCG TIC/G]CCTCCTGT GCGCAACCTACA TCAGT	C	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O14531 DIHYDROPYRIMIDINASE RELATED PROTEIN-4 (DRP-4) (ULIP4 PROTEIN) - Homo sapiens (Human), 572 aa.	1.6E-306	
655	cg43955051	494	GTTCTGACTTAA AGCAAAAATACA CIG/A]GCATAGAT TGCAACAGCAAA GAAGT	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD10823 SQUALENE EPOXIDASE (EC 1.14.99.7) - HOMO SAPIENS (HUMAN), 574 aa.	1.9E-305	8

656	cg43951838	1686	TAGCCACCGCCT TGTCACAGACGA C[G/C]GTCATCC GCTCCTCTATCC CGTTGA	G	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14194 DIHYDROPYRIMIDINASE RELATED PROTEIN-1 (DRP-1) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 1) (CRMP-1) - Homo sapiens (Human), 572 aa.	3.5E-304	4 (4p16.1)
657	cg42682985	315	CTGATCCTGGCT GAAGAGGTTCCA G[C/T]GACACTTG AATAGTAACITTT GTTT	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene REMTREMBL- ACC:D1020806 (LAMBDA) DNA FOR IMMUNOGLOBULIN LIGHT CHAIN - HOMO SAPIENS (HUMAN), 541 aa (fragment).	2.00E-301	22
658	cg43917155	474	CAGTCCTTAAGA AAAGGGAGTATG G[A/C]TCAAAGTA CACTCAGAATAA TTTCA	A	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAB87763 EMBRYONIC LUNG PROTEIN - HOMO SAPIENS (HUMAN), 568 aa.	2.00E-301	
659	cg43255486	1152	TCAAGCCCAACA AGCTTCGAAATG G[C/A]CACAAAG GGCTTCGGATCT TCTGCA	C	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q14451 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 7 (GRB7 ADAPTER PROTEIN) (EPIDERMAL GROWTH FACTOR RECEPTOR GRB-7) (B47) - Homo sapiens (Human), 532 aa.	6.70E-294	17
660	cg43255486	1686	TCATCCTGCCGA GCGAGGAGGAG GG[C/T]CGCCTG TACTTCAGCATG GATGATG	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q14451 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 7 (GRB7 ADAPTER PROTEIN) (EPIDERMAL GROWTH FACTOR RECEPTOR GRB-7) (B47) - Homo sapiens (Human), 532 aa.	6.70E-294	17
661	cg43926493	1341	CGCTGCTGAAGT GGACCGAGTACA C[G/A]CCAGATC CTAACCATGGCT TCTATG	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27715 CGI-06 PROTEIN - HOMO SAPIENS (HUMAN), 574 aa.	1.40E-293	20

662	cg43316305	1345	TGTTGGGCTCCT GTTGCTCACACA A[G/A]GAGCGCC TGAGTATCCTCC GGGCAG	G	A	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75708 HIRIP3 PROTEIN - HOMO SAPIENS (HUMAN), 551 aa (fragment).	8.70E-292	
663	cg42903434	103	AGGGCTGCAGC CACGGTCTCCAG AT[A/G]TTGCCCA GCCTGTCCAGCT GCAGAG	A	G	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P51690 ARYLSULFATASE E PRECURSOR (EC 3.1.6.-) (ASE) - Homo sapiens (Human), 589 aa.	2.30E-291	
664	cg42903434	67	CCCTAAGGCACC AGCAGAGGGGG AA[C/T]GGGCCA CAGCAGGGCTG CAGCCACG	C	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P51690 ARYLSULFATASE E PRECURSOR (EC 3.1.6.-) (ASE) - Homo sapiens (Human), 589 aa.	2.3E-291	
665	cg43949262	837	GCTGCTCTCTCA CCACTGCAAGCT C[C/T]GCGTCCC ACGCAGTGTAC TGAGCA	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa.	9E-290	
666	cg43995003	1790	TTTGTGGAATGA CATCAAATGGTT T[C/T]ACCATTC AGACCCAGATGA TAGAG	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P10155 60 KD R0 PROTEIN (60 KD RIBONUCLEOPROTEIN R0) (RORNP) (SJOJREN SYNDROME TYPE A ANTIGEN (SS-A)) - Homo sapiens (Human), 538 aa.	1.9E-289	1
667	cg43926814	645	AACCAAAAGGAT CTTCCTCAAAC G[A/C]ACTGGTC CTTCTCGGCCTC TCGTC	A	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA-62) - Homo sapiens (Human), 536 aa.	5E-289	14
668	cg44028870	446	AGAAAATAAAA TGTCGACCTCGT C[C/T]TTGAGGC GCCAGATGAAGA ACATCG	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA83017 KIAA1065 PROTEIN - HOMO SAPIENS (HUMAN), 641 aa.	5.6E-288	

669	cg40918088	1907	CAAAAGCCACAG AGGGCCGGATC ATTATACAGTGG AGGATCACTACC CGCAAG	T	A	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51854 TRANSKETOLASE 2 (EC 2.2.1.1) (TK 2) (TRANSKETOLASE RELATED PROTEIN) - Homo sapiens (Human), 557 aa.	1.8E-287	X (Xq28)
670	cg43129343	1526	TGGTCGAAGGTC AGGGCGAGAAG AACTGTGTGACCT TCTGGGGGAGA CCGCJGC	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P27918 PROPERDIN PRECURSOR - Homo sapiens (Human), 469 aa.	2.2E-286	X (Xp11.4)
671	cg43931056	1275	TGGCCATGGAGA GACATGGACTTG ATTCTCATCAAGT AATTTCTGTAAC CTTCG	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15020 ORF - HOMO SAPIENS (HUMAN), 963 aa.	4.5E-286	12
672	cg43968641	3598	CGATGGCCAGG CCATCGATGAAA TTATGJTGAGG CCGTCGCTCAGA GTGATCA	A	G	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
673	cg43949830	1018	TTGAGATGTAGC ACTCACATGCTT TGAJTTTCCTAA ATAATTTATAACC TCAG	G	A	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment).	2.7E-281	16
674	cg43949830	793	TTTTCATGTCTAT TTTTCTTTTGA T/CJCTCCAGCA AGTAGATTGATA TTTT	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment).	2.7E-281	16

675	cg44002920	1168	TCTGCAGCAGCA GTGAATCAGATA C[A/G]TTGGGATT TTTCAAATACTG GCACA	A	G	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
676	cg44002920	644	CAAAAGTTTCTC AGTGCTGCTTTC C[C/T]GCACTGTC ATAGAAATCTCT GATCC	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
677	cg43922691	1088	TGGCTGGAAAGT TAATTCCTGTGC A[C/T]CAAGTGAG AGGTTTGAAAGA GAAGA	C	T	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.5E-278	17
678	cg43922691	416	ACGAGGACGCG TTGCTGCGGCGT CT[G/A]CGAGGC CCGAGGGTTCAA GAACATG	G	A	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.5E-278	17
679	cg43922691	788	CCACATCAACTT CTCTTCCAAGAG G[C/A]ATCTTGAA GATGAAGAACTG CCAGC	C	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.50E-278	17

680	cg43984386	374	CGCGGAGGGTGC ACCAACGTGGG GTC/T/CJCTGTTG CTCACCCCGCAG GAGAACG	T	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00401 N-WASP - HOMO SAPIENS (HUMAN), 505 aa.	5.90E-277	
681	cg42935995	1294	CAATCTTCGTGC TCAGGTAGATTA G/C/TJTCCTCTGT CCGTGCGCATACT CTGGA	C	T	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q12774 PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE) - Homo sapiens (Human), 519 aa.	1.00E-274	
682	cg43929467	717	AAACTTGGTGG AGTTCACAGATG A/A/GJGAGGGAT ATGGTCGTTATC TCGATC	A	G	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12874 SPICESOME-ASSOCIATED PROTEIN SAP 61 - HOMO SAPIENS (HUMAN), 501 aa.	1.30E-274	1
683	cg43947753	641	TCCCCGAGCGT GTAGGAGCAGT GCG/A/GJTCGTG GTCCCTCCCTAT GCAGCCTG	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13610 PERIODIC TRYPTOPHAN PROTEIN 1 HOMOLOG (KERATINOCYTE PROTEIN IEF SSP 9502) - Homo sapiens (Human), 501 aa.	7.10E-274	12
684	cg43333012	1838	TGTTTCATGAGCT TTGGAAAAGCTG C/T/CJAATAAGCC CTCAATCCGAGT TCGGG	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA- COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.50E-272	11 (11q23.3)
685	cg43333012	1861	GCTAATAAGCCC TCAATCCGAGTT C/G/TJGGTCATTT CCACAAACTGTC GAGAA	G	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA- COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.50E-272	11 (11q23.3)
686	cg43333012	407	CAGCTCCCTCTT CTTGGTATTACA A/A/GJATTTCATA CTTATCCACTAG GAAAG	A	G	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA- COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.50E-272	11 (11q23.3)

687	cg43926574	972	AAGATCTAAGAC ATTAATAGTATC [A/G]AGAAGTACA CAGGCACCACTA ATAA	A	G	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P43490 PRE-B CELL ENHANCING FACTOR PRECURSOR - Homo sapiens (Human), 491 aa.	1.10E-268	7
688	cg42869211	1895	TGCACTGAAAAG CTTGATTCTCTAC ATTCTGGAAAAA ACCAAAAGCACC AGCAA	T	C	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15397 ORF, COMPLETE CDS - HOMO SAPIENS (HUMAN), 508 aa.	7.00E-267	9
689	cg43031103	1702	CCCTCCCTTGG TTGAGGAGACAG CTA/GGGGGCTG GTGTGAGGTGCA GCACCC	A	G	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60240 PERILIPIN - HOMO SAPIENS (HUMAN), 522 aa.	6.30E-266	
690	cg43313186	495	TCTCATTCCAA GATCTTCAAGGG ATTCTGGCAGCT GACCAGACAGA GGCCCT	T	C	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTROPHIN - HOMO SAPIENS (HUMAN), 505 aa.	8.30E-265 (20q11.2)	20
691	cg43922182	1285	CTTCCCGCGGG AGCCGCGGCC AAGTCTTGACCC ACAGCCTCAGCT TCTCGGG	T	C	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.10E-261	2
692	cg43922182	1476	CCTCCGCGGCC TCCACGCCCTCG GGC/GGCCCG ACATGCTGCGCC TCCGCGG	C	G	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.10E-261	2
693	cg27359628	196	GAGACAGCGTG CCACACAACCAC CCCTCJACCAAGT TCAAGGTGACAA ATGTGG	T	C	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALLING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.30E-260	

694	cg43980777	999	ATAATTTCTGAA ATCCATGGGCTC TTA/GGTACAATC TGGGTCGTGA GCAAG	T	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.20E-259	2
695	cg43980777	882	CATGCTTGCTTC TCAGTCCCCCGC TTC/TGAGGCTTC TGCGGGCGCCT CCTCCT	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.20E-259	2
696	cg43986498	1090	CGGAGGAGGAG CTGGAGCGGCT GGA[G/A]GAGGC CTGCGACATGGC GCTGGAGC	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa.	1.30E-255	19
697	cg43986498	1664	CCGGAAGCAGG CCAACCGTATGA GC[A/T]NCGGAG AGATCGAGGAG GACGCCCTA	A	T	???	???	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa.	1.30E-255	19
698	cg39711096	941	ACGTGGAGGTG GACATGTCGGGA GA[C/T]TTGGGT GGCTGTTGAACC TCTTCC	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18428 LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP) - Homo sapiens (Human), 481 aa.	1.00E-251	
699	cg39711096	953	ACATGTCGGGAG ACTTGGGGTGG CTG[C/T]TGAACC TCTCCACAACC AGATTG	G	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18428 LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP) - Homo sapiens (Human), 481 aa.	1.00E-251	
700	cg42101957	279	TTTATGTAAATAA TGGGTTTCGGTC [G/A]TTGTTAAGA TGTGTGCCAA TGAC	G	A	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04279 SEMENOGELIN I PROTEIN PRECURSOR (SGI) [CONTAINS: SEMINAL BASIC PROTEIN; ALPHA- INHIBIN-92; ALPHA-INHIBIN-31] - Homo sapiens (Human), 462 aa.	5.50E-251	20 (20q12)

701	cg44910581	1321	CAACTGCCTGTC CAAGTGTGGCG C[G]A[CAACACTT GGACCTCGTCCT AGTT	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa.	5.80E-251	
702	cg44910581	2649	AACTGGACAAAG CATTAGCTTGTT TTT[C]CGAAATGC TATCAGGGTCAA TCCTA	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa.	5.80E-251	
703	cg43950250	675	GTTCTCTACTT CGGGTGGGAAG TC[G]A[GGGTTCT GGAATTGCTGCA TGAGTI	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P11928 ORNITHINE DECARBOXYLASE (EC 4.1.1.17) (ODC) - Homo sapiens (Human), 461 aa.	7.00E-251	2 (2p25)
704	cg43962278	371	AGAGGGTGAGG GTCTGGAGGACT CCTT[A]GTGGTG CAGGCCATCTCC CGGATAG	T	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBL-NEW- ACC:AAD01211 ASPARTYL AMINOPEPTIDASE - HOMO SAPIENS (HUMAN), 472 aa.	1.50E-250	2
705	cg44027341	957	GCACTGGTTTCC GCCTCCGACCTG TTA[G]GCTGGCC TGCTTTCCTCTC GGGATT	A	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P00439 PHENYLALANINE-4-HYDROXYLASE (EC 1.14.16.1) (PAH) (PHE-4- MONOOXYGENASE) - Homo sapiens (Human), 452 aa.	1.60E-246	12
706	cg43996564	739	AGAGGGCACCC CGCAGGCTCAG GGG[C]GJCCACC ACCAGGCGTGA GCTGGATGG	C	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa.	2.90E-245	3
707	cg43980318	600	GCCCAGTTTATT CGTCCAAAGCTG C[AT]GGGAGTG GACTCAGGATGT GCGACC	A	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.60E-244	1 (1cen)

708	cg43985156	1497	CTCTCAAGTTCA TGCTGACGAATC TTT/GJAAAGTGGG GTCCTGCTTGGG TGTCCT	T	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75595 BCL-2-INTERACTING PROTEIN BECLIN - HOMO SAPIENS (HUMAN), 450 aa.	1.80E-243	17
709	cg42897932	675	ATTATATCTCTG GGATCCAGACTA TTT/CJGGACATAG GGTAATTGTATC TGATG	T	C	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA32662 KIAA0017 PROTEIN - HOMO SAPIENS (HUMAN), 1217 aa.	8.20E-241	16
710	cg43936335	747	AAAGGGAATGA GGAGGAGTAGT GGTATTTGCGA GCAGGTTCTCGG AGGGACC	A	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74919 KIAA0896 PROTEIN - HOMO SAPIENS (HUMAN), 1230 aa (fragment).	8.50E-239	8
711	cg44013460	1019	TCAGTGAGTTGA AAAAGCTGGACT TTC/GJCCAGCTC CAATTGGACCCA GCAGCA	C	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.60E-237	1
712	cg44013460	1040	ACTTCCCAGCTC CAATTGGACCCA GTC/GJAGCAGAA TTCGTATTTGTT GAACCA	C	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.60E-237	1
713	cg44013460	1043	TCCAGCTCCAA TTGGACCCAGCA GTC/GJAGAAATTC GTATTTGTTGAA CCAGGG	C	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.60E-237	1
714	cg43948360	2144	CCACACCTGTCA GATCGGGCGAG CTTG/CJCGGAAC GCGTCAGCCCA GGACTGGA	G	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O88746 TOM1 - MUS MUSCULUS (MOUSE), 492 aa.	5.10E-234	22

715	cg43982127	363	CCAAGAAGAAGAC TGTTGTTGAACT GIC/TJGTTGCACA AAGTTTCTTGAC CTCTT	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.10E-233	7
716	cg43982127	678	TAACTGGGGTT CTTTCTCAGACC C[G/A]GACATCCT CTTGTTGATGTT AAACT	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.10E-233	7
717	cg439840463	1031	AGAAATGGCTGC AGCGCTGGAAC C[A/G]GGCCCTC CTCCGCTCAGAC TCAGCT	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99771 JIP-1 - HOMO SAPIENS (HUMAN), 467 aa.	3.10E-232	
718	cg43983074	206	CGGACCTCAACC GCAAGGACAAAGT TTT/CJCCCGCCAT CACCCACCTCAA GTTC	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD31087 VITAMIN D RECEPTOR INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 873 aa.	3.20E-228	19
719	cg43984330	868	CGAGACCCCGC TTCTCCCGGTTG TC[A/G]CTGAGCA GTGGGGTTATGG TGTACA	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P32121 BETA-ARRESTIN 2 - Homo sapiens (Human), 409 aa.	8.50E-223	17
720	cg43999712	467	CCCTGGCAGTG GCCGCTGTGCTA TA[C/T]CACAAGA TGAACAGCGGG AAGCAGG	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.30E-221	2
721	cg43984204	1151	GCATCGCCACAT CCCTGGATGGCT TTC/TGACGTGCG GTCCGTGCAGCA GCAGC	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60864 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa.	5.40E-221	19

722	cg43994204	1157	CCACATCCCTGG ATGGCTTCGACG TTC/TGCGTCCGT GCAGCAGCAGC GGCAGG	C	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60664 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa.	5.40E-221	19
723	cg43960557	1813	TGAAATCAAGGG CCTGGTAGACGA GT/CJGAGTAGA GGTATTCCACCT TCTTAC	T	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa.	2.70E-220	22
724	cg43251548	1238	ATAGTCAGGTTG ATTGGACTTACG ATT/CJCCAAATGA ACCTCGATACTG CAATT	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60394 PAC CLONE DJ0872F07 FROM 7Q31, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 408 aa (fragment).	2.70E-217	
725	cg43068795	633	CTCCTTCTTTCT CCTTCCTCTGTT C/CJCGTTCCTC TTTCATATCTCTA AGTA	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB51071 HYPOTHETICAL 295.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 2701 aa.	2.80E-215	1
726	cg43990581	767	ACCCGTACCTCC CGCTCGTCACCG ATT/CJGAGGACA GCTGGTACAGCA AGTGGC	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60651 RAP2 INTERACTING PROTEIN 8 - HOMO SAPIENS (HUMAN), 405 aa.	1.60E-214	17
727	cg43083763	776	CCCTGAACGCCA CTCCAGGGACCT C/A/GJCTCATCTC CTTCAGTGACAA GGCCA	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P21549 SERINE-PYRUVATE AMINOTRANSFERASE (EC 2.6.1.51) (SPT) (ALANINE- GLYOXYLATE AMINOTRANSFERASE) (EC 2.6.1.44) (AGT) - Homo sapiens (Human), 392 aa.	1.10E-211	2 (2q36)
728	cg43984681	666	ACCCAGCCTTCA TCCGGGCCCTGG GT/GJGGCGGG GTCGGCAACTAC AAGTTAG	G	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O15382 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.42) (BCAT(M)) - Homo sapiens (Human), 392 aa.	1.30E-210	19 (19q13)

729	cg44927668	1463	ATCAGGCTGCGT TTTTGAGTCAAG C[C]/TTCACAGAT GTACGACTCCCTC TTTGA	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC: CAB4885 DJ462023.2 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 406 aa.	2.10E-210	1
730	cg43948416	2020	TTTGGACGAC CCCGTAAGAAAT TTT/CJTGCAATGCT ATTAAGTGCATC CATAG	T	C	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC: AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.70E-206	11
731	cg43959472	1584	TCTTGAGCCACA CGATGCCCGCAG GTA/GJCGCGTG AAGGGTTCTCG TTGATCT	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC: O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.40E-203	15
732	cg43921081	528	ACAAGAGAGAG AATTATCACCG GTT/CJGATGTTGA ACCAACAGATGC GGAAT	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC: Q99733 NUCLEOSOME ASSEMBLY PROTEIN 1- LIKE 4 (NUCLEOSOME ASSEMBLY PROTEIN 2) (NAP2) - Homo sapiens (Human), 375 aa.	3.10E-202	11
733	cg44128902	965	AGATGGAGTCAG CAGATCAGGCC GTT/CJGCTGAG CTCAACGGGACC CAGGIGG	T	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC: P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1.00E-201 (1p36.2)	1
734	cg44128902	761	GGGATCGAGAC CGAGACCGAGA GGGTT/GJCCCTTC CGCAGGTCGGA TTCATTCC	T	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC: P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1.00E-201 (1p36.2)	1
735	cg44128902	797	GGTCGGATTTCAT TCCCTGAACGGC GTA/GJCCCCCTA GGAAAGGGAATA CTCTCT	A	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC: P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1.00E-201 (1p36.2)	1

736	cg43289239	822	TCACCACCCCTGC CCCATGTGCAGA A/A/GJTACCTGAA GTCCGTACGCTA CATTG	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15059 KIAA0351 - HOMO SAPIENS (HUMAN), 557 aa.	1.50E-199	9
737	cg43320965	1607	GTGATACAAGGC AGAGCCTGCAG CA/A/GJTCCATGC CTCCCTGTGAGC CACCAT	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBL-NEW- ACC:AAD30184 HYPOTHETICAL 43.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 391 aa.	5.30E-198	14
738	cg43944615	2020	CATAGCTGTAGT TTTTGCTGAGAT A/C/TJGTGGCCAA AGTTGGCTTCAC CTTTT	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14877 FRPHE - HOMO SAPIENS (HUMAN), 346 aa.	1.30E-192	
739	cg43935935	777	TCCAGTCAAGAA TCCATTTCTAAC T/CJTGATCCAGC TCAGTTGGGATG TACT	T	C	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60735 GA17 PROTEIN - HOMO SAPIENS (HUMAN), 374 aa.	1.70E-192	X
740	cg43984795	2166	CCACGAGGTAGT CTTCCCGGATAA T/G/AJTGCTCCAC ACGGATCCGAG CICGTT	G	A	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53990 HYPOTHETICAL PROTEIN KIAA0174 - Homo sapiens (Human), 364 aa.	5.80E-192	16
741	cg43980381	460	ACACCCTCAGGA CCAAGAAGAACA CT/AJGCCATTGT CAAGCGCTGGA GCGACC	T	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03385 GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM A (RALGEF) - Mus musculus (Mouse), 852 aa.	5.60E-191	9
742	cg43998402	1312	GTGCAAAACCCAC TGTTTCTCATCT C/C/GJGCTATTAG CTCCGAGGGGT GCATCG	C	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.60E-189	2

743	cg43933608	390	CC TTGAGTTTCA GGAGGGGCTGT AA[G]AGTGAAGA AGCATGAAACTC AGTCTC	G	A	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa.	4.50E-189	8
744	cg43249389	924	GCTTCAACCGGT CCCGGGAGTATC A[G]A[CTCAACGA CTCTGCCAAATA CTACC	G	A	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09471 GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 1 - Homo sapiens (Human), 353 aa.	1.40E-188	15
745	cg43947129	1282	TTCTATTTTGGG GCTCCACTGGAC A[A]CJACGTAGAA TCCTTGAGAATT ATCAA	A	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P10658 PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP) - Oryctolagus cuniculus (Rabbit), 370 aa.	3.00E-188	
746	cg43927276	1007	CAGCCTATGGAG GCCTCAATGAGA A[A]GJTCITTTGT AGATGGCTTGAA TTTTA	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P50616 TOB PROTEIN (TRANSDUCER OF ERBB-2) - Homo sapiens (Human), 345 aa.	3.10E-186	17
747	cg43957632	893	TGCTCCCGCCGC CCAACATGTTCA T[G]A[GTGCTGTC CACGTGGTTCTC CACCA	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185 2 (2q33)	
748	cg43957632	1081	GCTCGGAGCCC GGGTGGGGATA GCA[G]CJGCGAG CCCCTGGCCGC AGCGCGGGG	G	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185 2 (2q33)	

749	cg43950796	369	AGTAGTACCGCT GCCAGCCCTGTC GTTCTGTCGGCT CTTCCTCAGGAG CAGGGA	T	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45684 C14ORF3 PROTEIN - HOMO SAPIENS (HUMAN), 338 aa.	2.5E-184	
750	cg44001387	770	GCTGCTCGTTG TGCTCCCAGGCA C/A/GJ/CACAAGG GCTCCCTGAAGC CCCACG	A	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O14832 PEROXISOMAL PHYTANOYL-COA ALPHA-HYDROXYLASE PRECURSOR (PHYTANIC ACID OXIDASE) - Homo sapiens (Human), 338 aa.	8.4E-184	10
751	cg43917229	245	GCCCACTTGCAA CCAGGAGAGCAT TTC/TCTAAAGAA GAAAGGGCTGA CAGATG	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75381 PEROXISOMAL MEMBRANE ANCHOR PROTEIN HSPX14P - HOMO SAPIENS (HUMAN), 377 aa.	1.6E-180	1
752	cg43981031	525	CTGCTATCCCTT TATGAGAGGGAG A/C/TJAAGGTCTG AAGTTTGTTC CAAAG	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34057 CGI-62 PROTEIN - HOMO SAPIENS (HUMAN), 325 aa.	1E-178	
753	cg43919917	1068	ATGACTCAGAGC AGGTGCCCCAG GC/A/CJCTCCGC CGGCTCCGCC GCGCAGCC	A	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60808 BK833B7.1 - HOMO SAPIENS (HUMAN), 339 aa.	3.5E-178	22
754	cg43989723	426	AGCTGCGGGC CGGAGCGAGGC TGA/G/AJATCCG GGTCTTCCTCCA GCAGCTCA	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13486 PSE-BINDING FACTOR PTF DELTA SUBUNIT - HOMO SAPIENS (HUMAN), 334 aa.	1.5E-175	
755	cg43931789	116	CGGCAGCGTCG CTGGAGCTGTG GCT/G/CJAACAAA GCCACAGACCCA AGCATGT	G	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14564 HYPOTHETICAL 67.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	2E-175	16

756	cg43967532	3684	TCATGGCGATGC AGACGTCCCCCT C[G/C]GGGAAC TGTCACACTTAA GCATCT	G	C	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.30E-174	8
757	cg43967532	3843	AGAGCCGAGCAG AGGAAGACCTG GGT[G/C]CCGGC GTGGCAGTCTT GTTGAGCA	G	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.30E-174	8
758	cg43250735	1560	TGATGATGTGGC TCTGGAACCTGT T[G/A]AAGTAGAT AGAACCGTTGTA GACCA	G	A	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q62609 NEURONAL OLFACTOMEDIN- RELATED ER LOCALIZED PROTEIN PRECURSOR (NOEL) (1B426B) - Rattus norvegicus (Rat), 485 aa.	1.20E-173	9
759	cg43918085	877	CACCCATGGGAC CATCTGACCCAG G[A/G]CCCATG GAAAATTAGGTC TGTAG	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45899 HYPOTHETICAL 37.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 361 aa.	1.90E-173	
760	cg43927536	1855	GAGCTGGTGTG GTAACCTCTGGT AC[A/G]AATTGG AAGAACTGGCAT ATGCAG	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60667 ANTI-FAS-INDUCED APOPTOSIS - HOMO SAPIENS (HUMAN), 390 aa.	3.80E-172	
761	cg43923012	1198	CTAACTCTACCA CTGCATTCCAC C[A/G]TAAAGACT GTACATGTCATC TGCAA	A	G	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43210 HYPOTHETICAL 37.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 330 aa (fragment).	9.10E-171	X
762	cg43941339	1200	TGGAGTCTGGC TGTCACATGGT C[A/G]TCATCATC TTCATCATCCAT ATCAT	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10451 OSTEOPOINTIN PRECURSOR (BONE SIALOPROTEIN 1) (URINARY STONE PROTEIN) (SECRETED PHOSPHOPROTEIN 1) (SPP-1) (NEPHROPONTIN) (UROPOINTIN) - Homo sapiens (Human), 314 aa.	8.20E-170 4 (4q21)	

763	cg43251632	646	TAAGTTGTTGT GTGTCACTGTGA C[G/A]GCTCCCA CGGTTGTTTCT TTGGCA	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD38537 TRANSPORTIN-SR - HOMO SAPIENS (HUMAN), 975 aa.	2.50E-169	
764	cg44032718	435	GGGAGGCACCT GCCACCCAGGC CTC[G/A]TCTACT ACTCAGCTGACT GATACCC	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76058 DJ1409.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE) - HOMO SAPIENS (HUMAN), 606 aa.	5.70E-169	X
765	cg44032718	807	CAGGTGGCCGA AGGGTCTCAAAG GCTT/CICTAATGG CCTCAATGGCCC GCAGGG	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76058 DJ1409.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE) - HOMO SAPIENS (HUMAN), 606 aa.	5.70E-169	X
766	cg43959938	1549	TGCATCCAGCAC ACTTCTTGGCCA C[A/G]AAGTTCTT GTAGCAATCCAC GCAGT	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13642 SKELETAL MUSCLE LIM-PROTEIN 1 (SLIM 1) (SLIM) (FOUR AND A HALF LIM DOMAINS PROTEIN 1) (FHL-1) - Homo sapiens (Human), 280 aa.	5.20E-168	X
767	cg43329903	874	TCCGGATCCTCC CAGCCCAGAGC CG[A/G]GCCCTC GGAGGCCCTCC AGAATACC	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
768	cg43329903	883	TCCAGCCCCAGA GCCGAGCCCTC GG[A/G]GGCCCT CCAGAATACCTG GGACAAA	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
769	cg43329903	892	AGAGCCGAGCC CTCGGAGGCCC TCC[A/T]GAATAC CTGGACAAAGA CACAGGC	A	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12

770	cg43329903	895	GCCGAGCCCTC GGAGGCCCTCC AGA[A/G]TACCTG GGACAAAGACAC AGGCTGG	A	G	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16684 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
771	cg43329903	917	AGAATACCTGGG ACAAAGACACAG G[C/T]TGGAGGA CGAGGAGGACG AGGAAGA	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16684 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
772	cg43329903	952	AGGAGGACGAG GAAGAGGCTGAA GG[C/T]GGGGG CTGGCCAGCCTT CGCCAAAT	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16684 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
773	cg43949591	1809	TAAGAACACCTA TCCTGACTTCAT C[A/G]AGATCTTT TAAAACCCATT AAAAA	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43008 HYPOTHETICAL 19.5 KDA PROTEIN - HOMO SAPIENS (HUMAN), 367 aa.	2.60E-166	18
774	cg43949591	1812	GAACACCTATCC TGACTTCATCAA G[A/G]TCTTTTAA AAACCCATTAA AATCG	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43008 HYPOTHETICAL 19.5 KDA PROTEIN - HOMO SAPIENS (HUMAN), 367 aa.	2.60E-166	18
775	cg43949591	1824	TGACTTCATCAA GATCTTTTAAAAA [C/T]CCATTAAAA ATCGGAACCCAGG TCTG	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43008 HYPOTHETICAL 19.5 KDA PROTEIN - HOMO SAPIENS (HUMAN), 367 aa.	2.60E-166	18
776	cg43924431	1015	TTTCATTTTCATT CTCTTGAGCATT C[T]TGTTCTATAT TATTAGCTACTT CAC	C	T	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16637 SURVIVAL MOTOR NEURON PROTEIN 1 - Homo sapiens (Human), 294 aa.	4.20E-166	5

777	cg43951985	856	TGATTCCAGCAT CATGGCAGGTAT TTT/CJACCACATC TGTCACATTCTT ATAGG	T	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43357 HYPOTHETICAL 55.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 505 aa.	2.50E-164	22
778	cg43949202	1179	TTGACTTCTCTTT TTCCAGTTCCTC G/AJGCAAGGCCA CAGGTGCAGTTC TTAC	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75207 HYPOTHETICAL 33.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 312 aa.	6.30E-163	16
779	cg43986422	891	CCTTGTGTCCT TTCCTTTATTGAG JA/GJCTCTCAAAC TGCCATTGAATA TAGG	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P04898 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-1 SUBUNIT (ADENYLATE CYCLASE-INHIBITING G ALPHA PROTEIN) - Homo sapiens (Human), and Bos taurus (Bovine), 353 aa.	6.30E-163	7 (7q21)
780	cg44015739	526	CATCACTGTCCG TGAGACCTATCC A/AJGJCGCGTGA AGGGGTTCTGT GTGTA	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q03969 HEPATIC LECTIN H2, VARIANT (ASIALOGLYCOPROTEIN RECEPTOR H2) - HOMO SAPIENS (HUMAN), 287 aa.	2.80E-160	17 (17p)
781	cg43986534	766	ACTTCTGCTACG AATCCCCCTTCC C/G/CJCGGGTGG CCACCACCCAC CGCCCC	G	C	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75900 METALLOPROTEASE MMP21/22A - HOMO SAPIENS (HUMAN), 390 aa.	4.70E-160	
782	cg42720055	609	GAGGAGTGGCA GTATTCATTGGG CA/AJ/CJCCACA GAGGTCGTGAA GTCAGAC	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P25874 MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN 1 (UCP 1) - Homo sapiens (Human), 307 aa.	1.60E-157	
783	cg43287561	637	CAATCTGGCCTT TCTGCCGGGTTT C/C/AJGGATTAC TTCTTCCCTGGG AAGAA	C	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)

784	cg43287561	661	CCGGATTACATT TCTTCCTGGGAA C/A/GJAACCCCTCT ATTGACCAGGAT GGTGA	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
785	cg43287561	673	TCTTCCTGGGAA CAAACCCCTCTAT TIG/TJACCAGGAT GGTGACTCCCAA GTCAG	G	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
786	cg43287561	693	CTATTGACCAGG ATGGTGACTCCC A/A/GJGTCAGAG CAATGGAAAGGA GTAAACA	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
787	cg43287561	697	TGACCAGGATGG TGACTCCCAAGT C/A/GJGAGCAAT GGAAAGGAGTAA CAACAT	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
788	cg43287561	703	GGATGGTGACTC CCAAGTCAGAGC A/A/GJTGGAAG GAGTAACAACAT AGCCCG	A	G	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
789	cg43287561	709	TGACTCCCAAGT CAGAGCAATGGA A/A/GJGGAGTAA CAACATAGGCC CACTT	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
790	cg43287561	715	CCAAGTCAGAGC AATGGAAAGGAG T/A/GJACAACATA GGCCCCACTTTC AGTTG	A	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)

791	cg43287561	733	AAGAGTAACAA CATAGGCCCCAC TTT/CITCAGTTGA GGATAATCTGCC AGCAT	T	C	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
792	cg43287561	769	ATAATCTGCCAG CATCACGTGCCT CTT/CJCGGACAG GGTCCACCATGG TCCGAG	T	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
793	cg43287561	793	CTCGACAGGG TCCACCATGGTC CGA/GGGCATT ATGTACAGCTCC TTGGAAT	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.4E-156	9 (9q34)
794	cg43254730	1641	GTGGCTCATTC AGAAGCTGAAC CIA/GAGGAGCA GCTGGTTCTCC TGGACA	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43800 NIPSNAP1 PROTEIN - HOMO SAPIENS (HUMAN), 284 aa.	1.80E-156	22
795	cg43298828	424	TGATCTCAGCCT TCTGGATCTCCC CIA/GITTCACATA CGGAGAGACTCT CAGAG	A	G	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92984 INTERFERON-INDUCED LEUCINE ZIPPER PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	1.10E-155	17
796	cg43060941	358	CTGCTGCTGTGT CCAGGCTCTCTT TTT/CJGCTTTCTC CACTATTTTATCT TTCA	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P70287 RETINOBLASTOMA BINDING PROTEIN 6 (PACT) - MUS MUSCULUS (MOUSE), 1587 aa (fragment).	4.90E-153	
797	cg43919239	407	CATGCATGGCTG CAGCATAGAACC TCA/GCCACATTC CTCGTTGGGGTT GCCCT	C	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	

798	cg43917036	2502	TCGGGGAAATGT AGTACCAGTTGT TTG/C/GGCAGAC GGAAATGCGGT AATGCT	G	C	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13239 PUTATIVE SRC-LIKE ADAPTER PROTEIN (SLAP) - HOMO SAPIENS (HUMAN), 276 aa.	1.30E-148	8
799	cg43927534	538	CCCGCTCCTGG GGGAGGTAGTC ATG/G/A/CTGTG GGGCCCTGAGG TAGAGGGGC	G	A	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P23249 PROTEIN MOV-10 - Mus musculus (Mouse), 1004 aa.	9.00E-148	1
800	cg43965798	1352	GGTCTGTTTGA TGAAGTGGAAC C/A/G/AACAGCTC CCTCAGGCACAG AACCA	A	G	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9E-148	1
801	cg43950886	894	TGTCCTTCAGT ATTTCATCCCTG C/A/G/CTGTCTA GCACCCCTGTCCG TGGAG	A	G	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q60921 HUS1+-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 280 aa.	8.1E-147	
802	cg43971525	829	CTGGTGAGGCC ATTTCTCTCGC TTT/C/JTCTGTT CAGCCTCCGGA CCAATCA	T	C	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75337 LIPRIN- BETA2 - HOMO SAPIENS (HUMAN), 783 aa (fragment).	1.2E-143	11
803	cg43999829	665	GCCTGCTGTCAC CAGGGGCGAGG CT/G/C/JATCACCA TCGAGATCAACC CCGACT	G	C	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P21864 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (Human), 271 aa.	2.1E-143 (22q11.2)	22

804	cg43308029	1020	ACAGTTACCGCG TGTAACAATG C/C/AJGGCCCA AGGATGAGGAC CAGGACT	C	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43819 CDNA HOMOLOGOUS TO YEAST SCO1 & SCO2 GENES AND C.ELEGANS CO1F1.2 GENE - HOMO SAPIENS (HUMAN), 266 aa.	6.7E-143	22
805	cg43024858	413	GCGAGAGCAGC GACTTCGAATGC AAT/CJAGATGC TAGAGGCGCAG GAGGAGC	T	C	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q60438 HT PROTEIN - CRICETULUS GRISEUS (CHINESE HAMSTER), 348 aa.	2.3E-142	22
806	cg43309726	616	ACTGTAAGAAGG ACCTGCTCCGCC G/CJGACGTGC TGTAACAAGG GCCGGC	G	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83064 KIAA1112 PROTEIN - HOMO SAPIENS (HUMAN), 694 aa (fragment).	5E-136	
807	cg43309726	623	GAAGGACCTGCT CCGCCGGGACG TG/CJTGTACTA CAAGGCCGGC TGGACAT	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83064 KIAA1112 PROTEIN - HOMO SAPIENS (HUMAN), 694 aa (fragment).	5E-136	
808	cg43994220	323	TCGGGGTGTAG CCAGAGTCGGCT TC/GAJGTGGTG AGGTCAGCGCCT CGGGCCA	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19
809	cg43948495	1189	TCCTACTCCTCC GTTCCCTCATATG G/GJTGAATGGG TTGTCTCTCCAC GGTCAC	G	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
810	cg43942432	811	TGTACTGCAGGG GATGCTCTGCCG G/CJTCCAGGGA CAACAGCCTTTC TCTTGC	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60573 CAP-BINDING PROTEIN 4EHP - HOMO SAPIENS (HUMAN), 245 aa.	5.30E-134	2

811	cg42910848	319	CGCAACACTAGA GACGCTCTCTGG CT/C]GCCATCAG GGGACTCGGAG GTAGGG	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPREMBL-ACC:O14988 GTPASE- ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment).	3.10E-132	
812	cg42910848	484	TGAAGATCTTTT CATAGTACTCGA TTC/TAGCAGTTC AGTGAACATGTT CAGGG	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPREMBL-ACC:O14988 GTPASE- ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment).	3.10E-132	
813	cg43918879	330	TGACGGGGAAG ATGGTCTGACC CG[G/A]GCCAAG GCCTCGGAGCT GCACAGCG	G	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMIF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa.	3.00E-131	21
814	cg43918152	358	AAAGTAATGGTC CAACAGACAGTT A/C/T]GCAGCCAT TTCAGAAAGTGA TGGAT	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
815	cg43918152	362	ATGGTCCACAG ACAGTTACGCAG C/C/T]ATTCAGA AGTGGATCGATT GCAGT	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
816	cg43918152	431	GTAATGGAGAG AAGAACAACACGG A/G/A]CGCTTGG AAGCCCTCGATG CCAATT	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
817	cg43918152	448	AACAAACGGAGC GCTTGAAGCCCC TTC/TGATGCCAA TTCTCGGAAGCA AGAAG	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)

818	cg43918152	503	GGAAAGAAAAGG CAATAAAGGAGC TTG[A]GAAGAGT GGTATGCGAGG CAGGACG	G	A	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
819	cg43918152	509	AAAAGGCAATAA AGGAGCTGGAA GA[G]ATGGTATG CGAGGCAGGAC GAGCAGC	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
820	cg43918152	518	TAAAGGAGCTGG AAGAGTGGTATG C[G]A]AGGCAGG ACGAGCAGCTAC AGAAGA	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
821	cg43918152	521	AGGAGCTGGAA GAGTGGTATGCG AG[G]A]CAGGAC GAGCAGCTACAG AAGACAA	G	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
822	cg43918152	542	CGAGGCAGGAC GAGCAGCTACAG AA[G]A]ACAAAGG CAAACAACAGGG TGGCAG	G	A	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
823	cg43918152	548	AGGACGAGCAG CTACAGAAGACA AA[G]A]GCAAAACA ACAGGGTGGCA GATGAAG	G	A	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
824	cg43928955	182	ACTCTTATGTGA AGTCTACCAAGC TTTC]GTGCTCAA GGGAACCAAGG CGAAGA	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.30E-129	

825	cg43917824	584	CAGTGGTGGTGT TCAGATTTTCC AAGGCTCAGATCC GGTGT	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00236 KIAA0251 - HOMO SAPIENS (HUMAN), 820 aa (fragment).	1.30E-128	16
826	cg43917824	674	TCGGCCGGGAG AGGCACTCGTGT GATTCGCGCTG AATCGCTGGCTG GGAGAAC	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00236 KIAA0251 - HOMO SAPIENS (HUMAN), 820 aa (fragment).	1.30E-128	16
827	cg44128041	132	GGCAGTATGAGA ACAGCGAAGGG GGTTCJTGATG GAGGACTATGAC TACGTTT	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.80E-128	
828	cg43926784	1082	ATACAAGCCATT CATAAACCTCAT C[G]A[CT]GATGCA GAGTGTGTCATA TTTGA	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB44334 CYSTEINE CONJUGATE BETA-LYASE - FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES), 419 aa.	6.70E-127	
829	cg43985142	894	ACAGTGAGATGG CTGGGAAGTAA C[C]A[CCCTCAAA AATATCTTTGTAA GCCA	C	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60660 ASH2L1 - HOMO SAPIENS (HUMAN), 628 aa.	8.00E-127	
830	cg43975901	682	CAGTTAAAGGCG TCACAGGACATG A[A]G[GTCTGCAA TTATTTCTGGAAT GTG	A	G	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30288 GOODPASTURE ANTIGEN-BINDING PROTEIN (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 624 aa.	2.60E-125	
831	cg43307940	788	GATCAAGTCCCT CACCTATACGGC A[A]T[ATCTGT GTGTTCACTAA CAATG	A	T	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P09661 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa.	8.10E-125	15

832	cg44028574	1607	AGGCCGAGTTCA GCCTTCTGCAGG A/A/G]CATCTGG GTGAGGGTCCA GCGAATG	A	G	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD27724 CGI-15 PROTEIN - HOMO SAPIENS (HUMAN), 329 aa.	4.00E-122	20
833	cg43958446	421	CGGGGCCATCT CAGATGGTCTCA TC/A/G]TCGCTCA TGTCACAGATCT CAGCAG	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43069 HYPOTHETICAL 73.5 KD PROTEIN - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 650 aa.	3.10E-120	
834	cg44002087	380	AATTCAACAACG AAATCAATATGA A/C/A]GAAAAGGT GAAAAGGCCACCA AAGCT	C	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60712 HYPOTHETICAL 26.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 236 aa.	2.90E-119	
835	cg29350504	989	CTGTAAATAGATT CCTCACTGCTTG A/A/C]AGGCTTTC TATGGTCTCCCT TGCAA	A	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05814 BETA CASEIN PRECURSOR - Homo sapiens (Human), 226 aa.	4.70E-119	4 (4q21.1)
836	cg43067745	180	TCCCTACCTTAG AAGAAAGGGAGG TG[G/A]TAGATGA AATGAACTGTAT GAAGAG	G	A	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.90E-118	
837	cg43067745	210	TGAAATGAACTG TATGAAGAGCCA C/T/C]AGCCTGG CCCACACACAGA AGAAAG	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.90E-118	
838	cg43067745	225	GAAGAGCCACTA GCCTGGCCCCAC AC/A/G]CAGAAG AAGGACTGGCC CGTCTTCT	A	G	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.90E-118	

839	cg43919033	1483	CCGTGGGTTCCCTC CGAGGCTCTGTG GTC/TGTGGGCA TGCAGGCGTAGT TCCATT	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46893 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.20E-117	1 (1q12)
840	cg43919033	1511	ATTGTCTGTCTCAG AACCTTCCTTCT TGA/CTGAAGAT GCTCCTCACGGC CACTA	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46893 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.20E-117	1 (1q12)
841	cg43919033	1577	GACACTGGTAGC TGAAGCCTTGCC GGA/JTCAAATT CACCCACCCATC ATGCG	G	A	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46893 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.20E-117	1 (1q12)
842	cg43948724	1702	CATCTCATGAGT GTGCCCCATGG GTG/TCCCTCCC CTCTCAGCATTT CCTTGT	C	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.90E-114	16 (16q21)
843	cg43036780	144	CTGTAACATCTT CCTCTTCCCCAT C/GA/JGGTTGA ATCTATTGAAAT GTATAC	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa.	1.50E-110	
844	cg43325007	854	ACGGGTCCAC CTGGGTTTCAGG GATG/AJTAGCCC TTCCTACAGCC AGCGGC	G	A	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa.	4.80E-110	20
845	cg42807145	903	GGCACTTCTCGG ACTCTCCAACT TTC/TGCAGTGAA TTTGGAGGGTT GCTGG	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50461 LIM DOMAIN PROTEIN, CARDIAC (MUSCLE LIM PROTEIN) (CYSTEINE-RICH PROTEIN 3) (CRP3) (LIM-ONLY PROTEIN 4) - Homo sapiens (Human), 194 aa.	1.10E-108	11

846	cg43296554	173	CGGTACACGGTCTC GTCTCTCTCCTG C[C/T]CTCATCAG TGGCCTTCTCTC TTGGG	T	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15527 SURFEIT LOCUS PROTEIN 2 - Homo sapiens (Human), 256 aa.	6.40E-108	9
847	cg43997383	293	TCGAGGACCTGT CTGAAGACTTGG A/A/GTGGAAAT TATCTATGTGGG CTCTG	G	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43363 HYPOTHETICAL 23.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 204 aa.	8.00E-108	
848	cg43941085	500	GGGCTGGGTTT GCTCCCAGTTTC C[G/T]GGCTACC GAGGATTTTCAGT ATGTGC	T	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P53673 BETA CRYSTALLIN A4 - Homo sapiens (Human), 195 aa.	8.10E-108	22 (22q11.2)
849	cg43947512	425	TCAACAGGTTAG GAGAGTTGATCC TTC/TAACCTCTGA GAGCAGCCGCT ATCAGT	T	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q14197 DS-1 PROTEIN - Homo sapiens (Human), 206 aa.	2.10E-107	17
850	cg43947512	570	TCATAGAATCAG GATAGAAAACAT G[C/A]NTCGGGA AAGGCTGAGACA AAAGAG	A	???	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q14197 DS-1 PROTEIN - Homo sapiens (Human), 206 aa.	2.10E-107	17
851	cg43979124	1071	CTCATCAAAGGA ATGCACTAGGAT TTC/TGGCGGG GGTCTTTCTGGT TCCTGT	T	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43023 TRANSMEMBRANE 4 SUPERFAMILY PROTEIN - HOMO SAPIENS (HUMAN), 204 aa.	2.10E-107	
852	cg43945125	680	AGGACTTGTGT GGTACGTGCCTC G[C/G]GCCAGCA TGCCCTTGGGAG CCTCCT	G	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P52566 RHO GDP- DISSOCIATION INHIBITOR 2 (RHO GDI 2) (RHO-GDI BETA) (LY-GDI) - Homo sapiens (Human), 201 aa.	2.70E-107	12

853	cg42854459	287	AGGGTAACCGCA AGTACTTGGTGA C[A/G]TTATGGAG GTTTATGGCATA CAGAG	A	G	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD41342 HEPARANASE - HOMO SAPIENS (HUMAN), 543 aa.	3.50E-107	
854	cg42823937	543	CCAGGTCCAGG GGGTAGGTCAGT GA[A/T]GCGGCT GTCGTTCCAGCC AGTGCGC	A	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43378 R29893_1 - HOMO SAPIENS (HUMAN), 216 aa (fragment).	4.40E-107	
855	cg42385149	259	TGGCGAACCA GCCAGGACTGC GC[G/A]CCGCCG GCCCGCGCGCG GCICACCT	G	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA77398 TEN-M3 - MUS MUSCULUS (MOUSE), 2715 aa.	1.70E-105	
856	cg43991689	688	GGGCTTCGGTGT TGAACACGTAGG C[A/G]TCCAGGC TGAGCAGGTTTG GGTCAT	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD45504 ENDOPLASMIC RETICULUM ALPHA- MANNOSIDASE I (EC 3.2.1.113) - HOMO SAPIENS (HUMAN), 863 aa.	2.50E-104	
857	cg43963123	1595	AGAACTTGACCG TGGTCACAGTTC TT[A/G]CCACCCTG GACCCTCTCGGT GGCCT	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.70E-104	17
858	cg43972159	1519	TGGCGCCATCA CCTTCTTGATGT C[A/G]TCCCTGGC CCGGCTACGGG TCTCGG	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa.	2.60E-102	7 (12q24.1)
859	cg43943283	1114	ATGTGAGCGAAT TGGGCCCTTGTA C[A/G]CAAGGAG GCAAAGTTATT GGGGAA	A	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76994 INTRONIC PROTEIN 259 - DROSOPHILA MELANOGASTER (FRUIT FLY), 259 aa.	1.10E-101	5

860	cg43980312	2517	CTTCGGCTGGGT CCATTTTCCTTC T/A/GAGTCAGAG AGGTGAACCTTC TCTT	T	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.90E-101	8 (8q22)
861	cg42028329	109	CGGCGGCCAAG GAGAACCCGTG CAG/A/GAAATTC CAGGCCAACATC TTCAACA	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
862	cg42028329	220	TGACGCGAGGCAA AACCATTATG GT/C/GGCTGGC TGCTCCTGGCTC CAGATG	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
863	cg42028329	223	CGCAGGCAAAAC CCATTATGGT G/C/TJGGCTGCT CCTGGCTCCAGA TGGCA	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
864	cg42028329	247	GCTGGCTGCTCC TGGCTCCAGATG G/C/GJACCGACT TTGACAACCCAG TACACC	C	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
865	cg42028329	268	ATGCAACCGACT TTGACAACCCAG T/A/GJACCGGT CTCGGAAATGGC AGCGAC	A	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
866	cg42646578	422	ACCGATCACGGT TTTCAAGTCTC T/G/AJTGAGCATA TCTTGCATAAGT CTTGT	G	A	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD31085 KU70-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 288 aa (fragment).	2.40E-99	

867	cg43925352	207	AGGAGTTGCAGC GGCGGCTGAAG CGC/TCTCTACC CGGCCGTGGAC GAACAAG	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment).	3.70E-97	6
868	cg43981552	454	TCATGTTGGCGA GCTATTTCTTAT TCATCCATGTTT GGAGGAGTCAT GGTCT	C	A	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75915 JWA PROTEIN - HOMO SAPIENS (HUMAN), 188 aa.	2.80E-96	3
869	cg43935925	597	GAGTACTCTCCA GAGGCTGGAGG TTTC/TGTGCGGA GTTGTACATGT GGTTGA	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa.	4.60E-98	16
870	cg43971745	1560	GAGGGTCTCTCA GGCTCAGGGGT CTG/GC/CGCC AGGGTGGGGAT GGGAGTGAG	G	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P41271 ZINC FINGER PROTEIN DAN (NO3) - Homo sapiens (Human), 180 aa.	2.00E-95	1
871	cg43922566	874	CACCAGGTGCCT CTGCAACAATGA A/GTACTCTGG CCAGTGGGCGA GGTATT	A	G	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40190 N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT - HOMO SAPIENS (HUMAN), 178 aa.	3.40E-93	20
872	cg43988495	1510	CCAAGTCTACCT CTGGGGGGGACG CC/T/C/GGCTCA GCCCCCGCAGA CC/GCCCCA	T	C	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.40E-92	3
873	cg43955549	1295	GACTATGAGCAA AGGAACAGTTTC C/CACATATTTG ACATTTTCCCA GAAG	A	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA82983 KIAA1031 PROTEIN - HOMO SAPIENS (HUMAN), 940 aa (fragment).	1.70E-91	16

874	cg43978148	805	TAAACAACCTCC TGCACAGTCTGC A[A/G]CTTCCTGA GGCCTGTTCTGA AATAA	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75201 HYPOTHETICAL 64.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment).	4.00E-90	16
875	cg42341305	100	AACAGACTTTGC CAGATGAATATT C[G/C]AGTACAG ACACACCGTATC CCGGCA	G	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60309 KIAA0563 PROTEIN - HOMO SAPIENS (HUMAN), 870 aa.	8.10E-90	
876	cg42341305	124	CGAGTACAGACA CACCGTATCCCG G[C/T]AGCCTACC TCCAGAACTCCG GGTGA	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60309 KIAA0563 PROTEIN - HOMO SAPIENS (HUMAN), 870 aa.	8.10E-90	
877	cg42341305	130	CAGACACACCGT ATCCCGGCAGC CT[A/G]CCTCCAG AACTCCGGGTGA AGGCAG	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60309 KIAA0563 PROTEIN - HOMO SAPIENS (HUMAN), 870 aa.	8.10E-90	
878	cg42463588	275	TTATTAATTCAAA GGCATCTCTGAC [A/G]TATGCTGAA GCTCAGTTGAGA ATTG	A	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA76852 KIAA1008 PROTEIN - HOMO SAPIENS (HUMAN), 928 aa.	8.20E-90	
879	cg43924895	200	AGGTTGGAGATC TCATCTATGGCC A[G/A]TTTGTGGT TGCTAATAAAGA CATGG	G	A	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34097 CGI-102 PROTEIN - HOMO SAPIENS (HUMAN), 220 aa.	1.30E-89	9
880	cg43969092	638	GGCCGGCCATC AGCACGCCCTTC AC[G/C]CGTTCTC CCTCCTCACTGC ACTCGT	G	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74913 KIAA0890 PROTEIN - HOMO SAPIENS (HUMAN), 1194 aa.	6.30E-89	

881	cg43955651	521	CACACTCTCTGT GCATCGGCTTGC GIC/TGTGTCCG GGTGAAGGAG TTGAACG	C	T	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.10E-87	2
882	cg43970868	507	TCTGGCTCTGGG ATATTCTGGCCT CIC/TGACITTCAC ACCGGATGAGA GAGCTA	C	T	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19508 Y39A1C.2 PROTEIN - CAENORHABDITIS ELEGANS, 1066 aa.	9.80E-87	12
883	cg43068353	456	AAAATCCTCTTT GGTTGACTTAA T/CJTCTGTATTAG AAGAACCCTTTG TGG	T	C	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49792 NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD NUCLEOPORIN) (P270) (RAN-BINDING PROTEIN 2) - Homo sapiens (Human), 3224 aa.	1.00E-86	2
884	cg43250258	123	AAATGATAGCAT CCAATAATGTCC CIG/AJATACITTC TTCTTGTGAAGA GAGT	G	A	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34116 CGI-121 PROTEIN - HOMO SAPIENS (HUMAN), 175 aa.	2.60E-86	2
885	cg43934734	1040	GTATGGAAATCT CATCCGGCTCCC CIC/TJTGCTACTC CGGCAGGTCAAT TTCT	C	T	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.10E-84	20
886	cg43934734	617	GTCAAGCTGCCA AACTGCCAAAGT AIC/TJTCCTGCAG CTCCAGCAGGG CCCGGA	C	T	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.10E-84	20
887	cg43986941	398	TTGCACTAAAAG GATCTGTAGCTT TT/CJCCAGCTGA GAATGGAGTTCA GAATA	T	C	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16044 PREPRO-MELANIN- CONCENTRATING HORMONE - HOMO SAPIENS (HUMAN), 165 aa.	3.10E-83	12 (12q23)

888	cg43989507	273	GCAGGAGTGGA AACCAGTAGCTG TC[G/A]TCGGC CACATGTCCTTG AAGGGGA	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P36639 7,8-DIHYDRO-8- OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE) - Homo sapiens (HUMAN), 156 aa.	3.90E-83	7 (7p22)
889	cg43970119	426	CCATTAGTAGGC AAATGTGCTCTG C[G/A]AATTCTCG GATGGCACCAC GGCCAC	G	A	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88719 CMP-N- ACETYLNEURAMINIC ACID SYNTHETASE (EC 2.7.7.43) (ACYLNEURAMINATE CYTIDYLTRANSFERASE) (CMP- SIALATE PYROPHOSPHORYLASE) (CMP-SIALATE SYNTHASE) - MUS MUSCULUS (MOUSE), 432 aa.	1.00E-82	12
890	cg43120215	1007	GGCAGCACTTG GACAGGATGCTG AA[G/C]CCGGCT GCAATGAAGATG AC	G	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P78524 P126 (P70) - HOMO SAPIENS (HUMAN), 1137 aa.	1.30E-82	7
891	cg44007579	95	GCTACCGCAGC CGCTGGTTCGTG TT[C/T]GACGCGC GCCGCTGCTACC TTTACT	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83007 KIAA1055 PROTEIN - HOMO SAPIENS (HUMAN), 868 aa (fragment).	2.20E-82	
892	cg43322319	622	ATGCCTACAAGA CTATGAAAGAGG A[C/T]GAAAAAAG ATACAATGAAAG AATT	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB41267 HYPOTHETICAL 66.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 609 aa.	1.20E-81	
893	cg43917139	113	CTTGGCTGGTGG CCGGCTTGGGT T[C/T]GCTTGTAC ATTCAGCACATA ATCAT	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA76671 CARBONIC ANHYDRASE VB - HOMO SAPIENS (HUMAN), 317 aa.	2.50E-81	X
894	cg43321624	660	AATAACGTGGAT TATGAGGGGCCT C[G/A]GTCACAG CCTGCAGTTCGT AGGGGA	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60377 P1.11659_5 - HOMO SAPIENS (HUMAN), 188 aa (fragment).	1.10E-80	9

895	cg42903644	671	TGGTGCCTGTCA GCAAGCCCGGT GC[A/C]CTTCGTC GCTCCCTGTCCC GCTCCA	A	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:O15273 TELETHONIN - Homo sapiens (Human), 167 aa.	1.40E-80	17
896	cg43969140	425	CAAAGATGGACA CCAGCGAATCAT CTT/CJAGTAATAA GTCTGTCTCCTT CCCAA	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.70E-80	
897	cg43969140	515	CGCCTTGTGG GCTCGGCCCCA CTC[G/T]CCAGTC ACAAAGGCATCA TTAACAC	G	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.70E-80	
898	cg43969140	605	CCTCAGCCTGCT CCACAAACCCTG G[C/G]AGGTGTG TCTTGAACATC CAGGGG	C	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.70E-80	
899	cg44024149	417	ATTCCACAGAA TGATCAAGTTGA C[G/C]ACAGGAA AGGAAGCCGCA CTCAGTT	G	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa.	5.30E-79	1 (1p35)
900	cg44024149	453	AAGCCGCACTCA GTTATGGCTTCT A[C/T]GGCTGCC ACTGTGGCGTG GGTGGA	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa.	5.30E-79	1 (1p35)

901	cg43969316	338	GCTCGAGCTACA GTGGACTACTTG A/GA/JCGACATCA TATTCACACCAA AAATG	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
902	cg43969316	371	ATATTCACACCA AAAATGTAGAAG A/C/TATAATTGA TAGTTTACGGGA TGAAG	C	T	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
903	cg43969316	374	TTACACACCAAAA ATGTAGAACACA T/A/TATTGATAG TTTACGGGATGA AGGGA	A	T	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
904	cg43969316	377	ACACCAAAAAATG TAGAACACATAA TT/A/JGATAGTTT ACGGGATGAAG GGATTG	T	A	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
905	cg43969316	443	AGCGGAGGGAG TACGATGAAGAG AC/A/TJGTTCGAT GGGCAGACGCT GTCATAG	A	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
906	cg43969316	458	ATGAAGAGACAG TTCGATGGGCAG A/C/TJGCTGTCAT AGCTGCGGGAG GTGATG	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
907	cg43327305	199	CACCTGCCTTAA AATTTAAGGTTG A/A/GAATTTCTT CTGTATGGGATC CCCAT	A	G	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46606 PHOSPHATIDIC ACID- PREFERRING PHOSPHOLIPASE A1 - BOS TAURUS (BOVINE), 875 aa.	6.10E-78	

908	cg43973026	689	ACAAGGTACTAG CTATGACCAACC G/A/GAACTTGTC ACCCAAGTCTAC AGGGT	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P52434 DNA-DIRECTED RNA POLYMERASES I, II, AND III 17.1 KD POLYPEPTIDE (EC 2.7.7.6) (RPB17) (RPB8) - Homo sapiens (Human), 150 aa.	1.00E-75	15
909	cg43931888	295	CCTGGCCACCC CAACGCCGAAC GC/C/GTCCAGG GAGGCCACCT GGGAACCC	C	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16192 ORF3 5' OF PD-ECGF/TP - HOMO SAPIENS (HUMAN), 157 aa.	1.00E-75	22
910	cg42897014	515	TGCGCTCCTGCG GCCGGGCCCG GC/G/A/TCGCGT GGCAGCGCCAG GAGGCAGA	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa.	1.70E-75	11 (11q13)
911	cg43155233	81	AGGATGCATTAA ATACAACTGAGA A/C/T/AAATTGCT TGATGCATATAC TCAGA	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB48427 HYPOTHETICAL 88.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 785 aa (fragment).	5.60E-75	
912	cg44012742	226	CCCCCATCCAGA ACATCTCATCCA A/T/C/GTGTCTAGA GGAGTCCGCCAT CTCCG	T	C	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20487 SIMILAR TO RAT TRG GENE PRODUCT. NCBI GI: 1109880 - CAENORHABDITIS ELEGANS, 2018 aa.	1.80E-74	
913	cg36728314	198	TGGAGTGTGG CAGTGGGAGGG AC/G/A/TCGATCC GAAGCTCTTTCT GGCTGG	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83051 KIAA1099 PROTEIN - HOMO SAPIENS (HUMAN), 804 aa.	1.30E-73	
914	cg43932428	588	CAATGGCCCGCT CGATTTGCCAA G/C/A/ACCTGGTT ATTGGGTATGGC CCGTC	C	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60869 EDF-1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa.	2.50E-72	

915	cg43934599	837	AGAGGGAAAAAG CCAGCAAGACCC A[G/A]AAGCTTTT CCATAGGCTTAG AGAGG	G	A	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34127 CGI-132 PROTEIN - HOMO SAPIENS (HUMAN), 137 aa.	3.70E-71	10
916	cg43045396	269	AGGAGCAAGCC AGCTGCCCTTCAC TC[T/C]CGGACAT AAATTCTGGTGC AGACCA	T	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.20E-70	15
917	cg43045396	386	GGCCGTCCCCTT CAAGAAGAGTTT G[C/G]GTGCAGT GGATCTTGTCT CATTCT	C	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.20E-70	15
918	cg43045396	503	TGAAGTTGATCT CAGTGGTGCGC AC[C/G]GTGGTG GATGCTTGATG TAGAACT	C	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.20E-70	15
919	cg43045396	617	GCATGGCGTTCA CACCAGTGCCT T[C/G]AGCAGCT CGTCGAAATTCT CGCTGC	C	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.20E-70	15
920	cg42696021	431	GCTTCACACAGT GGCTGTGCCGC CTT[G/C]ACAAATG AAGTGAACCGGA AGCTGG	T	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
921	cg42696021	449	GCCGCCCTTCACA ATGAAGTGAACC G[G/C]AAGCTGG GCAAGCCTGATT TTGACT	G	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	

922	cg42696021	467	TGAACCGGAAGCT TGGGCAAGCCT GAT/CJTITGACT GCTCAAGAGTTG ATGAGC	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
923	cg42696021	470	ACCGGAAGCTG GGCAAGCCTGAT TTT/CJGACTGCT CAAGAGTTGATG AGCGAT	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
924	cg42696021	485	AGCCTGATTTTG ACTGCTCAAGAG TTT/GJGATGAGC GATGGCGTGAC GGCTGGA	T	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
925	cg42696021	494	TTGACTGCTCAA GAGTTGATGAGC GJA/CJTGGCGTG ACGGCTGGAAG GACGGCT	A	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
926	cg42696021	500	GCTCAAGAGTTG ATGAGCGATGGC GTT/CJGACGGCT GGAAGGACGGC TCCTGTG	T	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
927	cg42921698	532	AGACCACTCCG ACGTGTCCAGCC G(GT)GGGTTGA AATGCAGGGCG GCATCGG	G	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.30E-69	19
928	cg42921698	547	TGTCAGCCCG GGTTGAAATGC AG(GC)GCGGCA TCGGAGCCCTG CTCCTCCC	G	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.30E-69	19

929	cg42921698	664	TGCCAGGGCGG ATGCCCTCGG CAG[C/T]GAGGA CTTGTTGGGGA CGTTGGACA	C	T	Ser	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.30E-69	19
930	cg42721336	1100	CCAGCTCCTGTG CTGGCCTCTTCA TTC/TGCCCTCACA CATCGGCTTCGA CTGGC	C	T	Ile	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P34629 PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-) - Caenorhabditis elegans, 491 aa.	3.30E-69	
931	cg43930848	573	TACGGGCGCGC GTGCGCACTCC GCAI/GJCGCGT TCAGGACCCCG GCGCGGGCA	A	G	Leu	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75817 RIBONUCLEASE P PROTEIN SUBUNIT P20 - HOMO SAPIENS (HUMAN), 140 aa.	7.90E-69	7 (7q21)
932	cg43323149	526	GCCTGACTAGTG TGCTGAGCACCA GIC/TJGGAAGCC CTACAGACGGAC TCAGCG	C	T	Ser	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
933	cg43323149	541	TGAGCACCAGC GGAAGCCCTACA GA[C/T]GGACTCA GCGTCATGCAAG GGCCCT	C	T	Asp	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
934	cg43323149	547	CCAGCGGAAGC CCTACAGACGGA CT[C/T]AGCGTCA TGCAAGGGCCCT ACAGCG	C	T	Leu	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
935	cg43323149	550	GCGGAAGCCCT ACAGACGGACTC AG[C/T]GTCATGC AAGGGCCCTACA GCGAAA	C	T	Ser	Silent- Coding	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1

936	cg43323149	553	GAAGCCCTACAG C ACGACTCAGC GTCTATGCAAG GGCCCTACAGC GAAACAG	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
937	cg43323149	577	TCATGCAAGGGC A CCTACAGCGAAA CAGGCGCCAGCT TTGCTGCCCTTT CAGGGG	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
938	cg43323149	589	CCTACAGCGAAA T CAGCCAGCTTTG CTTATGCCCTTTC AGGGGGCACAC TGAGTG	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
939	cg43323149	595	GCGAAACAGCCA T GCTTGTCTGCC TTCTCAGGGG GCACACTGAGTG GTGGCA	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
940	cg43323149	607	GCCTTGTCTGCC A TTTCAGGGGGCA CTATGCTGAGTG GTGGCATTCTCT CCAGTG	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
941	cg43323149	616	CCCTTTCAGGGG T GCACACTGAGTG GTCTGCGCATTCT CTCCAGTGGCAA GGGAA	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
942	cg43323149	646	TTCTCTCCAGTG C GCAAGGGGAAAT ATCTAGCCGGTT AGAAAGTCAAGC CGATG	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1

943	cg43323149	650	CTCCAGTGGCAA GGGAAAATACAG C[C/A]GGTTAGAA GTTCAAGCCCGAT GTCCA	C	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
944	cg42017985	338	ACAATCTATGCA GTGAAAGAGCTT A[C/T]GATCCTAA GCAGTTCCATAA TAGGG	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P56180 PUTATIVE PROTEIN- TYROSINE PHOSPHATASE TPTE (EC 3.1.3.48) - Homo sapiens (Human), 551 aa.	1.80E-68	
945	cg43942922	234	CCACATCTCAGG CCACTAGGGC AG[A/G]ACAAATA GGTCTCTGTCA AGAGCC	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
946	cg43942922	345	TCACCTCTGAGC CCACATCTCAGG C[C/T]ACTAGGG GAAGAAAAAATA GGTCCT	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
947	cg43942922	366	AGGCCACTAGG GGAAGAAAAAAT AG[G/A]TCCTCTG TCAAGACCCCTG AAACAG	G	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
948	cg43271511	252	ATGACGGCACTG TCAGAAAGGAAT C[C/T]GGCATTCC GTCAGGCAAAAT TGAGG	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD15557 T-CELL RECEPTOR GAMMA CHAIN, TRGV9 - HOMO SAPIENS (HUMAN), 137 aa.	3.40E-68	7 (7p15)
949	cg42831353	788	GCACCGCGGCG GTGGTGAGGAC ACA[G/A]GCTGC GGTGTAAAGCCC GCGTCACCG	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD37863 PUTATIVE NADH OXIDOREDUCTASE COMPLEX I SUBUNIT - CAENORHABDITIS ELEGANS, 237 aa.	1.30E-67	22

950	cg43973869	385	TGGGGGCACAA CTGGCGCTGATA CC[C/T]TGGGTG GAAAAGATCAGA ATGACAG	C	T	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD36983 MAP KINASE PHOSPHATASE-LIKE PROTEIN MK- STYX - HOMO SAPIENS (HUMAN), 313 aa.	3.10E-67	7
951	cg4399983	413	CTTCCAAATTAG CTTCAGTTTCA GT[A/G]AGCAAC CATTAAATCCTAT ATAAA	T	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43446 HYPOTHETICAL 34.0 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 299 aa.	1.00E-66	
952	cg43080742	266	AGACGGTGGCC TCGCTGTGGCC GGC[G/C]CTGCA GGAAC TGGCCC GGTGTGGGA	G	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P53603 FORMINOTRANSFERASE- CYCLODEAMINASE (FTCD) [INCLUDES: GLUTAMATE FORMINOTRANSFERASE (EC 2.1.2.5) (GLUTAMATE FORMYLTRANSFERASE) FORMINOTETRAHYDROFOLATE CYCLODEAMINASE (EC 4.3.1.4)] - Sus scrofa (Pig), 541 aa.	2.20E-66	21
953	cg43827424	304	CGCAGTATTCA GAGAAAAGTATA CT[A/C]CTCAGCT GAAGTACCCGCA CCCTC	T	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O77503 TRANSLATION INITIATION FACTOR EIF2C - ORYCTOLAGUS CUNICULUS (RABBIT), 813 aa.	1.90E-65	
954	cg43919145	1731	CCTCAACAGACT GCCTTTGTTTAC TG[A/T]CTGGAGA AGATAGCAAAAG AGTAG	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB52430 DJ703H14.1 PROTEIN - HOMO SAPIENS (HUMAN), 485 aa (fragment).	3.20E-65	1
955	cg42381630	261	CGACCTATTATT GGCCTAGACCAA G[G/A]CGCTATGT ACAGCCTCCTGA AATGA	G	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.90E-64	

956	cg42381630	267	ATTATTGGCCTA GACCAAGGCGC TATTCGTACAGC CTCCTGAAATGA TTGGGC	T	C	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.90E-64	
957	cg43132517	529	TCCATCTTCAGA CACCCCCCGTC TTC/TCTGACAG GGGAGTTGGCC TTCCAG	C	T	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa.	2.60E-63	
958	cg43132517	556	CTGCACAGGGA GTTGGCCCTTCCA GT[A/G]GGTGT GCTCTTCTGTCT TGACGTC	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa.	2.60E-63	
959	cg43950549	237	AGAAACCGGATG ATGCACAGTATT A/C/T/TGTCAAAG AGCTTATTGTCA CATTG	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	1.40E-62	
960	cg43950549	432	GACAAAAATTAG ATAGTGCAGATA C/C/T/AATTTCAG TGACTGGATTAA AAGGT	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	1.40E-62	
961	cg43969918	863	TTGCGGCCACTT GGGCTTGAGAA T/G/A/GCAGCTTT TCCTCGGCCAGC CCCTG	G	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P43331 SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) - Homo sapiens (Human), 126 aa.	2.90E-62	22
962	cg43950850	526	CCGTCGCGATC GGCCTCCGCCG GATC/TJAGGTTA TCAATCAGGCCG GAGCAGT	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O95298 NADH-JBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I- B14.5B) (CI-B14.5B) - Homo sapiens (Human), 119 aa.	7.80E-62	11

963	cg42672206	593	GCCTGAGACCA CTAACCTTGAT TTTCJTTACAGG CTCAGAGACCAT GGAAC	T	C	Lys	Lys	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to SPTREMBL- ACC:O55129 MICROTUBULE- ASSOCIATED PROTEIN 6 (STOP PROTEIN) - MUS MUSCULUS (MOUSE), 906 aa.	1.30E-61	
964	cg44926550	1939	CTGCACAGGTCA CAATATATTATA [G]GCTTTTCCC AACTTAACCAGG TGTC	G	A	Ala	Ala	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to SWISSPROT- ACC:P51808 PROTEIN 91/23 - Homo sapiens (Human), 116 aa.	2.10E-61	X
965	cg43918476	2024	TGAGCATGACCC GATCTTGAACCT CAGCTGTACTG CAGGTTAACTAC CTGT	A	G	Ser	Ser	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34122 CGI-127 PROTEIN - HOMO SAPIENS (HUMAN), 121 aa.	6.30E-61	2
966	cg43285334	682	CGGTGACCCGG GCGTCAGTGTC CC[G]ATAACCAG AGTAGGCCAGCA GTGATC	G	A	Tyr	Tyr	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa.	1.90E-60	1
967	cg42313635	272	GGGTGAGCAGC AAACAGGAGGTG AC[AG]CAGATTC CTGCAGCTCTGA GTGICC	A	G	Thr	Thr	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to REMTREMBL- ACC:G598237 T CELL RECEPTOR ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 134 aa (fragment).	8.00E-60	
968	cg43985327	429	TCGCGCAGGCC AGACAGCGGTG CAG[AG]CCGCC CCCTGGCAGGT CGGGGTCTGA	A	G	Gly	Gly	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa.	2.10E-59	1
969	cg43939569	691	GCATCCTCAGCT CGGAGATGAATT C[G]CTTCCGGA TCAAGAAGTAGA ACTGA	G	T	Arg	Arg	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32455 GANGLIOSIDE EXPRESSION FACTOR 2 HOMOLOG - HOMO SAPIENS (HUMAN), 117 aa.	3.50E-59	17

970	cg43924537	521	ATCCATTGGCTT TATCCACAGCCT G[C/A]AGGACTC GCTGGATGCTCT CCTTGT	C	A	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTRMBL- ACC:Q08726 CHROMOSOME XV READING FRAME ORF YOR262W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 347 aa.	1.20E-58	
971	cg43920127	340	AAAGATGCAGTT CATAATGTTCTC C[C/A]GATTCAGG AACTCTTATGCT GTGTC	C	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTRMBL- ACC:O75273 R26984_1 - HOMO SAPIENS (HUMAN), 508 aa (fragment).	3.10E-58	15
972	cg40968986	217	CGCGCCTCCTG CTGGCTGCACTG GTG[C/C]CAGGAC TATGTGCAGATG AAGGCCA	G	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)
973	cg40968986	262	AGCCAGTGAG CTGGAGCAGGA GCAIAGJGAGAG AGAGGGCTCCA GAATCATTG	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)
974	cg40968986	304	GAATCATTGCCC AGAAGAGAGCCT GTT[C/G]GACACTG CCACCTGTGTGA CTCATC	T	C	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)
975	cg40968986	361	CAGGCTTGCTGA GCAGATCAGGG GGT[C/G]TGGTG AAGAACAACCTTT GTGCCCA	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)
976	cg40968986	379	CAGGGGGTGTG GTGAAGAACAAC TTT[C/G]TGCCCCA CCAATGTGGGTT CCAAAG	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)

977	cg42165815	217	GGATCCTGGCCTA CGGAGAAGCGG TCJA/GJTAGAAAG GAGAGCGCAAC AGGTAGT	A	G	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD22466 PEROXISOMAL BIOGENESIS FACTOR 16 - HOMO SAPIENS (HUMAN), 336 aa.	3.50E-57	
978	cg43052776	294	AGGGTGGGAGA TTCCTGATGGGA ACG/AJAATTCTC CAGACAGCAGA GATGGTG	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43247 HYPOTHETICAL 34.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 323 aa (fragment).	3.60E-57	
979	cg43999272	459	AGAAGGCGGTG ACTCCAGCTCCT CC/C/TJATAAAGA GGTGGGAGCTG	C	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD05427 NADH-UBIQUINONE OXIDOREDUCTASE B14.5A SUBUNIT - HOMO SAPIENS (HUMAN), 113 aa.	3.20E-58	19
980	cg43300763	922	TCCTCGG CTCGGCGAAGG AGCATCTTTGAA TA/C/TJCAACGCA TAGAGCTGGACC CCAGCA	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q18500 HYPOTHETICAL PROTEIN C36E8.3 - CAENORHABDITIS ELEGANS, 476 aa.	3.20E-56	
981	cg43319008	251	TTAAATTATATAG CAGCATCACCAA [C/T]CAACAGAG GAGATACCTTGA GAAGC	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA20786 KIAA0328 PROTEIN - HOMO SAPIENS (HUMAN), 1661 aa (fragment).	9.20E-56	2
982	cg43869932	1228	CGTTCCTGCACCG A TCTCCTCCGAG CJA/GJTTGAATT CTTCCCCTTGTA GAIGT	A	G	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20124 SIMILAR TO S. CEREVISIAE YJU2 PROTEIN - CAENORHABDITIS ELEGANS, 323 aa.	1.10E-55	
983	cg43835092	99	TGGAGCGGTGC CAGCAGCAGGC GAA/C/TJGAGGT GACGGAAATTAT GCGTAACA	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD28992 VAMP5-LIKE PROTEIN HOMO SAPIENS (HUMAN), 116 aa.	1.80E-55	2

984	cg43942680	699	CGGAGGAGAGC GCCCTCAATCAC GTG/CJAGACAC CCGAGCGACGA AGCCGAGG	G	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38498 T-CELL ACTIVATION PROTEIN - HOMO SAPIENS (HUMAN), 127 aa.	1.80E-55	10
985	cg43269198	536	GCTGGCAGTCTA CCACGCTGATTT G/GA/AACTCGCT GGAAGGCAACAT TTCAA	G	A	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB41301 DJ596C15.1.1 (NOVEL PROTEIN) (ISOFORM 1) - HOMO SAPIENS (HUMAN), 162 aa (fragment).	1.80E-55	20
986	cg43917388	701	GGATGTCCACAT TGACCACGTGCA C/A/GJGGCTGGC AGGTCTCCTGTT CTCTGG	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q22453 SIMILARTO LDL RECEPTOR-RELATED PROTEIN. NCBI GI: 1055166 - CAENORHABDITIS ELEGANS, 1357 aa.	2.30E-55	1
987	cg43917989	775	TGGGCATGCTTG CTGGGGCCGCC AC/G/TJGGTGCT GCTCTTGGCTCA C/TATGT	G	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.30E-55	11
988	cg43917989	793	CCGCCACGGGT GCTGCTCTTGGC TC/A/GJCTTATGT GGTCGCCCTTGCT GGTCT	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.30E-55	11
989	cg43917989	796	CCACGGGTGCT GCTCTTGGCTCA CT/T/CJATGTGGT CGCCTTGCTGGT TCTGAG	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.30E-55	11
990	cg43917989	808	CTCTTGGCTCAC TTATGTGTGCGC C/T/CJTGCTGGTT CTGAGCCCTGG GGCTCG	T	C	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.30E-55	11

991	cg41684708	357	AGCAATCGACCA ATACAGCTGTGA C[C/T]CTGACTGG CTAGTAGTCTCT GGCAC	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P47892 LYMPHOTACTIN PRECURSOR (CYTOKINE SCM-1) (ATAC) (LYMPHOTAXIN) (SCM-1- ALPHA) - Homo sapiens (Human), 114 aa.	2.00E-54	1
992	cg43332460	324	GGAACATCTGGG TCAGCTCCGTGT CT/C]CCAAACTC CTGGGGGAGGT GGTAGA	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q91579 RIBONUCLEOPROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 462 aa.	5.40E-54	
993	cg42855650	520	CCGGGCCCTC ATAGGAGAGGAA GC/T/C]CGGGAG GTGGCCAGGCG GCAGGAAG	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O00230 CORTISTATIN PRECURSOR [CONTAINS: CORTISTATIN-29; CORTISTATIN-17] - Homo sapiens (Human), 105 aa.	7.90E-53	
994	cg42803443	49	TCACCGCCAGGA GGACGCATTG GC/G/C]GAACCC AGAGCCAGCGAT GCGCAC	G	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45012 573K1.15 (MM17M1-6 (NOVEL 7 TRANSMEMBRANE RECEPTOR (RHODOPSIN FAMILY) (OLFACTORY RECEPTOR LIKE PROTEIN)) - MUS MUSCULUS (MOUSE), 309 aa.(fragment).	1.90E-51	
995	cg44027270	229	CAGAGTCCATTA CTTTCTTCTGTT [A/G]AATTTCAT GTTGTTGCTTTT CTG	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14737 TFAR19 - HOMO SAPIENS (HUMAN), 125 aa.	2.20E-50	
996	cg44027270	489	GTTGGCCGCGCAT CACCAGGATCCT G/T/G]CGGCTAA ACTTGGGTCATA ACAAC	T	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14737 TFAR19 - HOMO SAPIENS (HUMAN), 125 aa.	2.20E-50	
997	cg41588177	226	CATTCTTGTCCT TTTCTCAAAGA C/A/G]TCGGCGA GGTAATTGTGC CCTTT	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P31151 S100 CALCIUM-BINDING PROTEIN A7 (PSORIASIN) - Homo sapiens (Human), 100 aa.	4.50E-50	1 (1q21)

998	cg44010855	651	CCTGGAACGAGAC AGCGCAGGGTC TA[C/T]GAAGAAT AGGGTGAAAAAC CTCAGA	C	T	Tyr	SILENT- CODING	UNCLAS- SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38944 NJAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa.	5.80E-50	5
999	cg44917490	446	CTCGGGCTCGG CTGAAGGGGTG AAG[G/A]GGGCC GGGTCAGGGTC GTTCCCTCCA	G	A		SILENT- NONCODING	amyloid	Human Gene SWISSPROT-ID:P51693 AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP) - HOMO SAPIENS (HUMAN), 650 aa.	0.00E+00	19
1000	cg43921977	3515	CAGCCGCGGAC CGTAGCTGGCAG TA[C/T]CCGCTCC TGCCGCCCGCTC CGCCTCA	C	T		SILENT- NONCODING	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0.00E+00	20
1001	cg43921977	442	GGAATTCGTGAC AAGTTCAAAAG A[G/A]AACTTCCT TTGTTTAAATGCA GCTG	G	A		SILENT- NONCODING	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0.00E+00	20
1002	cg42840476	5048	TGTAATCCCAGC TCCTTGGGAGGC TA[G/A]GACAGG AGGATTCCTTGA GCCCTG	A	G		SILENT- NONCODING	apoptosis	Human Gene SWISSPROT-ID:O14727 APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1) - HOMO SAPIENS (HUMAN), 1194 aa.	0.00E+00	
1003	cg43970780	245	GGCAGGAGATAA ACCATCCAGCAG AT/GTTTTCTGT GTAAAAACATTT ATTTT	T	G		SILENT- NONCODING	apoptosis	Human Gene SWISSNEW-ID:Q92785 ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM) - HOMO SAPIENS (HUMAN), 391 aa. Jcds:SWISSPROT-ID:Q92785 ZINC- FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM) - HOMO SAPIENS (HUMAN), 391 aa.	2.30E-212	11

1004	cg44001801	997	AGTAAATATCCC CTTGGCTGTGTT TT[<i>gap</i>]GTCAAA CATTGGGATTCT TTTTGCC	T	gap			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1005	cg44001801	1041	TTTGGCCAAAGTG CAACATGACTC TTAGGCCACTGTT ACCACCAATTGC AGTGG	A	G			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1006	cg44001801	1050	GTGCAAAACATGA CTCTACCACTGT TTAGGCCACCAAT TGCAGTGGACAC AGCCA	A	G			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1007	cg44001801	1238	AATCAGAGAAC AAAAGACAGCAC C[C/ <i>gap</i>]AGAAAG TTCTTCCCTGTT GAATCA	C	gap			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1008	cg44001801	270	TATTTTAAAGCTA TAACAGATTTTG C/GJACATAAAGC CAAAACAGATTG TTTT	C	G			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10

1009	cg44001801	571	CAGCTCACTCCA TCTCAGTCAGTG G[C/T]TTTGTCT TGTCATGGCTCC ATTTT	C	T			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1010	cg44001801	714	AAACCTCTTCCC ATTATCCTCATA G[C/A]CCTGGGT GTGGTAACAGCT TCTTGC	C	A			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1011	cg44001801	747	GTGGTAACAGCT TCTTGCTGTTTG G[C/G]TTCCTTT TATCATCTATGTA AGTC	C	G			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1012	cg44001801	755	AGCTTCTTGCTG TTTGCTTCTCT TT[A/T]ATCATCT ATGTAAGTCAAT TTCCT	T	A			SILENT- NONCODI NG	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1013	cg43921971	1242	CAGCTGCATTAA AACAAAGGAAGT TT[C/T]CCTTTTG AACTTGTACAGA ATTCC	T	C			SILENT- NONCODI NG	apoptosis	Human Gene Similar to SWISSPROT- ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	6.10E-68	
1014	cg43042134	636	TAATAAAATTAATT CTAAAGTTTAGA[T/C]GATGTTTTG GTTCTTCTTCAT GAAA	T	C			SILENT- NONCODI NG	apoptosis Inhib	Human Gene SPTREMBL-ID:Q13489 INHIBITOR OF APOPTOSIS PROTEIN 1 - HOMO SAPIENS (HUMAN), 604 aa.	0.00E+00	11

1015	cg43983747	26	TTTTTTTTTTT TTTTTTTTTTT[C /TTTCATTAACTT CTGGGCTTTATT TA	C	T				SILENT- NONCODI NG	apoptosis inhib	Human Gene Homologous to SWISSPROT-ID:Q92843 APOPTOSIS REGULATOR BCL-W (KIAA0271) - HOMO SAPIENS (HUMAN), 193 aa.	2.1E-101	
1016	cg43983747	28	TTTTTTTTTTT TTTTTTTTTTT[C /TTTCATTAACTT GGGCTTTATT TT	C	T				SILENT- NONCODI NG	apoptosis inhib	Human Gene Homologous to SWISSPROT-ID:Q92843 APOPTOSIS REGULATOR BCL-W (KIAA0271) - HOMO SAPIENS (HUMAN), 193 aa.	2.1E-101	
1017	cg43324271	2553	CCTGTTAAAAAG AAAGTGCAGTCA G/ATTTCTAAGC CCTGTTCAAGAG CTTCG	A	T				SILENT- NONCODI NG	apoptosis recep	Human Gene SWISSPROT-ID:Q13546 SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP) (RECEPTOR INTERACTING PROTEIN) - HOMO SAPIENS (HUMAN), 671 aa.	0	6
1018	cg43917593	306	CAGATAAGCAAG TGAGATCCCTCTG G/C/TCCTTAATC ATCAATATACTC AAATG	C	T				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSNEW-ID:Q99460 26S PROTEASOME REGULATORY SUBUNIT S1 (P112) - HOMO SAPIENS (HUMAN), 953 aa.	0	2
1019	cg43987714	2968	AGTGACCACCAG GGGCTCTGAACT G/C/TAAGCTGATG TTATCAGCAGGC CATGC	C	T				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa. pcis:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.	0	3

1020	cg43987714	2992	GCAGCTGATGTT ATCAGCAGGCCA T[G/gap]CATCCT GCTGCCAAGGG TGGACACG	G	gap				SILENT- NONCODING	ATPase_ associated	Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.lpcis:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.	0	3
1021	cg43924820	1166	CAAATACCTGGA TTTTTTTTTTTTT gap/TGTACACTG GTTTCATAGATCG GCACT	gap	T				SILENT- NONCODING	ATPase_ associated	Human Gene SWISSNEW-ID:Q14974 IMPORTIN BETA-1 SUBUNIT (KARYOPHERIN BETA-1 SUBUNIT) (NUCLEAR FACTOR P97) (IMPORTIN 90) - HOMO SAPIENS (HUMAN), 876 aa.lpcis:SWISSPROT-ID:Q14974 IMPORTIN BETA-1 SUBUNIT (KARYOPHERIN BETA-1 SUBUNIT) (NUCLEAR FACTOR P97) (IMPORTIN 90) - HOMO SAPIENS (HUMAN), 876 aa.lpcis:SPTREMBL-ID:Q14974 NUCLEAR FACTOR P97 - HOMO SAPIENS (HUMAN), 876 aa.	0	17
1022	cg43944573	820	AGGAGCCACCTT TGCTGGGCTCG GC[C/gap]TCTAC CAAGCAGAAATG CGATTACA	C	gap				SILENT- NONCODING	ATPase_ associated	Human Gene SPTREMBL-ID:Q99721 TBP-ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 947 aa (fragment).	0	20
1023	cg43277630	3793	ATCATGTTTCTG AGACCACAGTTT A[A/C]AACAGGTG TGCCTGTTGCTT TCTTC	A	C				SILENT- NONCODING	ATPase_ associated	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)

1024	cg43277630	3794	TCATGTTTCTGA GACCACAGTTTA A/CACAGAGGTGT GCCTGTTGCTTT CTCC	A	C				SILENT- NONCODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)
1025	cg43277630	4360	TCGTGGGGTTCA GTAGAGAAATCA A/GTTTGACTAGC GCCTGGCCTTGT GTGGC	G	T				SILENT- NONCODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)
1026	cg43277630	4504	CCACAGCACCCCA GAAGGGAGCAT CTA/GTTTACCT GGCAGTGGCTCT CAGAGC	A	G				SILENT- NONCODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)
1027	cg4320091	21	TTTTTTTTTTTT AGGGGGC[G/A]G GACATGCTTTAT TTTCAGCCACAG	G	A				SILENT- NONCODING	ATPase_ associate d	Human Gene SWISSPROT-ID:Q13608 PEROXISOME ASSEMBLY FACTOR-2 (PAF-2) (PEROXISOMAL-TYPE ATPASE 1) (PEROXIN-6) - HOMO SAPIENS (HUMAN), 980 aa.	0	6 (6p21.1)
1028	cg43247872	1766	GTTGATAACCAT ATGCACCTTAACA TTT/gapJATATTCT ATAAACATTAAAG TAGTGC	T	gap				SILENT- NONCODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21
1029	cg43247872	1802	ACATTAAAGTAGT GCCAGTTATGAG A/gap/CJTCCCA GTTCTTACTAAAT IGTATT	gap	C				SILENT- NONCODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21
1030	cg43247872	1878	TATCACATGTAA CTAATAATTGAA C/GTATACATTGA AGGACCGTGTG ATGT	C	G				SILENT- NONCODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21

1031	cg43247872	1943	GGTTGGAAGATA GCAGTATTATTA G[C/gap]ATAAGC TGCATACGTAAT ATTACGT	C	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21
1032	cg43247872	2121	TATTCAATGTTT CAGCACCATATA A/G]TAGAAATAC CCAATTATATTCT AGT	A	G				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21
1033	cg43958825	101	CGTGAGACTGG GGCTGGCCTGT GTG[C/gap]CCTA GGCGTAGTATTG TAGGTTGGC	C	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	7.8E-228	11
1034	cg43958825	103	TGAGACTGGGG CTGGCCTGTGTG CC[C/gap]TAGGC GTAGTATTGTAG GTGGCCT	C	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	7.8E-228	11
1035	cg43958825	38	TTTTTTTTTTTT TTTTTTTTTTTTTT GJTITGACCCTA AACCATCTTTAT T	T	G				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	7.8E-228	11
1036	cg43975309	160	TAGTGATAGAA CATTTCACAATTA [C/T]ACTCATCTT TTACATAACATCT TGA	C	T				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SPTREMBL-ID:Q93529 F18C12.2 - CAENORHABDITIS ELEGANS, 2245 aa.	5.8E-184	3
1037	cg43975309	553	AACAAATGTGCT TACATACACCAA G[A/gap]AAAAAA AAATTC TTGTG ACCCACT	A	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SPTREMBL-ID:Q93529 F18C12.2 - CAENORHABDITIS ELEGANS, 2245 aa.	5.8E-184	3

1038	cg43300636	224	GGTCAGGAAGG AGGCTGCGCAG GAC[C/gap]TGCA GTGGGCCCTAGT CATCTGTGG	C	gap				SILENT- NONCODING	ATPase_ associated	Human Gene SPTREMBL-ID:Q29466 VACUOLAR H ⁺ -ATPASE SUBUNIT (EC 3.6.1.34) (H ⁺)-TRANSPORTING SYNTHASE) (H ⁺)-TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (CHLOROPLAST ATPASE) (COUPLING FACTORS (F(O), F(1) AND CF(1))) - BOS TAURUS (BOVINE), 838 aa.	1.7E-175	
1039	cg43945992	1220	CCGATCTCCACT GTTGGGTGGGT GG[G/gap]CCCTG CCGGGACCCTG CTCACAGGC	G	gap				SILENT- NONCODING	ATPase_ associated	Human Gene SWISSPROT-ID:P13686 TARTRATE-RESISTANT ACID PHOSPHATASE TYPE 5 PRECURSOR (EC 3.1.3.2) (TR-AP) (TARTRATE-RESISTANT ACID ATPASE) (TRATPASE) - HOMO SAPIENS (HUMAN), 323 aa.	1.1E-173 (19p13.3)	19
1040	cg43918426	356	GCAGTCGAGCG CCACGGCTGCTC AT[C/T]GGATGAT CCAGGATGGGT CCTTGGC	C	T				SILENT- NONCODING	ATPase_ associated	Human Gene SWISSNEW-ID:O42908 HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 882 aa.	4.7E-155	20
1041	cg43918426	427	CGAGGATGGCC AGGCCGTGTGT GCT[C/T]TCCCA GTGCCGAGGTA CCTATCGC	C	T				SILENT- NONCODING	ATPase_ associated	Human Gene SWISSNEW-ID:O42908 HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 882 aa.	4.7E-155	20
1042	cg43918426	445	GTGTGCTCTTCC CAGTGCCGAGG TA[C/T]CTATCGC TCACGGCCAGG AGCTTGT	C	T				SILENT- NONCODING	ATPase_ associated	Human Gene SWISSNEW-ID:O42908 HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 882 aa.	4.7E-155	20
1043	cg43918426	193	TTTTTTTTTTTT TTTTTTTTTTTT TTGCCTTAGAGA GGGCAGTTTAT TGT	G	T				SILENT- NONCODING	ATPase_ associated	Human Gene SPTREMBL-ID:Q25531 40-KDA V-ATPASE SUBUNIT - MANDUCA SEXTA (TOBACCÓ HAWKMOOTH) (TOBACCÓ HORNWORM), 348 aa.	7.2E-154	

1044	cg43947105	1689	TCTCGTTCTTCG TCATGGTGTGCG C[G/gap]CGGACG GCGAGAGGAGC TGGGCGCG	G	gap			SILENT- NONCODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.6E-152	
1045	cg43947105	1763	GCGGAGGCGCG TCCCGGCTCCG GCG[G/gap]CGCA GCCCGGAGACG GCAGTGAAGG	G	gap			SILENT- NONCODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	
1046	cg43947105	492	CTGTTGACATCA AAATATGACAGT T[G/gap]TTATATC CATAAAATATTTA CATAG	G	gap			SILENT- NONCODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	
1047	cg43947105	575	TAAACCAACATAA AAAGAGGACAAG A[C/A]CCCCATCC TACATGTTTGA ATCAG	C	A			SILENT- NONCODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	
1048	cg43947105	587	AAAGAGGACAAG ACCCCATCCTA C[A/G]TGTGTTGA ATCAGGTGTTCA CCGGT	A	G			SILENT- NONCODING	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	

1049	cg43947105	609	TACATGTTTGGG ATCAGGTGTTCA C/C/G/GGTCCT ATCTGGCGACTG TAACT	C	G				SILENT- NONCODI NG	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	
1050	cg43927442	303	TGTTTTTTTTT TTTTTTTTTTTTT ATCCACATTCAG TTCTTTTATTAA T	T	A				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to SWISSNEW-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa. lpcis:SWISSPROT-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.	6.40E-146	17
1051	cg43927442	304	TGTTTTTTTTT TTTTTTTTTTTTT AJCCACATTCAGT TCITTTATTTAAT T	T	A				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to SWISSNEW-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa. lpcis:SWISSPROT-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.	6.40E-146	17
1052	cg43972614	146	GTTGTTTTTTTTT TTTTTTTTTTTTT AJATCGAGAATTC ACTGTTTATTGT G	T	A				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G2791859 RIBOSOMAL PROTEIN S4 Y ISOFORM - HOMO SAPIENS (HUMAN), 263 aa.	1.00E-140 (Yp11.3)	Y
1053	cg43972614	148	TGTTTTTTTTT TTTTTTTTTTTTT AJCGAGAATTC CTGTTTATTGT GCA	T	A				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G2791859 RIBOSOMAL PROTEIN S4 Y ISOFORM - HOMO SAPIENS (HUMAN), 263 aa.	1.00E-140 (Yp11.3)	Y
1054	cg43918496	1850	GCTTGCTGGTTT TATTGCAAGAA A/T/CJAAGTAGCA TTGCAGTAGTCT ACTT	T	C				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to SWISSPROT-ID:P54813 YME1 PROTEIN HOMOLOG (EC 3.4.24.-) - CAENORHABDITIS ELEGANS, 676 aa.	2.80E-136	10

1055	cg43284434	2578	ATCAGAGAGGAA TAAAAAGACATT TTT/gapJATAATTT ATTCTGCTCCAT TCCCTT	T	gap			SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
1056	cg43284434	2751	GTGGACCTAAAT TCCATTATCATC [C/gap]TTTATTAA TTCAGCCAGTGT ATCCA	C	gap			SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
1057	cg43284434	2877	CTGAATAGAAAT GTATAGCGATGA C[C/T]TCTTAAT ATAATTTGATTTG ACTG	C	T			SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
1058	cg43284434	3312	ATACTAGTTAAT TCTCCATTCCC C/TACTACACAG AGAGGTGAGCTT TCAA	C	T			SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
1059	cg43974574	1219	AAACCACTTAA TGTGAAGGAACA A[C/gap]AGCAAC AAGACCAGTATG ATATACC	C	gap			SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G2687400 VESICLE SOLUBLE NSF ATTACHMENT PROTEIN RECEPTOR - HOMO SAPIENS (HUMAN), 232 aa.	1.40E-116	14
1060	cg43967912	2065	GGAGACTCCGG GAGCCGAAAGT GAA[G/gap]CGGG TCCCGCACCAAG GAGACGTTG	G	gap			SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREVISIAE VACUOLAR H(+)-ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa.	5.60E-108	8
1061	cg43954224	3379	GATTTGTGCAT GTAGTTCAGTCT A[C/G]TGTGGTA GCATGACAGAAA GTGGG	C	G			SILENT- NONCODI NG	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	3.70E-103	1

1062	cg43250373	1641	TATGCTGGCTGG AGTGAGGAAAA A[agap]TCGTCC AGGAGCATTTT CCTCCAT	A	gap			SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to TREMBLNEW- ID:G2921585 ECTO-ATPASE - MUS MUSCULUS (MOUSE), 495 aa.	1.40E-100	10 (10q24)
1063	cg43250373	2397	CAGTTACAACCTC AGGGTCACAAAA A[agap]TGCATC TTCCAATGCATA TTTTTAT	A	gap			SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to TREMBLNEW- ID:G2921585 ECTO-ATPASE - MUS MUSCULUS (MOUSE), 495 aa.	1.40E-100	10 (10q24)
1064	cg4386887	104	AAGTAAAGTGAA TGAAACCATTTG TIG/AJATTAAGAT ACATAGACAGAA CTTCA	G	A			SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:000393 P97 HOMOLOGOUS PROTEIN - HOMO SAPIENS (HUMAN), 277 aa (fragment).	7.90E-93	16
1065	cg4386887	136	ATACATAGACAG AACTTCAATGTA G[agap]AAAAA AAAGACCTTGCT GGGAAAC	A	gap			SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:000393 P97 HOMOLOGOUS PROTEIN - HOMO SAPIENS (HUMAN), 277 aa (fragment).	7.90E-93	16
1066	cg4386887	145	AGAACTTCAATG TAGAAAAA A[agap]AGACCTT GCTGGGAACA GATGAIGA	gap	A			SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:000393 P97 HOMOLOGOUS PROTEIN - HOMO SAPIENS (HUMAN), 277 aa (fragment).	7.90E-93	16
1067	cg43869125	681	AATGGACAATAA AGGACTGAGGG AG[agap]GGGCT AGAAAATGATTG ATTTTCT	A	gap			SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:P18708 VESICULAR-FUSION PROTEIN NSF (N-ETHYLMALIMIDE- SENSITIVE FUSION PROTEIN) (NEM- SENSITIVE FUSION PROTEIN) - CRICETULUS GRISEUS (CHINESE HAMSTER), 744 aa.	1.40E-79	17
1068	cg43972161	186	TTTTTTTTTTTT TTTTTTTTTTTTT AJAAAAATTTTAA TCTTTAATTCCTG T	T	A			SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	

1069	cg43972161	306	AGCCCTGGGT CGGGCGGGGT CCC[C/gap]TGGG CCGCCGGGGG GTCCACATGC	C	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1070	cg43972161	314	GGTCGGGCGG GGTCCCCTGGG CCG[C/gap]CCGG GGGTCCACAT GCAGCCCCCTG	C	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1071	cg43972161	316	TCGGGGCGGG TCCCCTGGGC GCC[C/gap]GGGG GGTCCACATGCA GCCCTGGG	C	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1072	cg43972161	342	GGGGGTCCAC ATGCAGCCCCTG GGT[C/gap]GGGG CCGGCGGGGG TGAGGTCCG	T	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1073	cg43972161	405	TTGCTGAGTCC GGCCGGTTGGG GC[C/gap]GCCGC TAGCGCGCTG GCTGGGCAG	C	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1074	cg43943233	1023	GCAAGCAAAAC AAAGCTATACT TTG[A]GCAGTGG TATTCAACCACC ACTTAT	G	A				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:O15511 ARP2/3 COMPLEX 16 KD SUBUNIT (P16-ARC) - HOMO SAPIENS (HUMAN), 151 aa.	3.90E-75	

1075	cg43943233	320	TATCAAAAACAG CAAAGAGTTTAT A/A/G/AATTTCTG CACCAGTTTGCA CATAA	A	G			SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:O15511 ARP23 COMPLEX 16 KD SUBUNIT (P16-ARC) - HOMO SAPIENS (HUMAN), 151 aa.	3.90E-75	
1076	cg43917062	179	GGAGACAAATAC ACAAATAACTAG A/A/T/TACAAGGC AGTAAACAAGAG TGGGC	A	T			SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSNEW- ID:O42945 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPBC16H5.10C - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 735 aa.	6.10E-65	17
1077	cg43917062	76	ACTGAGTGACTA CTATGTGCAAAG C/A/gap/CTATGC TAGGTGCATGAA AGATACA	A	gap			SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSNEW- ID:O42945 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPBC16H5.10C - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 735 aa.	6.10E-65	17
1078	cg44022155	1279	GAGAGCTGGCC GAGCAGCCCTG GCC/A/G/CCGCT GCCCGCCGGCC CCCTGAGGT	A	G			SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:Q12697 PROBABLE CALCIUM- TRANSPORTING ATPASE 9 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1472 aa.	1.50E-63	1
1079	cg44015998	172	AGCCAGCGGAT GGCTGTGGGG TCC[C/gap]AGCT CAGTCTTCCAAG GGCGAGACT	C	gap			SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:P39986 PROBABLE CALCIUM- TRANSPORTING ATPASE 6 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1215 aa.	1.50E-53	
1080	cg44015998	268	GCCCTGTGGG GTTCCCGCCAG CG[G/gap]CAGCC AGGGTGGGCAG TGGGTACCA	G	gap			SILENT- NONCODING	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:P39986 PROBABLE CALCIUM- TRANSPORTING ATPASE 6 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1215 aa.	1.50E-53	

1081	cg43917679	327	CAAGAAGGGAAC AGGATTATTAG AIC/TJCATTCCA GGACAGGGACC CAGGGG	C	T				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:P46467 SKD1 PROTEIN - MUS MUSCULUS (MOUSE), 444 aa.	4.30E-53	16
1082	cg43917679	549	CAGAGCTTGGG CTGGGGTTGCA GGG[G/gap]CATC AGCCAATCTGCT CTCAAGGAG	G	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:P46467 SKD1 PROTEIN - MUS MUSCULUS (MOUSE), 444 aa.	4.30E-53	16
1083	cg43917679	837	GTAGGAAGAGCA GTGTCCACTGTG T[G/gap]CCCCAG GGCAGTGGAGT GTCTCTGT	G	gap				SILENT- NONCODI NG	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:P46467 SKD1 PROTEIN - MUS MUSCULUS (MOUSE), 444 aa.	4.30E-53	16
1084	cg43966234	2339	AAAAATCACCAA TGGAATTTTCA TTT/gap[GATATAA ATACTTGATACAT ATGATT	T	gap				SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05165 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 702 aa.	0.00E+00 (13q32)	13
1085	cg43966234	2357	TTTTCATTGATAT AAATACTTGATAC A/gapJTATGATTT GTACTTCTGCTG TGAGA	A	gap				SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05165 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 702 aa.	0.00E+00 (13q32)	13
1086	cg43966234	2363	TTGATATAAATAC TTGTACATATGA T/GTTGTACTTCT GCTGTGAGATTC CCT	T	G				SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05165 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 702 aa.	0.00E+00 (13q32)	13

1087	cg43009431	3003	CTCCCCAAACGGC CGGTAATGCCG GG[C/gap]GTCCC CGAGACGCGGC TGCCTGTCC	gap			SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P50747 BIOTIN-PROTEIN LIGASE (EC 6.3.4.-) (BIOTIN APO-PROTEIN LIGASE) (BIOTIN-[METHYLMALONYL-COA- CARBOXYLTRANSFERASE] LIGASE (EC 6.3.4.9) / BIOTIN-[PROPIONYL- COA-CARBOXYLASE (ATP- HYDROLYSING)] LIGASE (EC 6.3.4.10) (HOLOCARBOXYLASE SYNTHETASE) (HCS) / BIOTIN- [METHYLCROTONOYL COA-CARBOXYLASE] LIGASE (EC 6.3.4.11) / BIOTIN-- [ACETYL-COA- CARBOXYLASE] LIGASE (EC 6.3.4.15)) HOMO SAPIENS (HUMAN), 726 aa.	0.00E+00	21 (21q22.1)
1088	cg43920913	1770	CCATTCCTGCCT A TTTGCAATCATG A/ATTACCTGGGA ATCCAAATAGTT GGATA	T			SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)
1089	cg43920913	1777	TGCCTTTTGCAA G TCATGAAACCTG G[G/C]AATCCAAA TAGTTGGATAAC TTAGA	C			SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)
1090	cg43920913	1788	TCATGAAACCTG gap GGAATCCAAATA G[gap/G]TTGGAT AACTTAGAATAA CTAAGTT	G			SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)

1091	cg43920913	1796	CCTGGGAATCCA AATAGTTGGATA A[gap/G]CTTAGA ATAACTAAGTTTA TTAAAT	gap	G				SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)
1092	cg43920913	1801	GGAATCCAAATA GTTGGATAACTT A[G/T]AATAACTA AGTTTATTAAATT CTAG	G	T				SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)
1093	cg43920913	1809	AATAGTTGGATA ACTTAGAATAAC TTA/G]AGTTTATT AAATTCTAGAAA GATAA	A	G				SILENT- NONCODI NG	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.2E-288	3 (3q21)
1094	cg43931765	665	GCCAGGTGACAT GGCCAGGCACC TT[gap/C]CCTGT ACAGGCACTGTG GGCTCCTG	gap	C				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
1095	cg43931765	692	CTGTACAGGCAC TGTTGGGCTCCTG G[C/gap]CCAGGC TCACTAGAAGGT CTTCTCT	C	gap				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
1096	cg43918042	1005	TTAGAGGAGCA GTAGCAGCAGCA G[C/gap]AGGAGA AGATGCTGAGGA TGGGGAC	C	gap				SILENT- NONCODI NG	cadherin	Human Gene TREMBLNEW- ID:G2852363 NF-PROTOCOLADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa.	0	4
1097	cg43265972	2272	TGATGAGTTTAT TAGCTAAGTTAA A[A/gap]TTAATTT GAACCTTGATCT AAACCA	A	gap				SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCOLADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5

1098	cg43265972	2279	TTCAATTAGCTAA GTTAAATTAATT [T/gap]GAACCTTT GATCTAAACCAA AACAAA	T	gap			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCOLADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1099	cg43265972	2333	GGAAATAAAGC TGTAAGGAACCT TTT/gap]ATCAAG CATTCCAAAACC AACTAGA	T	gap			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCOLADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1100	cg43265972	2374	ACCAACTAGAAA TTACTTGAAGTTT [T/gap]CGAGTGA GCATTGCCTGTG CCAGTA	T	gap			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCOLADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1101	cg43265972	2484	TATTCAGCCAAT TTCATGGATGTA A[A/gap]CGATGG ATATAAATAATTG ATAGCA	A	gap			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCOLADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1102	cg43968898	212	ACGGGGGAGGG GGTCGCCCTTAGC GC[G/gap]TGGAC ACAGCACAAAC ACAACACG	G	gap			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCOLADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1103	cg43976826	1294	ACTGTCTTATTT TATTTTCATGTT gap/TCCCTCTTT TCCAGCATTGC AGTTT	gap	T			SILENT- NONCODI NG	cadherin	Human Gene TREMBLNEW- ID:G1881841 R NR-CAM 22=NEUROFASCIN HOMOLOG/IG-FNIII CELL ADHESION MOLECULE {ALTERNATIVELY SPLICED} - RATTUS SP, 1166 aa.	0.00E+00	7
1104	cg43976826	1638	TGTAATGCCTGG AAGATTAAGAAG C[C/gap]TACGGA GTAACAGGAGCC AAGAGTA	C	gap			SILENT- NONCODI NG	cadherin	Human Gene TREMBLNEW- ID:G1881841 R NR-CAM 22=NEUROFASCIN HOMOLOG/IG-FNIII CELL ADHESION MOLECULE {ALTERNATIVELY SPLICED} - RATTUS SP, 1166 aa.	0.00E+00	7

1105	cg43952088	4171	ACAACCCACCAA AGTTCCGCAGA GIC/GIGTATACCA GATGCTCTGTGC AGAAG	C	G				SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q15065 OB CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0.00E+00	16
1106	cg43952088	4172	CAACCCACCAA GTTCCGCAGAG CIG/CJTATACCAG ATGCTCTGTGCA GAAGC	G	C				SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q15065 OB CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0.00E+00	16
1107	cg43952088	4376	GAAAAAGCCTGT AGATTGTGAAC CIA/GJAAAGAGC CTATAGCTTGAA GGTAGA	A	G				SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q15065 OB CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0.00E+00	16
1108	cg43952088	4475	CAAGGACACTGT GACCGTCAAGAT CIG/TJCAGTAGAA GATGCTGATGAG CCCCC	G	T				SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL-ID:Q15065 OB CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0.00E+00	16
1109	cg43127783	4451	GGCTTCAGGGC GCACAGCATGAG AGIG/CJCTCTGT GCCCCCATCACC CTCGTTT	G	C				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00 (16p11.2)	16
1110	cg43127783	4541	CATCGTGGGGCT CTCAGTTCGGAT TTTC/CCCAGGCT GAATTGGGAGTG AGATG	T	C				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00 (16p11.2)	16

1111	cg43127783	4602	GGTCTGCACAG CTGGCCTCCCG CG[gap/G]TTGGG CAACATTGCTGG CTGGAAGG	gap	G				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1112	cg43127783	4607	TGCACAGCTGGC CTCCCGCGTTGG G[gap/T]CAACAT TGCTGGCTGGAA GGGAGGA	gap	T				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1113	cg43127783	4620	TCCCGCGTTGG GCAACATTGCTG GC[gap/C]TGGAA GGGAGGAGCGC CCTCTAGGG	gap	C				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1114	cg43127783	4679	GCCCCCGGTGC GGCTGCAGCTCA CC[C/gap]AGCCC CAGGGGCAGAA GAGACCCAA	C	gap				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)

1115	cg43127783	4756	ATATAGTACCTG AAAAAATGCCAA G[C/gap]ACAAGA TTATTTTTTAAA AAGCGT	C	gap			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1116	cg43127783	4759	TAGTACCTGAAA AAATGCCAAGCA C[A/T]AGATTATT TTTTTAAAAAGC GTACT	A	T			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1117	cg43127783	4760	AGTACCTGAAAA AATGCCAAGCAC A[A/T]GATTATTT TTTTTAAAAAGCG TACTT	A	T			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA- X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1118	cg44026923	187	GCTCTGTGCATG CGGGTGGGCTG GG[gap/C]CCCCA GGGGTGCAAGG ATGGAGTAG	gap	C			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0.00E+00	17 (17q11)
1119	cg44026923	181	CTGTGCATGCGG GTGGGCTGGGC CC[C/gap]AGGGG TGCAAGGATGGA GTAGCTGA	C	gap			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0	17 (17q11)

1120	cg44028923	258	GAGTCGGGAGG ACGCCTAGTGG GAC/A/GJTGGCG GGGTGGGGCA GGTGCGGT	A	G				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0	17 (17q11)
1121	cg42558238	2838	CACCGCCACATG GCTTCCTCCTGC G[C/T]GCATGTG CGCACACACACA CACACA	C	T				SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.lpcis:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)
1122	cg42558238	2889	CCACTCTCCTTG CTACCCAGAAAT C[C/gap]ATCTAA ATACCTGCCCTG ACATGCA	C	gap				SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.lpcis:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)

1123	cg42558238	3220	GGGAAAGCCCA GAAAAGGACAGA AA[C/T]GAAGTAG AAAGGGGCCCA GTCCTGG	C	T			SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.lpcis:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)
1124	cg43994411	1460	TC TTCAGAAAGT AGGCTTTCAAAT T[A/G]CTCTTC CATATTTTGTAG ATAT	A	G			SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.lpcis:SWISSPROT- ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.	0 2 (2q31)	
1125	cg43994411	1714	CAACATATTTC A GAAATGACTGT A/GCTAGGTGGT AAAACTGTTAGG GTAA	A	G			SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.lpcis:SWISSPROT- ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.	0 2 (2q31)	
1126	cg43994411	393	ATACAAATATTTG TTTATATTAGGC T/CJTACTAAATTA ATGACAACTTTG AAA	T	C			SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.lpcis:SWISSPROT- ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.	0 2 (2q31)	

1127	cg43980086	250	CCAAGTCCCAGG C ACTGGCTGATAG C[C/gap]TCTCCC AGTGGATAGCAG GTCCTAA	gap		SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:P38570 INTEGRIN ALPHA-E PRECURSOR (MUCOSAL LYMPHOCYTE-1 ANTIGEN) (HML-1 ANTIGEN) (CD103 ANTIGEN) (INTEGRIN ALPHA-IEL) - HOMO SAPIENS (HUMAN), 1178 aa.lpcds:SWISSPROT-ID:P38570 INTEGRIN ALPHA-E PRECURSOR (MUCOSAL LYMPHOCYTE-1 ANTIGEN) (HML-1 ANTIGEN) (CD103 ANTIGEN) (INTEGRIN ALPHA-IEL) - HOMO SAPIENS (HUMAN), 1178 aa.	0	
1128	cg43948700	159	AAGCTCTGAGCC C CGCCCCCTCTGG G[C/gap]CACAGT GGTAGGGATGG GGGAAGGG	gap		SILENT- NONCODI NG	cadherin	Human Gene TREMBLNEW- ID:G2739450 INTEGRIN BINDING PROTEIN KINASE - MUS MUSCULUS (MOUSE), 452 aa.	4.9E-251	11
1129	cg43948700	204	GAAGGGGATGG G ACCCCATGGCTG GG[G/gap]TAGTA CCATGACTGGAG GCGGGGGA	gap		SILENT- NONCODI NG	cadherin	Human Gene TREMBLNEW- ID:G2739450 INTEGRIN BINDING PROTEIN KINASE - MUS MUSCULUS (MOUSE), 452 aa.	4.90E-251	11
1130	cg43949264	14175	ATCGTGAGGTTT gap TCATCGGCTGTG C[gap/C]ATTTC CAACGTCITTTG GGATTTA	C		SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P33450 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 5147 aa.	6.20E-222	4
1131	cg43949264	14400	TGTTTCAACTG G AATTTGGTGGT G[G/T]TAGTGCCA TTATCTAGCACC CTGAT	T		SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P33450 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 5147 aa.	6.20E-222	4

1132	cg43949264	14436	ATCTAGCACCCCT GATTTTTTTTTT T/gap]ACTATAAC CAGGGTTTCATT CTGTC	T	gap				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P33450 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 5147 aa.	6.20E-222	4
1133	cg43949264	14436	TCTAGCACCCCTG ATTTTTTTTTTT gap/]ACTATAAC CAGGGTTTCATT CTGTC	gap	T				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P33450 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 5147 aa.	6.20E-222	4
1134	cg43956560	1579	TTCTGAGGAGAA ACAAATAAGACC AT/CJAAAGGAA AGGATTCATGTG GAATA	T	C				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:P14151 L- SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE- 1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1.00E-218	1 (1q23)
1135	cg42701303	989	GTGGCTCCACTT GCCCGTCTGCTT G[G/gap]CCCCAG GCTGCTCTTGTC CTGTTTG	G	gap				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:Q14242 P SELECTIN GLYCOPROTEIN LIGAND 1 PRECURSOR (PSGL-1) (SELECTIN P LIGAND) (CD162 ANTIGEN) - HOMO SAPIENS (HUMAN), 412 aa.	2.50E-215	12 (12q24)
1136	cg42701303	1083	CTCCGAGGAAG CCCAGAGCTGTG GA/A/TTGGGT CTGGGCACTCAG GGGTGGC	A	T				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:Q14242 P SELECTIN GLYCOPROTEIN LIGAND 1 PRECURSOR (PSGL-1) (SELECTIN P LIGAND) (CD162 ANTIGEN) - HOMO SAPIENS (HUMAN), 412 aa.	2.50E-215	12 (12q24)

1137	cg43977724	1602	TCATTCCCAACA ACATCCTCTGCC A/C/TJACACAACA AAACGTAAGTTT CATT	C	T			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT-ID:Q14982 OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR (OBCAM) (OPIOID-BINDING CELL ADHESION MOLECULE) (OPCML) - HOMO SAPIENS (HUMAN), 345 aa.	1.80E-182	11
1138	cg43958666	1161	AGTAAGACGTGA AAGGAATACACT TIGCJTGTTTAAG CACCATGGCCTT GATGA	G	C			SILENT- NONCODI NG	cadherin	Human Gene SWISSNEW-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa.lpcis:SWISSPROT-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa	1.20E-167 (3q13.1)	3
1139	cg43943478	366	GAGGAGAGGCC CTGACAAAGGAGG GC[C/gap]GCCCC TGCCCCGGGGTG AGGCTGCAC	C	gap			SILENT- NONCODI NG	cadherin	SAPIENS (HUMAN), 323 aa Human Gene Similar to SPTREMBL- ID:Q99971 CALCIUM AND INTEGRIN BINDING PROTEIN CIB - HOMO SAPIENS (HUMAN), 191 aa.	1.50E-98	
1140	cg43943478	398	CCCGGGGTGAG GCTGCACAGCG CCA[gap/G]CTCC AGGCTGGGCCA GCTTGGCCCCG	gap	G			SILENT- NONCODI NG	cadherin	Human Gene Similar to SPTREMBL- ID:Q99971 CALCIUM AND INTEGRIN BINDING PROTEIN CIB - HOMO SAPIENS (HUMAN), 191 aa.	1.50E-96	
1141	cg43943478	408	AGGCTGCACAG CGCCACTCCAG GCT[G/gap]GGCC AGCTTGGCCCCG CACTGGCAAC	G	gap			SILENT- NONCODI NG	cadherin	Human Gene Similar to SPTREMBL- ID:Q99971 CALCIUM AND INTEGRIN BINDING PROTEIN CIB - HOMO SAPIENS (HUMAN), 191 aa.	1.50E-96	

1142	cg43943478	410	GCTGCACAGCG CCACTCCAGGCT GG[G/gap]CCAGC TTGGCCCGCACT GGCAACAG	G	gap			SILENT- NONCODI NG	cadherin	Human Gene Similar to SPTREMBL- ID:Q99971 CALCIUM AND INTEGRIN BINDING PROTEIN CIB - HOMO SAPIENS (HUMAN), 191 aa.	1.50E-96	
1143	cg42924171	1026	CCCAACTTCCCC TGGAGCTCAGAG G[T/G]GTCCCCA CTGTACCAGCCT CTGATA	T	G			SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1144	cg42924171	1028	CAACTTCCCCCTG GAGCTCAGAGGT G[T/G]CCCCACT GTACCAGCCTCT GATAAG	T	G			SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1145	cg42924171	1160	TCTCTTTCTCGG TGATAAAACACA C[C/G]CGCTCCG GTGAGCCCCAGC GTCCCCCT	C	G			SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1146	cg42924171	1169	CGGTGATAAAAC ACACCCGCTCCG G[T/gap]GAGCCC AGCGTCCCCCTCC TTGGCTT	T	gap			SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1147	cg42924171	1177	AACACACCCGCT CCGGTGAGCCC AG[gap/G]CGTCC CCTCCTTGGCTT CCAGGAGC	gap	G			SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17

1148	cg42924171	1179	ACACACCCGCTC CGGTGAGCCCA GC[G/C]TCCCCT CCTGGCTTCCA GGAGCCC	G	C				SILENT- NONCODING	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1149	cg42924171	1184	CCGCTCCGGTG AGCCAGCGTC CCC[gap/C]TCCCT TGGCTTCCAGGA GCCCTGGGA	gap	C				SILENT- NONCODING	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1150	cg42924171	1204	GTCCCCCTCCTTG GCTTCCAGGAGC C[C/gap]TGGGAA GCATTTTAACT GGGTAGA	C	gap				SILENT- NONCODING	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1151	cg42924171	1208	CCTCCTTGCTT CCAGGAGCCCT GG[G/gap]AAGCA TTTTTAAC TGGG TAGAATCT	G	gap				SILENT- NONCODING	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1152	cg42924171	746	ATGCTGAGCCCG AGCACTAACCT C[C/gap]TGC GGC CCTAGCGACCCCT CAGGCTT	C	gap				SILENT- NONCODING	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1153	cg42924171	868	GCTCCCATCTGC CCCCCTGCAACA G[T/C]CGCAGGC TGCTTCCTCTCT CTGAGT	T	C				SILENT- NONCODING	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17

1154	cg42924171	869	CTCCCATCTGCC CCCCTGCAACAG TTC/TGCAGGCT GCTTCCTCTCTC TGAGTT	C	T			SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1155	cg42924171	907	CTCTCTCTGAGT TCCTCTGGGCTG C/C[gap]GCAGGC TCCCCTGGGAAT AGAGCAA	C	gap			SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1156	cg42924171	958	GACGTGAGTCCT AACCTGGCCACA G/C/T/TGGGGGA GGCAGAGCCAG CAGGTGG	C	T			SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1157	cg42924171	967	CCTAACCTGGCC ACAGCTGGGGG AG[G/gap]CAGAG CCAGCAGGTGG ACAGGTGTT	G	gap			SILENT- NONCODI NG	calcium_ channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L- TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1158	cg43246381	243	ACCTGGATTGT TTTCAGCTTTCT C/G/A/JATTTTCAC ATGCACGTTAGG CTATC	G	A			SILENT- NONCODI NG	calcium_ channel	Human Gene Similar to TREMBLNEW- ID:G259184 RYANODINE RECEPTOR/CALCIUM RELEASE CHANNEL - ORYCTOLAGUS SP, 4872 aa.	1.00E-73	12
1159	cg43933897	195	TCAGATGCCAGC TCTCCTCAGCGG A/C[gap]GCTCCT GATCCCTCAATT TGCCATC	C	gap			SILENT- NONCODI NG	calcium_ channel	Human Gene Similar to TREMBLNEW- ID:G259184 RYANODINE RECEPTOR/CALCIUM RELEASE CHANNEL - ORYCTOLAGUS SP, 4872 aa.	9.70E-66	

1160	cg43919581	2171	AGGAATGCCTCC TCCCTGGGCAGA A[A]gap[GTGGCC ATGCCACCCTGT TTTCAGC	A	gap			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P00750 TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68) (TPA) (T- PLASMINOGEN ACTIVATOR) - HOMO SAPIENS (HUMAN), 562 aa.	0.00E+00	8 (8p12)
1161	cg43919581	2357	TATAGTCACAAG AGCCACAGCAGG GC[C]gap[TCAAA GTTGGGCAGG CTGGCTGGC	C	gap			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P00750 TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68) (TPA) (T- PLASMINOGEN ACTIVATOR) - HOMO SAPIENS (HUMAN), 562 aa.	0.00E+00	8 (8p12)
1162	cg43946028	394	GAATCTCGTGCC TCAGCCTCCCAA G[T]C]AGCTGGG ATTACAGGCATG CACCAC	T	C			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P25774 CATHEPSIN S PRECURSOR (EC 3.4.22.27) - HOMO SAPIENS (HUMAN), 331 aa.	3.10E-185	
1163	cg43946028	403	GCCTCAGCCTCC CAAGTAGCTGGG A[T]C]TACAGGCA TGCACCACCGTG CTCGG	T	C			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P25774 CATHEPSIN S PRECURSOR (EC 3.4.22.27) - HOMO SAPIENS (HUMAN), 331 aa.	3.10E-185	
1164	cg43946028	468	TTTATAGTAGAGA TGGGGTTTCACC A[T]C]GTTAGCCA GGCTGCTCTTTA ACTCC	T	C			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P25774 CATHEPSIN S PRECURSOR (EC 3.4.22.27) - HOMO SAPIENS (HUMAN), 331 aa.	3.10E-185	
1165	cg43264626	197	ATAGACATTTCT ACCTTGAGGATA T[A]T]GAAGGGAA CTTAGGAAGTGA GAAGT	A	T			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.10E-183	1
1166	cg43264626	41	TTTGAATGTGTA CTAGATGCTATT T[A]T]TTAAACTG TAGACAGGAGAT AAATA	A	T			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.1E-183	1

1167	cg43264626	437	TGAAAAAGGTCA TGGGTGGAGAG AA[G/C]CAAAAGTA GGAAGGATCATT TGAAGC	G	C				SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.1E-183	1
1168	cg42926989	826	TCCTCGGTTCT ACGACCCCGAA G[G/gap]CAGATT TGTGTGGGGGA CCGGCGGG	G	gap				SILENT- NONCODI NG	cathepsin	Human Gene Homologous to SWISSPROT-ID:P08311 CATHEPSIN G PRECURSOR (EC 3.4.21.20) - HOMO SAPIENS (HUMAN), 255 aa.	1.7E-136	14 (14q11.2)
1169	cg42926989	908	AGGCCCCCTGCT GTGTAACAATGT G[G/gap]CCCCAG GCATCGTCTCCT ATGGAAA	G	gap				SILENT- NONCODI NG	cathepsin	Human Gene Homologous to SWISSPROT-ID:P08311 CATHEPSIN G PRECURSOR (EC 3.4.21.20) - HOMO SAPIENS (HUMAN), 255 aa.	1.7E-136	14 (14q11.2)
1170	cg42094318	1232	CCAACCCCTGAG CACCCCTATCAA C[C/T]CCCTATTG TAGTAAACTTGG AACCT	C	T				SILENT- NONCODI NG	cathepsin	Human Gene Homologous to SWISSPROT-ID:P20151 GLANDULAR KALLIKREIN 2 PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN) (PROSTATE) (HGK-1) - HOMO SAPIENS (HUMAN), 261 aa.	5.5E-110	19 (19q13)
1171	cg43982945	461	ACACATGTCAGG CTGGGGCAGCA GC[C/gap]ACTCT GATCAGCACCAG GTCCCGAG	C	gap				SILENT- NONCODI NG	cathepsin	Human Gene Similar to SWISSPROT- ID:Q26534 CATHEPSIN L PRECURSOR (EC 3.4.22.15) (SMCL1) - SCHISTOSOMA MANSONI (BLOOD FLUKE), 319 aa.	2E-80	11
1172	cg43982945	97	GGTACAAGTTT CCTGGACATGGA G[A/G]GGGACAC TATCCCTAAATC CAAGGG	A	G				SILENT- NONCODI NG	cathepsin	Human Gene Similar to SWISSPROT- ID:Q26534 CATHEPSIN L PRECURSOR (EC 3.4.22.15) (SMCL1) - SCHISTOSOMA MANSONI (BLOOD FLUKE), 319 aa.	2E-80	11
1173	cg43925458	591	TCTGGACATAAA TCTGCCATTATT [A/G]AACCATTC CTACAACAAATA AATA	A	G				SILENT- NONCODI NG	cathepsin inhib	Human Gene SWISSPROT-ID:P20810 CALPAIN INHIBITOR (CALPASTATIN) (SPERM BS-17 COMPONENT) - HOMO SAPIENS (HUMAN), 708 aa.	0	5 (5q15)

1174	cg43980411	1763	AGTAGGTATCCC TCCATGCCCTTC T[G]A[TAATAAAT ATCTGGAAAAAA CATT	G	A				SILENT- NONCODI NG	cathepsin inhib	Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG-SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa.	3.2E-222	18 (18q21.3)
1175	cg43971453	1029	CTGTAGCTGCCT CCTGCCCTCCGA A[G]gap]GCAGAA GGAATGAAAGAT GCACATT	G	gap				SILENT- NONCODI NG	chloride_ channel	Human Gene SWISSPROT-ID:P51788 CHLORIDE CHANNEL PROTEIN 2 (CLC 2) - HOMO SAPIENS (HUMAN), 898 aa.	0	3
1176	cg43971453	536	GGGTGTTAATGC CCACGTAGTGG G[G]gap]CCTCTG GCAGATCCTGCA TTCCAAG	G	gap				SILENT- NONCODI NG	chloride_ channel	Human Gene SWISSPROT-ID:P51788 CHLORIDE CHANNEL PROTEIN 2 (CLC 2) - HOMO SAPIENS (HUMAN), 898 aa.	0	3
1177	cg43971453	885	CCCCAACCCATC CTGCCAGGGCA GG[G]gap]CCTAT CTTCCTGCCCTCT GGAAGACT	G	gap				SILENT- NONCODI NG	chloride_ channel	Human Gene SWISSPROT-ID:P51788 CHLORIDE CHANNEL PROTEIN 2 (CLC 2) - HOMO SAPIENS (HUMAN), 898 aa.	0.00E+00	3
1178	cg43970982	5505	GACCAATGCCCT AATTAAAGAATTT [A/T]AAAAAGTTG TAATAGAGAATA TTTT	A	T				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0.00E+00	2
1179	cg43970982	5564	CTCTAATGTTGT GTGTTTTTTTTT [T/G]TGTGTGCTG GAGGGAGGGGA TTTAA	T	G				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0.00E+00	2
1180	cg42201364	2443	TTAAAAACAAC AACAAAAAACAA A[gap/G]CAACAA AAAAAAAATTAA AAAAAA	gap	G				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0.00E+00	6

1181	cg42201364	2818	GCCTTCATCAAT GAACCTTTTCAA A/gap/AJCCTTTCT ATGATTGCAGAG AAGCTT	gap	A				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0.00E+00	6
1182	cg42201364	3169	GTTTACCTACT CCCTATTACGA C/GJCAATAAAA TAACATCAATAG AATT	A	G				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0.00E+00	6
1183	cg42201364	3191	GACACAATAAAA TAACATCAATAG A/AJTITTAGGC TGAATTAAATTGA AAGC	A	T				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0.00E+00	6
1184	cg41035069	3660	GCTTTTTTTTTT TTTTTTTTTTTTT[gap]GGGAGTAAG CCAGGCATTAAA AGCA	T	gap				SILENT- NONCODI NG	collagen	Human Gene TREMBLNEW- ID:D1024188 TYPE XIX COLLAGEN A1 CHAIN - HOMO SAPIENS (HUMAN), 1143 aa.	0.00E+00	6 (6q12)
1185	cg43917054	12431	ACCGTCTTGATC GGAAAGCTCTTC CT/GJAATCGCTA ATCAGTCATTTC TTTCA	T	G				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)
1186	cg43917054	12851	GAGGATGCAACA AATGTGGCCAAG C[C/gap]TATCAA AGGAAATGAGAA TGACAGC	C	gap				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)
1187	cg43917054	12916	CAGAAAGTAGAGG GGGTGGGTGCG TA[A/gap]GGATG TGTGAGTTTTGC TTTTGACT	A	gap				SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)

1188	cg43917054	13001	TCTCAGAAGTCC CTGTTTATTCCA A[AT]TGCCATCC AGATGTGTGCAA TGTGG	A	T			SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)
1189	cg43917054	13008	GTCCCTGTTTAT TCCAAATGCCAT C[Gap]AGATGT GTGCAATGTGGC AACTGA	C	gap			SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)
1190	cg42740351	1048	TGAAGCTAAAA AGACAGCAGAAC T[G/C]GTATTTT CATCCTAAAGAA CAAAG	G	C			SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q28084 COLLAGEN ALPHA 3(IV) CHAIN - BOS TAURUS (BOVINE), 471 aa (fragment).	6.80E-174	2 (2q36)
1191	cg42740351	1047	GAAGCTAAAA GACAGCAGAACT G[G/C]TATTTTC ATCCTAAAGAAC AAAGT	G	C			SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q28084 COLLAGEN ALPHA 3(IV) CHAIN - BOS TAURUS (BOVINE), 471 aa (fragment).	6.80E-174	2 (2q36)
1192	cg42740351	1131	CTTTAACCAAC AATATTGCTCCA T[G/C]ATGACTTA GTACAAAGTTTC AATT	G	C			SILENT- NONCODI NG	collagen	Human Gene SWISSPROT-ID:Q28084 COLLAGEN ALPHA 3(IV) CHAIN - BOS TAURUS (BOVINE), 471 aa (fragment).	6.80E-174	2 (2q36)
1193	cg43968268	20	TTTAAATATATA CAAAGGACJATT TTATTATTAAACCA AAGAAAGGG	A	C			SILENT- NONCODI NG	collagen	Human Gene Homologous to SPTREMBL-ID:Q61428 TYPE III COLLAGEN - MUS MUSCULUS (MOUSE), 1464 aa.	8.20E-128	1 (1p21)
1194	cg43991318	328	AACAGCAATTAA AAACAACAACAA C[Gap]ACAAAA AAAAACATTAC AACCTGT	A	gap			SILENT- NONCODI NG	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.30E-73	1 (1p34)

1195	cg43991318	339	AAAACAACAACA ACAACAACAAAA A[A/gap]CATTCA CAACCTGTACACA GAGTCCT	A	gap				SILENT- NONCODI NG	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.30E-73	1 (1p34)
1196	cg43938820	487	TCTGCGGGAGG GAGGAGCAGAC GGG[G/gap]TTAG CACCCTTAATCT CGAGGGTCT	G	gap				SILENT- NONCODI NG	collagen	Human Gene Similar to SPTREMBL- ID:Q14040 ALPHA-1 COLLAGEN VI (AA 574-1009) - HOMO SAPIENS (HUMAN), 436 aa (fragment).	5.00E-59	21 (21q22.3)
1197	cg43938820	862	GGGCGTCTTGCT CAGGCTGGTGG GATTCJGCAGCA CAGAGGTGCCTA GGGAAGG	T	C				SILENT- NONCODI NG	collagen	Human Gene Similar to SPTREMBL- ID:Q14040 ALPHA-1 COLLAGEN VI (AA 574-1009) - HOMO SAPIENS (HUMAN), 436 aa (fragment).	5.00E-59	21 (21q22.3)
1198	cg39659519	2155	GTGTGTATGTGT GCGTGTGTGTAT G[C/T]GTGCATGT GTGTGTGTGTGT GTGTG	C	T				SILENT- NONCODI NG	collagen	Human Gene Similar to SWISSPROT- ID:Q99715 COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3063 aa. [pcis: SPTREMBL- ID:Q99715 COLLAGEN TYPE XII ALPHA 1 PRECURSOR - HOMO SAPIENS (HUMAN), 3063 aa.	4.10E-52	1 (1p35)
1199	cg43278293	369	TTTCCTGCCTCT GCCTTGACCCGA A[G/gap]GTCTTA CAGGAAGACAAT AAATAAA	G	gap				SILENT- NONCODI NG	collagen	Human Gene Similar to SPTREMBL- ID:Q14058 PRO ALPHA 1(II) COLLAGEN - HOMO SAPIENS (HUMAN), 288 aa (fragment).	6.50E-50	12 (12q13.1)
1200	cg43278293	370	TTTCCTGCCTCTG CCTTGACCCGAA G[G/gap]TCTTAC AGGAAGACAATA AATAAAT	G	gap				SILENT- NONCODI NG	collagen	Human Gene Similar to SPTREMBL- ID:Q14058 PRO ALPHA 1(II) COLLAGEN - HOMO SAPIENS (HUMAN), 288 aa (fragment).	6.50E-50	12 (12q13.1)

1201	cg43063256	2090	AGAGCCCTGAG CCCTCAAGAACT CA[CTGCCAGCT CAGCCCTACACC AGTTTC	C	T				SILENT- NONCODI NG	complem ent	Human Gene SWISSNEW-ID:P07358 COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 591 aa.[pcis:SWISSPROT- ID:P07358 COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 591 aa.	0.00E+00	1 (1p32)
1202	cg43281450	229	AATCCTCAGAAG AAGAAAGGG CC[C/gap]TTTGG GTTGTTTCAGGT AAAGTACA	C	gap				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0.00E+00	12 (12p13)
1203	cg43281450	368	GTCAGTTGTTTT TGTGTTTTTTTTT T[gap]CCACACTG CTCTCTGGATTC GAACC	T	gap				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0.00E+00	12 (12p13)
1204	cg43281450	368	TCAGTTGTTTTT GTTTTTTTTTTTTg ap/TJCCACACTG CTCTCTGGATTC GAACC	gap	T				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0.00E+00	12 (12p13)
1205	cg43049885	3106	CTCAAAGTTACT GACAAAATTAT TTTCTCTGTTAG TTTGAGATCATT ATTCT	T	C				SILENT- NONCODI NG	complem ent	Human Gene TREMBLNEW-ID:G386348 COMPLEMENT C6 - HOMO SAPIENS, 941 aa.	0.00E+00	5 (5p13)
1206	cg43049885	3303	GTAGCCTGTGAC ATTAAGCATTCT CIA/GJCAATTAGA AATAAGAATAAA AGCCA	A	G				SILENT- NONCODI NG	complem ent	Human Gene TREMBLNEW-ID:G386348 COMPLEMENT C6 - HOMO SAPIENS, 941 aa.	0.00E+00	5 (5p13)
1207	cg43933757	3223	GTTCAAGCGATT CTTGTCCTCAG CIC/TTCCCAAGC AGCTGGGATTAC AGGTG	C	T				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0.00E+00	5 (5p13)

1208	cg43958722	254	GAAACCAAGCCTG GGCAACATAGGA A/A/GJATCCTGTC TCTACAAAAAAT AAATT	A	G				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:P08174 COMPLEMENT DECAY- ACCELERATING FACTOR PRECURSOR (CD55) - HOMO SAPIENS (HUMAN), 381 aa.	3.40E-192	1 (1q32)
1209	cg43958722	287	CTCTACAAAAA TAAATTTCAAAA [C/gap]TTAGCCG GGTGTCGTGGC ACACACC	C	gap				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:P08174 COMPLEMENT DECAY- ACCELERATING FACTOR PRECURSOR (CD55) - HOMO SAPIENS (HUMAN), 381 aa.	3.40E-192	1 (1q32)
1210	cg43956185	308	TTTTGGAGTTTT TAGTTTTCCAAG[T/A]TTTAATATGG TGCTTTTAAGAA GAG	T	A				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
1211	cg43956185	423	AAAGGAGTAAAA CAATACTTAAAA ATT/AJTAATAATA GAACGATTTAA TACTA	T	A				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
1212	cg43956185	430	TAAACAATACIT AAAAATTAAATT A/GJAGAACTGAT TTAATACTAAAGT ICT	A	G				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
1213	cg43956185	471	CTAAAGTTCTGA ATAAAGGTGTGC ATT/CJTATTATGAT TGATTCTATCTTT TTGC	T	C				SILENT- NONCODI NG	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1
1214	cg43945714	1056	TACCCCCAACAC CACCCTTGCCC A/G/AJCCAATGCA CACAGTAGGGCT TGGTG	G	A				SILENT- NONCODI NG	complem ent	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)

1215	cg43945714	1063	AACAGCACCCCT TGCCAGGCCAAT G[C/G]ACACAGT AGGGCTTGGTGA ATGCTG	C	G				SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)
1216	cg43945714	1124	GAGTAAATAAAC TCTCAAGGCCA A[G/A]GAACAGT GGTCTAATTCAA CTCTGT	G	A				SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)
1217	cg43945714	1125	AGTAAATAAACT CTTCAAGGCCAA G[G/A]AACAGTG GTCTAATTCAAC TCTGTG	G	A				SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)
1218	cg43945714	1126	GTAATAAACTC TTCAAGGCCAAG G[G/A]ACAGTGG TCTAATTCAACT CTGTGT	A	G				SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)
1219	cg43945714	1160	CTAATTCAACTC TGTGTCCCAGCA C[C/gap]TGGCAC ACCAGAAGTGCC ATGCTCA	C	gap				SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)

1220	cg43947909	969	CAGAAAAAATG ATAATAAATGAG A/A/GJ/CACAAAAC ATATAATTTAAAT TTGG	A	G				SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17
1221	cg43947909	991	AGAACACAAAAC ATATAATTTAAAT T/CJTGCGTATTTT TTCCCCCATGAT ATTA	T	C				SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17
1222	cg43947909	326	ATTCAACAGGAG CTGATCAACCAA G/A/GJ/GCAGTCC ATCATCAGCGAG TATGAG	A	G				SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17

1223	cg43947809	575	ATAAATGAGCAC AGTGCACATTGT C/C/CCACACAC CTGAATTTTCAG TCACT	C						SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17
1224	cg43947809	839	ACATCTGTTCTT GGTCTTTTGTGA C/G/A/CAGGTTG AAGGGGGAGGA ATAGAAA	G	A					SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17
1225	cg43984382	141	CAGCCAGTCCTG GGGCTCTCAGA GC/C/gap/JAGCCC CCTCCCTTCAGC AGCTGAAG	C	gap					SILENT- NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:P02745 COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 245 aa.	8.8E-101	1
1226	cg43942011	2028	TTTTCTATGAAG AGCCCCAGATG GA/gap/AJGTTTT GGGGGGTGTCAT GGCCTGCT	gap	A					SILENT- NONCODING	complement	Human Gene Similar to TREMBLNEW- ID:E246058 COMPLEMENT RECEPTOR 2 - MUS MUSCULUS (MOUSE), 651 aa (fragment).	1.10E-69	1 (1q32)
1227	cg44028879	1058	TCCTCAGTCAGA GCTCGCCCTGTA G/C/GCTCTCTGT CTGTGCCCTCCC CTCCC	C	G					SILENT- NONCODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)

1228	cg44028879	1129	CTCCCTCTTGG GAATGTCAAAGT G[C/G]AAGATGC AGAAACCTGGGC GAACAA	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1229	cg44028879	119	AAATAGATATTTA AATGACTTTTATA T/AJAAAAATAATTC ACCACCTTCCAAG TAT	T	A				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1230	cg44028879	1152	TGCAAGATGCAG AAACCTGGGCGA A[C/G]AACACAG CCTAAAGACCGG CTCTGG	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1231	cg44028879	1168	CTGGGCGAACAA CACAGCCTAAAG A[C/G]CGGCTCT GGCTGGCGGCC CAGGAGG	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1232	cg44028879	134	TGACTTTATATAA AATAATTCACCA C/GJTTCCAAGTA TAAAAACAAAAT CTCA	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1233	cg44028879	137	CTTTATATAAAAT AATTCACCACCTT C/GJCAAGTATAA AAACAAAATCTC ACAG	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1234	cg44028879	183	CACAGTGCCTGA GCCAATGTCCTC T[C/GJTTGACTTC TCAGAGAACAGA AGGGG	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)

1235	cg44028879	188	TGCGTGAGCCAA TGTCCTCTCTTG A/C/GTTCTCAGA GAACAGAAGGG GTTCCT	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1236	cg44028879	232	GGTTCCTGAGCA GGTAGCCTGGG GG[G]gapJACACC AGAGGTGGCTCT GGGGCTCC	G	gap				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1237	cg44028879	460	AGGCTAAGCCCC ATATGCAAGTTC A/C/GTGCCTTC CCTAAGCTGTCTG GCATC	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1238	cg44028879	679	GCTCGTTGCCTA GGCCTCAGAGC CA/C/GJACCCAC AGGCTGGCCAC AAAGTGGG	C	G				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1239	cg42542486	1400	ACACTGCCGACA TCAGCATTGTCT C/G/AJGTACAGC TCCCTTCCCTGC AGGGC	G	A				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)
1240	cg42542486	1835	AGAAATTGCAA CTCACTGATTCT C/T/AJACATGCTC TTTTTCTGTGATA ACTC	T	A				SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)

1241	cg42542496	1668	CTTTTCTGTGATG AACTCTGCAAAG[G/A]CCTGGGCTG GCCTGGCAGTTG AACA	G	A			SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)
1242	cg42542496	1728	ACTAACCTTGAG A TCAGAAACAGA G[A/G]AAGGGTA ATTTCCTTTGCTT CAAAT	A	G			SILENT- NONCODI NG	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)
1243	cg41533258	1246	GTTTGACTCCCG T AACATCACCGAC G[T/C]GTCCTCCTG TTTTCTGGGTG GCCTC	T	C			SILENT- NONCODI NG	csf	Human Gene Homologous to SWISSPROT-ID:P09919 GRANULOCYTE COLONY- STIMULATING FACTOR PRECURSOR (G-CSF) (PLURIPOLIETIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.50E-107	17 (17q11.2)
1244	cg2752865	774	GGAGTGGCCTG C GACCTGCCCTG GGC[C/gap]ACAC TGACCCCTGATAC AGGCATGGC	C	gap			SILENT- NONCODI NG	csf	Human Gene Similar to SWISSPROT- ID:P04141 GRANULOCYTE- MACROPHAGE COLONY- STIMULATING FACTOR PRECURSOR (GM-CSF) (COLONY-STIMULATING FACTOR) (CSF) - HOMO SAPIENS (HUMAN), 144 aa.	5.00E-75	5 (5q31.1)
1245	cg43931046	2754	AACCTCTTCAAA A GAAATAGGAGCA A[A/gap]CCCCCA AGAGGCTTAATT TACCAAT	A	gap			SILENT- NONCODI NG	cyclin	Human Gene SPTREMBL-ID:P70413 CYCLIN D-INTERACTING MYB-LIKE PROTEIN - MUS MUSCULUS (MOUSE), 761 aa.	0.00E+00	7
1246	cg43931046	3843	AATTGTATATTCA T GTTTAACAGAAA[T/A]AAAAGAATAT TTGTCTTAAGAT GCA	T	A			SILENT- NONCODI NG	cyclin	Human Gene SPTREMBL-ID:P70413 CYCLIN D-INTERACTING MYB-LIKE PROTEIN - MUS MUSCULUS (MOUSE), 761 aa.	0.00E+00	7

1247	cg43920512	101	TGGCCTGGGCT GCGACCGGGA GCA/C]GACTAT TCCTTGGCCGGG TCGGTGC	A	C				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P20248 G2MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1248	cg43920512	103	GCCTGGGCTGC GACCGGGAGC AAG/C]CTATTC TTTGGCCGGGTC GGTGCGA	A	C				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P20248 G2MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1249	cg43920512	1574	GTGTACAGTTTT TAACCTTAGTTTT [gap/T]AATTTTAC AATCAATTTCTGA ATACA	gap	T				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P20248 G2MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1250	cg43920512	2224	GAATAAAAAATA CCCAGGGTCTT TTT/G]AATGGAAT AAATATCCCTTT AATA	T	G				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P20248 G2MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1251	cg43920512	95	GTAGGCTGGCCT GGCTGCGACC GG[C]GAGCAA GACTATTCTTG GCCGGGT	G	C				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P20248 G2MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1252	cg43920512	98	GGCTGGCCTGG GCTGCGACCGG GGA[G/C]CAAGA CTATTCTTTGGC CGGGTCGG	G	C				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P20248 G2MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1253	cg43927697	2010	AGCGGGGAGAA GCAGAACACCG GAG[G/gap]CCCG ACCAGCCAAGGA CCTACACCC	G	gap				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P14635 G2MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.60E-230	5 (5q12)

1254	cg43927697	609	CAGTAATATGTA CAGATGGCACAT GIG/gapJTGCCAA TTTTATTGTAAA TATAGT	G	gap				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P14635 G2/MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.60E-230	5 (5q12)
1255	cg43927697	620	CAGATGGCACAT GGTGCCAAATTT A/gap/GJTTGTAA ATATAGTACTCC AACTCA	gap	G				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P14635 G2/MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.60E-230	5 (5q12)
1256	cg43927697	628	ACATGGTGCCAA TTTTATTGTAAA [gap/GJTTGTAA CTCCAACCAAG TTTACA	gap	G				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P14635 G2/MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.60E-230	5 (5q12)
1257	cg43957094	1145	CCAAACATTTAT AATCAAGAGATT T/gap/AJTAATCAA TTATGTACTAGA ATCATA	gap	A				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6
1258	cg43957094	1145	CCAAACATTTAT AATCAAGAGATT T/gap/AJTAATCAA TTATGTACTAGA ATCATA	gap	A				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6
1259	cg43957094	1184	ACTAGAATCATA TTAAAGAAAAAC TT/gapJATTTTGC AAAAATAAAATC ACTTTC	T	gap				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6
1260	cg43957094	1189	AATCATATTAAA GAAAAACTTATTT TT/gapJGCAAAA TAAATCACTTTC CAATA	T	gap				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6

1261	cg43957094	800	TAAATACACTTT TAAATCAATATA gap/CJGGTACTTG ATTAATTTCCCT GAAAT	gap	C				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6
1262	cg43242733	1125	ACTGGATTATTA CAGCACCAAAAA A[gap/A]CTTCTCT GAAGCCTTTCTC CACAAAC	gap	A				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P51959 G2/MITOTIC-SPECIFIC CYCLIN G1 - HOMO SAPIENS (HUMAN), 295 aa.	1.30E-154	5
1263	cg43242733	1205	TGGATTAAAGCT ATGAAGCCTCAA A[A]gap]CATCAC GAGATAAGCATG ATGGTCT	A	gap				SILENT- NONCODI NG	cyclin	Human Gene SWISSPROT-ID:P51959 G2/MITOTIC-SPECIFIC CYCLIN G1 - HOMO SAPIENS (HUMAN), 295 aa.	1.30E-154	5
1264	cg43951588	138	AAGAGTTCTAAA CCAATAAGAAAA A[G/A]GGCACAAT GAAGCACACATC CCCAG	G	A				SILENT- NONCODI NG	cyclin	Human Gene Similar to SWISSPROT- ID:P37883 G2/MITOTIC-SPECIFIC CYCLIN B2 - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 397 aa.	2.10E-92	15
1265	cg43989364	569	TTAACCAGGCGT GGGCCTCATG CTA/TJGCAGTTC CAGCCACTCCG GAGGCTG	A	T				SILENT- NONCODI NG	cyclin	Human Gene Similar to TREMBLNEW- ID:G2688505 PUTATIVE CYCLIN G1 INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 154 aa.	9.70E-67	7
1266	cg43989855	1221	TTTCTTCCATATA AACACAGCTTTC C/gap]TTTTGCCG CAAGCATCTGAT GACGA	C	gap				SILENT- NONCODI NG	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.20E-293	2 (2p22)
1267	cg43989855	2882	ATGCATACCTTA AAATTCATGATA A[A/C]TCATGGAA CCCCACTATACT CACTA	A	C				SILENT- NONCODI NG	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.20E-293	2 (2p22)

1268	cg43143315	2383	GGTTACAAACCG TTTCAGGCCCTG C[C/gap]TACCAC ATTCACGTGTTG AATCTTT	gap			SILENT- NONCODI NG	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.lpcis:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa	1.90E-279	20
1269	cg43143315	2717	CTAGTGATTAC TGCGGCATTATT TTT/gap]GTTAGA GGACCTTAAAT TGTTTAT	gap			SILENT- NONCODI NG	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.lpcis:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa	1.90E-279	20

1270	cg43143315	2951	GATTAGGATCT GTGGTGCAGGG CAIAGapJTGTTTC AAAGTTTAGTCA CAGCTTA	gap			SILENT- NONCODI NG	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.lpcis:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513.aa	1.90E-279	20
1271	cg43143315	3398	TGTGAAATTATTT TTAGAATTATAA A/gapJTTACAGTC TTGTCAGATTTT ATCTG	gap			SILENT- NONCODI NG	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.lpcis:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513.aa	1.90E-279	20

1272	cg43143315	3411	AGAAATTATAAAATT CACGTCCTTGTCAT G/TATTTTCATCTG TATACCTTCAAAT TC	G	T			SILENT- NONCODI NG	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450-CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.jpcls:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450-CC24) (VITAMIN D(3) 24- HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.	1.90E-279	20
1273	cg34413296	1732	CGCTGTGAACAT GTCCAGGCGCG GCTT/gap]GCTTC TCCATCAATTGA AGAAGACA	T	gap			SILENT- NONCODI NG	cyto450	Human Gene SWISSNEW-ID:P05177 CYTOCHROME P450 1A2 (EC 1.14.14.1) (CYP1A2) (P450-P3) (P(3)450) (P450 4) - HOMO SAPIENS (HUMAN), 515 aa.jpcls:SWISSPROT-ID:P05177 CYTOCHROME P450 1A2 (EC 1.14.14.1) (P450-P3) (P450-4) - HOMO SAPIENS (HUMAN), 515 aa.	4.60E-278 (15q22)	15
1274	cg43309495	230	TTCTCTCCCTCC TCATCTGAGACA T[G/gap]GCAGCA GCCAGGAACCA CTGTGCCA	G	gap			SILENT- NONCODI NG	cytochro me	Human Gene SPTREMBL-ID:Q64639 CYTOCHROME P-450C27/25 (EC 1.14.14.1) - RATTUS NORVEGICUS (RAT), 540 aa.	1.90E-202 2 (2q33)	
1275	cg43923430	130	AGAACTGTATAG GAAGCATGGCG CT[gap/G]GGCAT CTGCTTCTGGTG AGGGCCCTC	gap	G			SILENT- NONCODI NG	cytochro me	Human Gene Similar to SWISSPROT- ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10

1276	cg43923430	132	GAACTGTATAGG AAGCATGGCGCT G[G/gap]CATCTG CTTCTGGTGAGG GCCTCAC	G	gap				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10
1277	cg43923430	2721	CTGATGCAATCA CACTGTGCTCTA G[G/gap]CGCTGC CCTAGGAGCCA GGAGCGGC	G	gap				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10
1278	cg43923430	2744	AGGCGCTGCC TAGGAGCCAGG AGC[G/gap]GCAG ATACTGCCTCCC CTTCAAGGC	G	gap				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10
1279	cg43923430	390	CCCACCTCTAAC ACTGAATGTCAC AIC[gap]TTTGAA CATGAGATTGG AGGGGAC	C	gap				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10
1280	cg43923204	1029	AAAATGCAGGCC CTGGCTCAGTCA CIC/AIAGGAAGG GGGTGCTCCGA GGCCTTT	C	A				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1281	cg43923204	114	TGTGAAGGCTGT AACAAGTTGTAG AIG/AIGCTTTTC CAGACATTCCTA TGCAA	G	A				SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17

1282	cg43923204	1258	TGGGGTTGGAG GAGAGATGTATA AA[gap/A]GACCC TCAAAGGGAAAA ATAATTCC	gap	A			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1283	cg43923204	277	CTGTTTAAATGTT GTTTAACTCTCC[C/T]ACCCCGACC AATGAATCCCTA CGGA	C	T			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1284	cg43923204	289	GTTTAACTCTCC CACCCCGACCAA T[gap/C]GAATCC CTACGGACCCAGC AGTGCCC	gap	C			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1285	cg43923204	296	CTCTCCACCCCC GACCAATGAATC C[C/gap]TACGGA CCAGCAGTGCC CTGGGAGA	C	gap			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1286	cg43923204	307	CGACCAATGAAT CCCTACGGACCA G[C/T]AGTGCCCT GGGAGACTGAG TAATGA	C	T			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1287	cg43923204	330	GCAGTGCCCTG GGAGACTGAGTA AT[gap/C]GAAA CATCCTGTCAAG CTTCAAGA	gap	C			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17

1288	cg43923204	378	AGACCTTTGGGC AGATGGGACTCT GTC/TAGACCCG TGGGAGCACAAA GGACTA	C	T			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1289	cg43923204	421	AAGGACTAAAA GCTGCAGGTAAC C/GA/TATTTGGT AACCGAGACCAC ACCTG	G	A			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1290	cg43923204	423	GGACTAAAAAGC TGCAGGTAACCG T/A/GTTTGGTAA CCGAGACCACAC CTGGC	A	G			SILENT- NONCODING	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1291	cg43275625	92	TTTCTTTTATTG AGAACATCTCAA A/GTCCCTTTGTC TGTATTGACAG CGTC	A	G			SILENT- NONCODING	deaminase	Human Gene SPTREMBL-ID:000465 DSRNA ADENOSINE DEAMINASE DRADA2C - HOMO SAPIENS (HUMAN), 714 aa.	0	21
1292	cg43318865	1205	GAGACCCCTGG AGGGCTGGAG TTT/T/gapJATCCA GCGCCTCGTCGT ATGTTTGG	T	gap			SILENT- NONCODING	deaminase	Human Gene SWISSPROT-ID:P20132 L- SERINE DEHYDRATASE (EC 4.2.1.13) (L-SERINE DEAMINASE) - HOMO SAPIENS (HUMAN), 328 aa.	1.1E-173	12
1293	cg43318865	1246	TATGTTTGGCTG AGCACCTGTGGC C/gap/CJTGCGTG CAGGTTAACTTC TTGTTAT	gap	C			SILENT- NONCODING	deaminase	Human Gene SWISSPROT-ID:P20132 L- SERINE DEHYDRATASE (EC 4.2.1.13) (L-SERINE DEAMINASE) - HOMO SAPIENS (HUMAN), 328 aa.	1.1E-173	12

1284	cg41626024	838	TGGGACCTTAGAA CACC GCCGCC CC[C/gap]TGCCC CACCTTTCCTTT CCTTCCTG	C	gap				SILENT- NONCODING	deaminase	Human Gene Similar to SWISSPROT- ID:P32320 CYTIDINE DEAMINASE (EC 3.5.4.5) (CYTIDINE AMINOHYDROLASE) - HOMO SAPIENS (HUMAN), 146 aa. cds:TREMBLNEW- ID:E1228801 CYTIDINE DEAMINASE (EC 3.5.4.5) - HOMO SAPIENS (HUMAN), 146 aa.	8.8E-78	1 (1p36.2)
1285	cg43967318	133	GGCACAGTGCT GGGAACACTAG GCC[C/gap]CTTC GGGACAAACCA GGGCCTTAAG	C	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0 (17p11.2)	17
1286	cg43967318	134	GCACAGTGCTG GGAAACACTAGG CC[C/gap]TTCGG GACAAACCAGG GCCTTAAG	C	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0 (17p11.2)	17
1287	cg43967318	210	GGAAGGCACATA ACTGGGACAGG CC[C/gap]TGGCG GGGAGTATTCAG AAGCCAAG	C	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0 (17p11.2)	17
1298	cg43967318	215	GCACATAACTGG GACAGGCCCTG GC[C/gap]GGGAGT ATTCAGAAGCCA AGTGGGT	G	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0 (17p11.2)	17
1299	cg44033747	3686	ATCTGTAATCAC ATTCTGAGTGT TTT/CCTCCTCTTT TTCTGTGTGAGG TTTTT	T	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P23378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa.	0 9 (9p22)	9 (9p22)

1300	cg44033747	3707	TGTTTCCTCTTT TTCTGTGTGAGG [T/gap]TTTTTTTT TTTTTAATCTGCA TTTA	T	gap			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P23378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa.	0	9 (9p22)
1301	cg44033747	3720	TTCTGTGTGAGG TTTTTTTTTTTTT T/gapJAATCTGCA TTTATTAGTATTC TAAT	T	gap			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P23378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa.	0	9 (9p22)
1302	cg43314766	267	GCTAAATGCAAC TGTTCCCTTTCTA [T/gap]AAAAATTAT TATCCTGCAAAA GTAGC	T	gap			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P00352 ALDEHYDE DEHYDROGENASE, CYTOSOLIC (EC 1.2.1.3) (CLASS 1) (ALDH1) (ALDH-E1) - HOMO SAPIENS (HUMAN), 500 aa.	7.2E-273	9 (9q21)
1303	cg43918671	1029	ACAATAAGTAGC TTTTTGCTTACA [T/C]ATTAGTGCA CTGAAACAAAAT ACTA	T	C			SILENT- NONCODING	dehydrogenase	Human Gene SPTREMBL-ID:Q14131 DIHYDROLIPOAMIDE DEHYDROGENASE - HOMO SAPIENS (HUMAN), 511 aa.	5.1E-272	7 (7q31)
1304	cg43918671	1218	GCTCCAGGAAA TTTCAGAAAAA A[T/gap]ATATATA ATCTTCTAATTCA AAAGT	T	gap			SILENT- NONCODING	dehydrogenase	Human Gene SPTREMBL-ID:Q14131 DIHYDROLIPOAMIDE DEHYDROGENASE - HOMO SAPIENS (HUMAN), 511 aa.	5.1E-272	7 (7q31)
1305	cg43918671	749	GGTTAAATAAAA CAAGTGAGAGAC C[A/G]TTTACTTA CATCAGTTCGGT TTATA	A	G			SILENT- NONCODING	dehydrogenase	Human Gene SPTREMBL-ID:Q14131 DIHYDROLIPOAMIDE DEHYDROGENASE - HOMO SAPIENS (HUMAN), 511 aa.	5.1E-272	7 (7q31)
1306	cg43996714	391	TCATTTCATGCTT CTTTATCCTCTT [T/G]CTTTAGAAG TTCACAGTGTTA TATA	T	G			SILENT- NONCODING	dehydrogenase	Human Gene TREMBLNEW- ID:G2979825 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.6E-266	11

1307	cg43398714	549	TATTATCCAGAA TAAACTTCTGTA C/C/AJTATTAAAT TCTTCAAGTATAT CTAG	C	A			SILENT- NONCODI NG	dehydrog enase	Human Gene TREMBLNEW- ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.6E-266	11
1308	cg43330439	86	GCTGACCCCTGTG TGAGGGCAAAAG GGT/CJTITTTTT TGCAGGAACAGT GGTTTA	T	C			SILENT- NONCODI NG	dehydrog enase	Human Gene TREMBLNEW- ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa.	2.1E-257	
1309	cg43330439	88	TGACCCCTGTGTG AGGGCAAAAGG TTT/CJTITTTTT CAGGAACAGTG GTTTAT	T	C			SILENT- NONCODI NG	dehydrog enase	Human Gene TREMBLNEW- ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa.	2.1E-257	
1310	cg43330439	92	CCTGTGTGAGG GCAAAGGGTTTT TTT/GJTGACAGG AACAGTGGTTTA TTGACC	T	G			SILENT- NONCODI NG	dehydrog enase	Human Gene TREMBLNEW- ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa.	2.1E-257	
1311	cg43330439	93	CTGTGTGAGGG CAAAGGGTTTT TTT/CJTGACAGG ACAGTGGTTTAT TGACCA	T	C			SILENT- NONCODI NG	dehydrog enase	Human Gene TREMBLNEW- ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa.	2.1E-257	
1312	cg43264442	3020	TACTTGTGCTCT GCTGAGAATGTA C/A/GJGTTTGAT TAAACATCCCAG GTCTC	A	G			SILENT- NONCODI NG	dehydrog enase	Human Gene TREMBLNEW-ID:G806944 UDP-GLUCOSE DEHYDROGENASE, UDPGDH=52 KDA SUBUNIT [EC 1.1.1.22] - BOS TAURUS, 468 aa.	8.6E-240	4
1313	cg43259523	1624	TCTGTCTTACTC TGTCACCCAGGG T/A/GAGGTGCA GTGGCGCGATCT CAGCTC	A	G			SILENT- NONCODI NG	dehydrog enase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR [EC 1.3.99.-] (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)

1314	cg43259523	1625	CTGCTTACTCT GTCACCCAGGCT ATGATAGTGCAGT GGCGGATCTCA GCTCA	G	A			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1315	cg43259523	1626	TGCTTACTCTG TCACCCAGGCTA GATGTCAGT GGCGGATCTCA GCTCAC	A	G			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1316	cg43259523	1642	CCAGGCTAGAGT GCAGTGGCGG ATCTTCAGCTC ACTGCAGCCTTG ACCTCC	C	T			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1317	cg43259523	1643	CAGGCTAGAGT CAGTGGCGCGA TCCTCAGCTCA CTGCAGCCTTGA CCTCCT	T	C			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)

1318	cg43259523	1859	GCTGGGATTACA GGGATGAGCCA CCAGJTGCCCTG GCTGGGTATTTA TATTATC	A	G		SILENT- NONCODING NG	dehydrog enase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/Branched chain specific precursor (EC 1.3.99.-) (SBCAD) (2- methyl branched chain acyl- CoA dehydrogenase) (2-MEBCAD) - Homo sapiens (human), 432 aa.	2E-229	10 (10q25)
1319	cg43259523	2043	GTTACATAGTAG GCAATTTTATC C[Agap]GTACTTT ATAGATTCAACT CTAAGT	A	gap		SILENT- NONCODING NG	dehydrog enase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/Branched chain specific precursor (EC 1.3.99.-) (SBCAD) (2- methyl branched chain acyl- CoA dehydrogenase) (2-MEBCAD) - Homo sapiens (human), 432 aa.	2E-229	10 (10q25)
1320	cg43259523	2365	AAATATTCAATAC AGTGTGGATAT T[Agap]CTGTCATG CACTATTTTCA GTTGA	T	gap		SILENT- NONCODING NG	dehydrog enase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/Branched chain specific precursor (EC 1.3.99.-) (SBCAD) (2- methyl branched chain acyl- CoA dehydrogenase) (2-MEBCAD) - Homo sapiens (human), 432 aa.	2E-229	10 (10q25)
1321	cg43259523	2383	TGGATATTCTGT CATGCACTATT TT[Agap]CAGTTG ACAAATTTCTGTAT TTTAAT	T	gap		SILENT- NONCODING NG	dehydrog enase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/Branched chain specific precursor (EC 1.3.99.-) (SBCAD) (2- methyl branched chain acyl- CoA dehydrogenase) (2-MEBCAD) - Homo sapiens (human), 432 aa.	2E-229	10 (10q25)

1322	cg43259523	2437	TACTGTTTCTTCA GTCATGGTTATT gap/A]GCACTTTA TCCTGAATAATA ATTCA	gap	A				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1323	cg43259523	2458	TTATTGCACTTTA TCCTGAATAATA A/G]TTCAGAAAT TGGGTTTTCGTT CAGT	A	G				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1324	cg43259523	2564	GAATGAGGGAG AGAAGGGGGCT GTA[G]C]AGTTTG AAAAAGCATATT CAATATT	G	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1325	cg43259523	2650	CTATTGTTTTC AATATAGTTTAT A[A]gap]ACAGGC AAAATGCAATAA AATATAT	A	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2- METHYL BRANCHED CHAIN ACYL- COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)

1326	cg43259523	2651	TATTGTTTGGCAAA TATAGGTTATAA[A/gap]CAGGCAAA ATGCAATAAAAT ATATA	A	gap			SILENT- NONCODI NG	dehydrog enase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/Branched chain specific precursor (EC 1.3.99.-) (SBCAD) (2- methyl branched chain acyl- CoA dehydrogenase) (2-MEBCAD) - Homo sapiens (human), 432 aa.	2E-229	10 (10q25)
1327	cg43259523	2656	TTTGGCAATATA GGTTATAAACAG G[C/gap]AAAATG CAATAAAATATAT ATCTGG	C	gap			SILENT- NONCODI NG	dehydrog enase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/Branched chain specific precursor (EC 1.3.99.-) (SBCAD) (2- methyl branched chain acyl- CoA dehydrogenase) (2-MEBCAD) - Homo sapiens (human), 432 aa.	2E-229	10 (10q25)
1328	cg43057018	1713	ATTTGATGAACC AAGGAAAGCCAT G[C/A]GTTTAAAC AAATATTTACATT TAAT	C	A			SILENT- NONCODI NG	dehydrog enase	Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.jpds:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.3E-209	4 (4q22)
1329	cg43057018	1805	CTGTTATATATAT GAATATTCCTAI T[C]GTTAAATAAT AATAATAACTAG TGT	T	C			SILENT- NONCODI NG	dehydrog enase	Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.jpds:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.3E-209	4 (4q22)
1330	cg44016790	1302	CCATCTTGAGCC ATGTCCCCCAGC C[A/gap]TGGCAT GGGTGCACTGTA AAGGCCA	A	gap			SILENT- NONCODI NG	dehydrog enase	Human Gene SWISSPROT-ID:Q02127 DIHYDROOROTATE DEHYDROGENASE PRECURSOR (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE) - HOMO SAPIENS (HUMAN), 396 aa (fragment).	1.4E-207	16

1331	cg44016780	1310	AGCCATGTCCCC CAGCCATGGCAT G[G/C]GTGCACT GTAAACGCCAAT CGGGGG	G	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:Q02127 DIHYDROOROTATE DEHYDROGENASE PRECURSOR (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE) - HOMO SAPIENS (HUMAN), 396 aa (fragment)	1.4E-207	16
1332	cg44016780	1311	GCCATGTCCCC AGCCATGGCATG G[G/C]TGCACTG TAAACGCCAATC GGGGGG	G	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:Q02127 DIHYDROOROTATE DEHYDROGENASE PRECURSOR (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE) - HOMO SAPIENS (HUMAN), 396 aa (fragment)	1.4E-207	16
1333	cg3000385	494	AACAGAGTGAAC TGAGCATCAGTC A[G/C]AAAAAGTC TATGTTGCAGA AATAC	G	C				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P40394 ALCOHOL DEHYDROGENASE CLASS IV MU/SIGMA CHAIN (EC 1.1.1.1) (RETINOL DEHYDROGENASE) (GASTRIC ALCOHOL DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 374 aa.	4.4E-202 4 (4q23)	
1334	cg3000385	530	TGTTTGCAGAAA TACAGATCCAAG A[G/C]AAAGACA GGATGGGCACT GCTGGAA	C	G				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P40394 ALCOHOL DEHYDROGENASE CLASS IV MU/SIGMA CHAIN (EC 1.1.1.1) (RETINOL DEHYDROGENASE) (GASTRIC ALCOHOL DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 374 aa.	4.4E-202 4 (4q23)	
1335	cg43923979	126	TATCTGTTTGG ATACATCTTTCAT [C/G]AGGACTCT GCCACATCCATA CTTIG	C	G				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192 3 (3p13)	
1336	cg43923979	179	CTTGTGGTGAGA GAGGATAAAATG TTTGTATATAAT TGTTATTCAAAG AACAT	T	G				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192 3 (3p13)	

1337	cg43923979	323	AATACCTGCTGT TGCTTTAGAAAT CIGAJTTTTCCGT TATGAATAGTCA GGTCT	G	A				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192	3 (3p13)
1338	cg43923979	330	GCTGTTGCTTTA GAAATCGTTTTT CIGJTTTATGAAT AGTCAGGCTCTTG CAGTA	G	T				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192	3 (3p13)
1339	cg43923979	69	ATCAAAACAAAC TAACAGTAAATG TJA/GTATTATAT GCTTTAATTTTAT ACAT	A	G				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192	3 (3p13)
1340	cg43998926	248	TGACCCAGACAG GGATATCATTTGC TJA/gapJAAAAAA AAAAATCCCCCTT GTGACC	A	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.3E-190	15
1341	cg43998926	260	GGATATCATTTGC TAAAAA AJA/gapJCCCCCT TGTGACCTGGGT ACATTTT	A	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.3E-190	15
1342	cg43998926	260	GATATCATTTGCT AAAAA AJgapAJTCCCCCT TGTGACCTGGGT ACATTTT	gap	A				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.3E-190	15

1343	cg43988926	339	AAGGGCCAAAG GAGGCCATGAGT TG[<i>gap</i>]CTTTG GTTGTGGGACA GAGGGTAA	T	<i>gap</i>			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.30E-190	15
1344	cg43988926	445	GAGAAGGGAGA GGAAGACAGGA AGG[G/A]AAAGG AGATGCCTGAGG GTCAAAAG	G	A			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.30E-190	15
1345	cg43948373	1817	AACATCCCTTAA TTTGAGGTGTC C[AT]GCAGCTGT TTTTGGAGAAGA CAAAG	A	T			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE- DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
1346	cg43948373	1828	ATTGAGGTGTT CCAGCAGCTGT TT[C]TGGAGAAG ACAAAGAAAATT AAAGT	T	C			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE- DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
1347	cg43948373	1845	AGCTGTTTTTGG AGAAGACAAAGA A[AG]ATTAAAGT TTCCCTGAATA AATGC	A	G			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE- DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
1348	cg43948373	1873	TAAAGTTTCCC TGAATAAATGCA TT[C]ATTATGAC TGTGACAGTGAC TAATC	T	C			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE- DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5

1349	cg43255016	114	AATATCATCAT GGCTCTGAAATG C[G/A]TCTAAAGA TGTCATTCTTAA GTCAA	G	A			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P29266 3- HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1.31) (HIBADH) - RATTUS NORVEGICUS (RAT), 346 aa (fragment).	3.40E-156	
1350	cg43255016	159	AGTCAAAAAATA CGTAGTAAGAAT G[T/A]ACAAGAAA GAAAAAAATATA AAAC	T	A			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P29266 3- HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1.31) (HIBADH) - RATTUS NORVEGICUS (RAT), 346 aa (fragment).	3.40E-156	
1351	cg43255016	168	ATACGTAGTAAG AATGTACAAGAA A[G/A]AAAAAAAT ATAAAAAACAAGT CTGCT	G	A			SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P29266 3- HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1.31) (HIBADH) - RATTUS NORVEGICUS (RAT), 346 aa (fragment).	3.40E-156	
1352	cg43941594	1818	CCGAGGACCGC CCTTGGAGTGGC AC[C/T]TTGTGAG AGGATGGCCTG CATAGAT	C	T			SILENT- NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3- PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3
1353	cg43941594	2210	TGTCCTTGTACC TCTGAGCCTTGA C[G/A]AAGGCATA TTCTGACAACTA ACGAA	G	A			SILENT- NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3- PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3
1354	cg43941594	238	TGTGGATGCCAT GGGGCCATGCT GT[A/gap]GTCAA AAGTTAAATGAA AAACCACA	A	gap			SILENT- NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3- PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3

1355	cg43941594	322	TCATTCAGATATT TGTTCCATATTA TTCAGGAGGGTG GATCCTAGCAAG GCAA	T	C			SILENT- NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3- PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8). (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3
1356	cg43941594	754	GCTACTTACTAG ACACCACAATTA G[C/gap]TTACAG CCCTTTATATATC TTTTAA	C	gap			SILENT- NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3- PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8). (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3
1357	cg43991070	297	GGGGTCAGCAAT TCCATTCTCTCT CTT[gap]CCGGCT CAGTTCAGAAAGC TGTGATG	T	gap			SILENT- NONCODING	dehydrogenase	Human Gene Similar to TREMBLNEW- ID:E321870 VERY-LONG-CHAIN ACYL- COA DEHYDROGENASE - MUS MUSCULUS (MOUSE), 656 aa.	4.70E-95	3
1358	cg44000219	353	AGCGCAGGCTCT GAGAGCCGGGA CG[C/A]GTACAG CTATGTGGTGGT GGGCGCG	C	A			SILENT- NONCODING	dehydrogenase	Human Gene Similar to SPTREMBL- ID:Q84644 CHOLINE DEHYDROGENASE (EC 1.1.99.1) - RATTUS NORVEGICUS (RAT), 441 aa (fragment).	3.30E-93	

1359	cg43104003	266	AAATGTTACCTTT TAGTTCACACTG C/TJTAATCCCTTA GTCCCCATAAAA TAA	T			SILENT- NONCODING	dehydrogenase	Human Gene Similar to SWISSNEW- ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa.lpcis:SWISSPROT-ID:P11586 C-1- TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934-aa.	7.10E-92	6
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1360	cg43104003	452	AAGAAATCTTTG GCCTATTTCAAC A/T/C/GTCTCCAG CATTGCATAACA GACAT	T	C				SILENT- NONCODING	dehydrogenase	Human Gene Similar to SWISSNEW- ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYL TETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa.lpcis:SWISSPROT-ID:P11586 C-1- TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYL TETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934 aa.	7.10E-92	6
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1361	cg43104003	547	AGTAGTCTGTTT C CAGGAGTCTGCA TTC/AJGGGTCCT GTGAGAGCCTTG TCCACT	A				SILENT- NONCODING	dehydrogenase	Human Gene Similar to SWISSNEW- ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYL-TETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa.jpcls:SWISSPROT-ID:P11586 C-1- TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYL-TETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934 aa	7.10E-92	6
1362	cg43990226	103	ACACATGAGCTG C TGGCTGCATTTT AIC/TACAGAAGC TGACACATCTCG CAGGA	T				SILENT- NONCODING	dehydrogenase	Human Gene Similar to SWISSPROT- ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	1.70E-88	10
1363	cg43990226	388	AAGATGGGAGCA C GCTGGGGGATG CTC/gapJCAGCA CAGTAGCCTGCC TATAGGAC	gap				SILENT- NONCODING	dehydrogenase	Human Gene Similar to SWISSPROT- ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	1.70E-88	10

1364	cg43990226	408	ATGCTCCAGCAC AGTAGCCTGCCT AT/CJAGGACTCC TCTGGCTCCCTC AGTCC	T	C			SILENT- NONCODING	dehydrogenase	Human Gene Similar to SWISSPROT- ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	1.70E-88	10
1365	cg43300900	479	CTTGGTCTGCGC TCCAGCGTGGG CCT/CJGGCTGT GCAGGCACGAG GTGTCCAT	T	C			SILENT- NONCODING	dehydrogenase	Human Gene Similar to SWISSPROT- ID:P29918 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3) (NADH DEHYDROGENASE 1, CHAIN 6) (NDH-1, CHAIN 6) - PARACOCCLUS DENTRIFICANS, 173 aa.	4.90E-61	
1366	cg44029571	1685	CCCAATGGAGAC TTTCTGATGCAT C[G/A]TTTCTTT GCTGTGCCAAAG CAGGT	G	A			SILENT- NONCODING	dehydrogenase	Human Gene Similar to SWISSPROT- ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	3.50E-53	7 (7p14)
1367	cg44029571	767	AGCCACCGGCA ACAAGAAGACCC AC[C/gap]TGACG GAGCTGCAGCG CCTCCTGGA	C	gap			SILENT- NONCODING	dehydrogenase	Human Gene Similar to SWISSPROT- ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	3.50E-53	7 (7p14)
1368	cg43918191	1244	CTGCCATGACTC ACAGGCAAGGA G[G/gap]CAGGTC TGCCACCTGCGG TGCCGCT	G	gap			SILENT- NONCODING	dehydrogenase	Human Gene Similar to SPTREMBL- ID:Q23612 SIMILAR TO SHORT-CHAIN ALCOHOL DEHYDROGENASE. NCBI GI: 1086671 - CAENORHABDITIS ELEGANS, 325 aa.	3.70E-51	14
1369	cg43918191	228	GGCTGCTGTTTC ACTGAGACAGGA C[G/A]AACCAACA AGTCCAAATGAG AAGAC	G	A			SILENT- NONCODING	dehydrogenase	Human Gene Similar to SPTREMBL- ID:Q23612 SIMILAR TO SHORT-CHAIN ALCOHOL DEHYDROGENASE. NCBI GI: 1086671 - CAENORHABDITIS ELEGANS, 325 aa.	3.70E-51	14

1370	cg43979857	133	ACTTTATTAAAGT TACTTTTCCAGAT G/AJAATTCAGTA AATATGGTAATA TAGG	G	A			SILENT- NONCODING	dehydrogenase	Human Gene Similar to SPTREMBL-ID:Q29259 NADH DEHYDROGENASE (UBIQUINONE) - SUS SCROFA (PIG), 128 aa (fragment).	4.00E-50	9
1371	cg43937259	397	CCCCCTGGAAAG TGATCCCGGCAT C/C/G/GAGAGCC AAGATGCCGGC CCACTTG	C	G			SILENT- NONCODING	desaturase	Human Gene SWISSPROT-ID:Q00767 ACYL-COA DESATURASE (EC 1.14.99.5) (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE) - HOMO SAPIENS (HUMAN), 359 aa. lpcds:SPTREMBL-ID:Q00767 ACYL-COA DESATURASE 1 (EC 1.14.99.5) (STEAROYL-COA DESATURASE 1) (FATTY ACID DESATURASE 1) - HOMO SAPIENS (HUMAN), 359 aa.	8.10E-194	
1372	cg44000579	1236	CTTACAGCCATT TCCTGAATGGCT G/gap/CJTGCGCT TCCCTCTGTCA TCCTCTT	gap	C			SILENT- NONCODING	desaturase	Human Gene Homologous to SPTREMBL-ID:Q00119 FUNGAL STEROL-C5-DESATURASE HOMOLOG HOMO SAPIENS (HUMAN), 236 aa.	6.20E-128	20
1373	cg44000579	47	CGCCGACCTTTT TTTTTTTTTTTTT T/AJTTTTAATTAT GATCAACTTTTAT TG	T	A			SILENT- NONCODING	desaturase	Human Gene Homologous to SPTREMBL-ID:Q00119 FUNGAL STEROL-C5-DESATURASE HOMOLOG HOMO SAPIENS (HUMAN), 236 aa.	6.20E-128	20
1374	cg43291836	264	TCTAAAGTGCCA GTATTATTACAC [T/gap]TTTTTTTTT TTTTTTAGCCAAA AGTC	T	gap			SILENT- NONCODING	dna_mn_bind	Human Gene TREMBLNEW-ID:G2828110 ZINC FINGER DNA BINDING PROTEIN 89 KDA - HOMO SAPIENS (HUMAN), 794 aa.	0.00E+00	3
1375	cg40993080	282	AAGTTATTGG TATCTTTGGAAA G/gap/GJAAATTA TAAAGATTCGTC TGGGAAA	gap	G			SILENT- NONCODING	dna_mn_bind	Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa.	0.00E+00	6

1376	cg4396292	37	TTTTTTTTTTTT TTTTTTTTTTTTTT ATTTTCTCTT ATATTCTACTTA T	T	A				SILENT- NONCODING	dna_ma_ blind	Human Gene SWISSPROT-ID:P33194 POSSIBLE DNA-REPAIR PROTEIN XP- E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DB) - CERCOPIHUS AETHIOPS (GREEN MONKEY) (GRIVET), 1140 aa.	0.00E+00	11 (11q12)
1377	cg4396292	198	GATGCTGAGGCT GTGGGCGAGCT TTTgap/TJCCCGG GACAACACACGTG GGAGAGCC	gap	T				SILENT- NONCODING	dna_ma_ blind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1378	cg4396292	208	GCTGTGGGCA GCTTTCCCGGA CA/A/GJCCACGT GGAGAGCCCGG CTCACCTG	A	G				SILENT- NONCODING	dna_ma_ blind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1379	cg4396292	224	CCCCGGACAAC CACGTGGGAGA GCC[G/A]GCTCA CCTGGTCCCCAC GGTGAGGC	G	A				SILENT- NONCODING	dna_ma_ blind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1380	cg4396292	264	CACGGTGAGGC GCAACAAGGAG GGG[C/T]TGGA CAGGCCAGGCA CCTTTATAA	C	T				SILENT- NONCODING	dna_ma_ blind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1381	cg4396292	612	ACCTTCCCCAGG ATCCAGAGGCTG G/A/GJGTGTGT TTTGGCGGGG AGTGAGG	A	G				SILENT- NONCODING	dna_ma_ blind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)

1382	cg43962927	613	CCTTCCCCAGGA TCCAGAGGCTG GA[G/A]TGTGGTT TTGGCGGGGA GTGAGGG	G	A				SILENT- NONCODING NG	dna_ma_ bind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1383	cg43962927	634	TGGAGTGTGGTT TTGGCGGGGA GT[G/A]AGGGGA AGGGACGTGCAT TTCCCAA	G	A				SILENT- NONCODING NG	dna_ma_ bind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1384	cg43968816	1025	TTCTGAGATGCG CACGAGGGAGG AA[A/gap]TTGCTT AGTCCACCATCA AGAGCCT	A	gap				SILENT- NONCODING NG	dna_ma_ bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA- BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1385	cg43968816	357	TAGCTTTAGTCA AAAAAACAAAA T[A/G]CATGAATG CAGGAATGTGA CAGGT	A	G				SILENT- NONCODING NG	dna_ma_ bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA- BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1386	cg43968816	431	CGAAGCGCAGC ATTAATTGAAGT GA[A/G]AAGTAAA GAAACGCTTTGT AGCCGC	A	G				SILENT- NONCODING NG	dna_ma_ bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA- BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1387	cg43968816	476	AGCCGCTCGGAT TTCCTTAGGGGA C[A/G]GCAAGTC AATGCTTATCAG CGGTCC	A	G				SILENT- NONCODING NG	dna_ma_ bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA- BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)

1388	cg43968816	482	TCGGATTTCCTT AGGGGACAGCA AGTTA/CAATGCT TATCAGCGGTCC TCAGAA	T	A			SILENT- NONCODING	dna_ma_ bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA- BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1389	cg43968816	555	GACCCATCTGAC TCAGTCTATTAA A/C/G/CCTGAAG GAAGGATACTCT TCAGAT	C	G			SILENT- NONCODING	dna_ma_ bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA- BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1390	cg44129390	4713	CACCAATACACA TAAATGGGGGAG G[ap/A]AAAGCT ATGAAACTGTAT AGGGCTG	gap	A			SILENT- NONCODING	dna_ma_ bind	Human Gene SWISSNEW-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa. pcis:SWISSPROT-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa.	0.00E+00	2 (2p16)
1391	cg44129390	4716	CAATACACATAA ATGGGGGAGGA AA[gap/A]GCTAT GAAACTGTATAG GGCTGTAT	gap	A			SILENT- NONCODING	dna_ma_ bind	Human Gene SWISSNEW-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa. pcis:SWISSPROT-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa.	0.00E+00	2 (2p16)

1392	cg44129390	5268	TCTGAATACATG TTAAAAAAAAAAAA [A/gap]TCAAAAG GAACGCAGAAGT GCTAGC	A	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene SWISSNEW-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa.lpcis:SWISSPROT-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa.	0.00E+00	2 (2p16)
1393	cg44005808	3654	CGTGTAACCAAA AGCCCTAAAATT C[C/gap]ACTGCG TTGTCCACAAGA CAGAAAGC	C	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa.lpcis:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	
1394	cg44005808	3835	ATCTAGCAATCA CAACACTGGCTG AIG/AJCGGATGC ATCTGGGGATGA GGTTGC	G	A			SILENT- NONCODING	dna_ma_ bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa.lpcis:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	

1395	cg44005808	3841	CAATCACAACAC TGGCTGAGCGG AT[G/gap]CATCT GGGGATGAGGT TGCTTACTA	G	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP-1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa.jpds:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	
1396	cg44005808	3962	TATTGTCATTAA GGTATCACGGTC [G/gap]CCACCTG GCATTCCCTTCTG ACCACA	G	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP-1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa.jpds:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	
1397	cg43258220	4244	AAAATCAGATCC GAGGCTTGTTT TTT[gap]CCCTTGTC TAGATATGTTTTA AAAGA	T	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene SPTREMBL-ID:Q00425 PUTATIVE RNA BINDING PROTEIN KOC (KOC) - HOMO SAPIENS (HUMAN), 579 aa.	1.30E-300	7
1398	cg43094267	1953	ACAGAGAACT ACGCAAAAAAG TTGTTGAAGTCA TGCAAACTCCTA CTTTA	G	T			SILENT- NONCODING	dna_ma_ bind	Human Gene SWISSNEW-ID:Q13422 DNA-BINDING PROTEIN IKAROS (LYMPHOID TRANSCRIPTION FACTOR LYF-1) - HOMO SAPIENS (HUMAN), 519 aa.	5.40E-285	7

1399	cg43950470	3069	ATTTTAACCTTAGA GCCTTTTTTTTg apTAAATTTTGTC TGCCCCAAGTTT TGTC	gap	T				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SPTREMBL-ID:P70568 RNA BINDING PROTEIN - RATTUS NORVEGICUS (RAT), 550 aa (fragment).	2.00E-271	X (Xq27.3)
1400	cg43931615	417	AGACACCTGAGC TCACTGGTGAAC TTC/TTGCTTCAA GTCCTCCTGCAA AGCAC	C	T				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SPTREMBL-ID:Q13148 TAR DNA-BINDING PROTEIN-43 - HOMO SAPIENS (HUMAN), 414 aa.	4.30E-227	20
1401	cg43931615	832	TTTCTCGCTCAT ACTAGCCTTTCA TIG/gapCCTCGG CACCACCATCAA TCCCACA	G	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SPTREMBL-ID:Q13148 TAR DNA-BINDING PROTEIN-43 - HOMO SAPIENS (HUMAN), 414 aa.	4.30E-227	20
1402	cg43952830	137	TCTTCTGATCAC AGATGGAGTGGA AATGAGGTTGAA AATGCCTTCTAG AATCC	A	T				SILENT- NONCODI NG	dna_ma_ bind	Human Gene TREMBLNEW- ID:G2801552 RNA BINDING PROTEIN ELAVL4 - MUS MUSCULUS (MOUSE), 346 aa.	2.90E-184	1 (1p34)
1403	cg43956159	1034	CATCTCATCTCA TGGTATACTCCT TATTCACACAAA ACATTCAAACCTA CTTTT	A	T				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
1404	cg43956159	1175	AACCATTAGCAT TCTCAGTGTGCA TIG/gapCTCACC GCAAAGGCTTAG GCGCCGC	G	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
1405	cg43956159	1195	GCATGCTCACGG CAAAGGCTTAGG CIGap/CJGCCGCT CGAAGGGCGG GTACCAGT	gap	C				SILENT- NONCODI NG	dna_ma_ bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10

1406 cg4396159	1250	GTCCAGGGTCAC CCACATACCATG C[gap]/C[ACCACG GGTGCTATGCCG CTTCCTA	gap	C			SILENT- NONCODI NG	dna_rna_ bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
1407 cg43971682	415	TTTTTGCTTTAT TGACTTTATTTT gap/TJAGTTTTTG TACATAAAGAAA AATCA	gap	T			SILENT- NONCODI NG	dna_rna_ bind	Human Gene SWISSPROT-ID:P52912 NUCLEOLYSIN TIA-1 (RNA BINDING PROTEIN TIA-1) - MUS MUSCULUS (MOUSE), 386 aa.	6.10E-157	
1408 cg43917883	2776	TGTTTGAACAG GAGAAATTTTTT T[gap]CCTTTTAA TTCTTTATTTTT TCTT	T	gap			SILENT- NONCODI NG	dna_rna_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.70E-138	1
1409 cg43917883	2884	CAAAGTGACCA ATTTTTTTTTTT T[gap]ACTGTGCT TCAAATAAATAG AAAAA	T	gap			SILENT- NONCODI NG	dna_rna_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.70E-138	1
1410 cg43917883	3009	CATGAGAGTGC TAGGCCTTTGAA T[gap]GCATAT GCCATTCTGGG AAATGCA	G	gap			SILENT- NONCODI NG	dna_rna_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.70E-138	1
1411 cg43917883	555	GCGGCCTCCAC GACTCCGTTCT CC[C/gap]GCCGC CCGGCATGGGC CTCAATCAG	C	gap			SILENT- NONCODI NG	dna_rna_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.70E-138	1
1412 cg43961456	1506	CATTGTTTCATT CCTGGCTATCTA G[gap]/A/AAAAAA AAAGTCAGTGGT ATGCCTT	gap	A			SILENT- NONCODI NG	dna_rna_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	

1413	cg43967456	1515	ATTCTTGGCTAT CTAGAAAAA A[gap/A]GTCAGT GGTATGCCCTTTA TACTTTT	gap	A			SILENT- NONCODI NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1414	cg43967456	1523	GCTATCTAGAAA AAAAAGTCAGT GIG/ATATGCCCTT TATACTTTACCT GTTA	G	A			SILENT- NONCODI NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1415	cg43967456	1593	TTGTTAATGTAT GTAGACTTAAAA GT/gapTTTTTTTT TTTTGTAAACCTT GAGGT	T	gap			SILENT- NONCODI NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1416	cg43967456	1604	GTAGACTTAAAA GTTTTTTTTTTTTT gap/TGTAAACCT TGAGGTTTTTGT ATTTT	gap	T			SILENT- NONCODI NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1417	cg43967456	1751	TAGTACTGTGAA ATCTATGTAGTT A[gap/A]ATCTCAA TAAAGAAATCAT TTTGA	gap	A			SILENT- NONCODI NG	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1418	cg44031794	336	CCGATCTCAGCC TTGCTGATCATC TTC/TGTACAGCA GCAGAAAATGAC CATGT	C	T			SILENT- NONCODI NG	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	2.40E-137	5
1419	cg43930612	629	GAGGTAGAGCG GGCGCGCGGCA GCG[G/gap]CGG GGATTACTTTGC TGCTAGTTTC	G	gap			SILENT- NONCODI NG	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q60668 ARE ELEMENT RNA-BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	1.30E-134	4 (4q21.1)

1420	cg43930612	668	GCTGCTAGTTTC GGTTCGCGCA GC[G/gap]GCGG GTGTAGTCTCGG CGGCAGCGG	G	gap				SILENT- NONCODING	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q60668 ARE ELEMENT RNA-BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	1.30E-134	4 (4q21.1)
1421	cg43933276	1461	AGCACACCTGC CTCTGGGAATAG G[G/gap]CTCACC CGCGCCGAGAG GTCTGGAG	G	gap				SILENT- NONCODING	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q64012 MERC=RNA- BINDING PROTEIN (ALTERNATIVELY SPLICED, EXON 1A) - MUS MUSCULUS (MOUSE), 296 aa.	1.20E-131	20
1422	cg43933275	256	GGGAGGGGAG GTAGTATGGGA AA[C/gap]CCCTG TGCTCTACCCCTC TGGCCTGG	C	gap				SILENT- NONCODING	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q64012 MERC=RNA- BINDING PROTEIN (ALTERNATIVELY SPLICED, EXON 1A) - MUS MUSCULUS (MOUSE), 296 aa.	1.20E-131	20
1423	cg43281802	280	GAGATTTCTTTT CCAGGCCCCAGG C[C/gap]TGTGAA AAACGATGGCTA AGTGTTA	C	gap				SILENT- NONCODING	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:P29558 SINGLE- STRANDED DNA-BINDING PROTEIN MSSP-1 - HOMO SAPIENS (HUMAN), 372 aa.	1.30E-122	12
1424	cg43935457	728	CAGAACTGGTTT CTTTTTTTTTTTT T[gap]CAAGTTT AGAGAACTAAAT TTGCA	T	gap				SILENT- NONCODING	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q62262 SPERMATID PERINUCLEAR RNA BINDING PROTEIN - MUS MUSCULUS (MOUSE), 648 aa.	6.00E-118	
1425	cg43973273	1019	CCATGGAAATGA TAAGGAATCAAA TTGTTTCTGCAT CAGTAATTTTAAT AAAG	G	T				SILENT- NONCODING	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q13097 DNA/RNA- BINDING PROTEIN - HOMO SAPIENS (HUMAN), 363 aa (fragment).	2.00E-112	

1426	cg43955901	20	TTTTTTTTTTT TTTTAT[G/T]TT GTAAATTTTACTT AGGCCATCA	G	T				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SWISSNEW- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA) - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SWISSPROT- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SPTREMBL-ID:Q91836 RNA BINDING PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.	9.40E-97	2
1427	cg43955901	24	TTTTTTTTTTT TTTTATGTTT[G/T JTAAATTTTACTT AGGCCATCATTT T	G	T				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SWISSNEW- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA) - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SWISSPROT- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SPTREMBL-ID:Q91836 RNA BINDING PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.	9.40E-97	2
1428	cg44922718	1197	CATACCTATCAA GCAGTTGCAGAT A[A/gap]TGAAAC ATTATCAGCTAT CAATAAT	A	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1428	cg44922718	1251	TTGGCACTTTCA CTTTGTTTATAA [A/gap]ATTTCCAA TACACTGTACCA CAGTT	A	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	

1430	cg44922718	1252	TGGCAGCTTCAC TTTTGTTTATAA A/gap]TTTCCAAT ACACTGTACAC AGTTA	A	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1431	cg44922718	1261	CACITTTGTTTAT AAAATTCCAAT A/gap]CACTGTAC CACAGTTATGTG TCTAA	A	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1432	cg44922718	1263	CTTTTGTTTATAA AATTTCCAATAC A/gap]CTGTACCA CAGTTATGTGTC TAAAC	A	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1433	cg44922718	1318	AGGATGTTAATG GAGTAATGACTG TTT(gap]CTACTG GCCAGGCGATG GGATCAGT	T	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1434	cg44922718	1356	CGATGGGATCAG TAGTGAATTCAG TTG(gap]CTTAAAA ACAAATGTACAA ACCICI	G	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1435	cg44922718	1372	GAATTCAGTGCT TAAAAACAAATG TTAGJCAAAACCTC TGAAGAGGTGG GACICG	A	G			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1436	cg44922718	1376	TCAGTGCCTTAA AACAAATGTACA A/gap]CCTCTG AAGAGGTGGGA CTCCATGT	A	gap			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	

1437	cg44922718	1447	CAATGATGAAG AATGGCCATGG C/CgapJAGCATG CAGCATTATTTC CATGTGC	C		gap			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to TREMBLNEW- ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1438	cg43931745	278	GCCTGGGCAGT AGGGAGAACTAC CC/C/GICTATCTC TCCAGGTACATC CCAGCT	C	G				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q02395 M96=METAL RESPONSE ELEMENT DNA-BINDING PROTEIN - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 373 aa.	2.00E-80	6
1439	cg43931745	369	GTGTGAATGGG GAGCTGGGCAG AGG[C/gap]AGGC TGTCAGAAAGAT GCCCCCTCC	C		gap			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q02395 M96=METAL RESPONSE ELEMENT DNA-BINDING PROTEIN - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 373 aa.	2.00E-80	6
1440	cg43920750	1030	CTGCCGCGACC CGGACTGCGCG CCA[G/gap]CACC CCCCTGCCGACA GCTCCGTCA	G		gap			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q60668 ARE ELEMENT RNA- BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	1.70E-77	4
1441	cg43918693	1192	GGGACGAGTT GATAAGCTGGGC GG[G/T]GGGGG GGGTCCACTGT CACTTGA	G	T				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:O01367 KH RNA BINDING PROTEIN (WHO) - DROSOPHILA MELANOGASTER (FRUIT FLY), 405 aa.	3.60E-74	6
1442	cg43918693	2361	GATTTTTCAT ACAGGGAGTTT [A/gap]AAAAAAA TACTTGAACAGT TTGCC	A		gap			SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:O01367 KH RNA BINDING PROTEIN (WHO) - DROSOPHILA MELANOGASTER (FRUIT FLY), 405 aa.	3.60E-74	6
1443	cg43918693	2443	TTCTCATATTTT TTAGGTGTAAAA[T/A]AAAGATTCA GTAATTTTAACTC AGA	T	A				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:O01367 KH RNA BINDING PROTEIN (WHO) - DROSOPHILA MELANOGASTER (FRUIT FLY), 405 aa.	3.60E-74	6

1444	cg43920744	180	GACAACACAACT TAAAAATGAACT TTCCTCTCCATT CCCTAAAGTTGC ATGTT	A	C				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q60688 ARE ELEMENT RNA- BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1445	cg43920744	196	AATGAACCTTACT TCCATTCCCTAA ATGATTTGCATGT TGAATGAACAGA ATCCC	G	A				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q60688 ARE ELEMENT RNA- BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1446	cg43920744	365	GCAGGCACCAAA TTAAAAA [gap]/AJGGGAGGG CTCATGAGCATA AGAAAC	gap	A				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q60688 ARE ELEMENT RNA- BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1447	cg43920744	365	GCAGGCACCAAA TTAAAAA [gap]/AJGGGAGGG CTCATGAGCATA AGAAAC	gap	A				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q60688 ARE ELEMENT RNA- BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1448	cg43920744	58	TTTTTGTAAAA AGGCTTTATTCAT T/gapTTTTTTGAT CAGGGAAGG ACAATC	T	gap				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q60688 ARE ELEMENT RNA- BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1449	cg43920744	63	TTTAAAAAGGCT TTATTCATTTTTT gapTTGATCAGG GAAAAGGACAAT CTCAAT	gap	T				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q60688 ARE ELEMENT RNA- BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	5.90E-73	4
1450	cg43144895	903	TGAGCCCACTGT GGTGCTCCTGCA G[G/gap]CTGAGC CACAACTGCTGG ACAGACA	G	gap				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	2.40E-59	11

1451	cg43327954	984	AACTGAAGCAGG CCTTGAAGCCTT GT[C]CCCTTGA GGACAAGAAACC CGAGG	T	C				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.50E-57	1
1452	cg43327954	985	ACTGAAGCAGGC CTTGAAGCCTTG TTC/TCCCTTGAG GACAAGAAACCC GAGGA	C	T				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.50E-57	1
1453	cg43936210	235	TAAATCAGTGG TGGAAGAGCCG AA[G]gap]GTTCG TATGAGCGAGGA TGATTCCC	G	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q50905 DNA-BINDING PROTEIN (ASGB) - MYXOCOCCUS XANTHUS, 375 aa (fragment).	2.20E-56	2
1454	cg43936210	236	AAATCAGTGGT GGAAGAGCCGA AG[G]gap]TTCGT ATGAGCGAGGAT GATTCCCA	G	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q50905 DNA-BINDING PROTEIN (ASGB) - MYXOCOCCUS XANTHUS, 375 aa (fragment).	2.20E-56	2
1455	cg43936210	308	CAACTTTGTGTCAG CAGCAGAACCG GA[G]gap]GGAGC CGCAATGTACGC CACACCAC	G	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q50905 DNA-BINDING PROTEIN (ASGB) - MYXOCOCCUS XANTHUS, 375 aa (fragment).	2.20E-56	2
1456	cg43936210	587	ACTTCATCGAAA GCACTTGTGGAT G[G]gap]TGTCTA AGCCACCAATAG TTTGCCCT	G	gap				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q50905 DNA-BINDING PROTEIN (ASGB) - MYXOCOCCUS XANTHUS, 375 aa (fragment).	2.20E-56	2
1457	cg43946971	245	AGCAGTTTGCCA TGGAGAGCTTGG G[G/C]CTGCACA CGGTGACCCCTTA GTGATG	G	C				SILENT- NONCODI NG	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	4.90E-52 (6p21.3)	6

1458	cg43917203	916	TCATCTTAGAAA GGTCTGGTCGCA TTC/gap]CTACGG GCCCGCTTCTTG CTGCTCT	C	gap				SILENT- NONCODING	dna_ma_ bind	Human Gene Similar to SWISSPROT- ID:O14846 CHROMODOMAIN- HELICASE-DNA-BINDING PROTEIN 1 (CHD-1) - HOMO SAPIENS (HUMAN), 1709 aa.	5.90E-50	14
1459	cg43980504	81	CACAGAACTATT GTAAACAATAT TTT/CITCAGTCGG TGATCATTGTAA TATAC	T	C				SILENT- NONCODING	dna_ma_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:P41134 DNA-BINDING PROTEIN INHIBITOR ID-1 (ID) - HOMO SAPIENS (HUMAN), 154 aa.]pcis:SWISSPROT- ID:P41134 DNA-BINDING PROTEIN INHIBITOR ID-1 (ID) - HOMO SAPIENS (HUMAN), 154 aa.	6.60E-74	20 (20q11)
1460	cg43298462	639	AACTGCAGAAAG GGCATTAAAG TTC/TTTTTTCATA AATAACGAATAT CACA	C	T				SILENT- NONCODING	dna_ma_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa.]pcis:SWISSPROT- ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa.	9.20E-67	3 (2p25)
1461	cg43298462	726	TTAGTTTTCTTC CATTTTTTTTTTg ap/T]CTTTTTTAAA AAGGTCCATTCA ACTT	gap	T				SILENT- NONCODING	dna_ma_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa.]pcis:SWISSPROT- ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa.	9.20E-67	3 (2p25)
1462	cg43971258	1074	AGAGAAAGAAAA CCAAAAGAAAGTC C[C/gap]GCTACA GTGACCTGCAAC GCGCGCA	C	gap				SILENT- NONCODING	dna_ma_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP- HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.]pcis:SWISSPROT-ID:Q02535 DNA- BINDING PROTEIN INHIBITOR ID-3 (ID- LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)

1463	cg43971258	146	TAAAGAACAAATA CTTTTTTTTTTTT ATTACACAAGTGT TTAAAAATCGTTT ATT	A	T				SILENT- NONCODING	dna_ma_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP- HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.lpcis:SWISSPROT-ID:Q02535 DNA- BINDING PROTEIN INHIBITOR ID-3 (ID- LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)
1464	cg43971258	245	CAGAAAGTCACC TTCCTGTAAAAA A[gap/A]GGTACA AAACCTATATAC TCTATTA	gap	A				SILENT- NONCODING	dna_ma_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP- HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.lpcis:SWISSPROT-ID:Q02535 DNA- BINDING PROTEIN INHIBITOR ID-3 (ID- LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)
1465	cg43971258	343	AAGACCAGCTCT GCCGCCGCCCTT GG[C/gap]ATAGT TTGGAGAGCAGC CACTCCTT	C	gap				SILENT- NONCODING	dna_ma_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP- HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.lpcis:SWISSPROT-ID:Q02535 DNA- BINDING PROTEIN INHIBITOR ID-3 (ID- LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)

1466	cg43971258	389	TCCTTCACACC TCCACGCTCTGA AAGAGACCTTA GAACCTGGGGT GGGGT	A	G				SILENT- NONCODI NG	dna_ma_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP- HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa. ipcds:SWISSPROT-ID:Q02535 DNA- BINDING PROTEIN INHIBITOR ID-3 (ID- LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)
1467	cg43949306	169	CTTCTCTATTAC AATCTGAAGAAT TCTCTCCTTTG GAAACCTTCAAT CCGG	T	C				SILENT- NONCODI NG	dynein	Human Gene SWISSPROT-ID:P38650 DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C) - RATTUS NORVEGICUS (RAT), 4644 aa.	0.00E+00	14
1468	cg43947402	256	CTTTTGAAGGAA AAGGCAGAGGC ATGTTTACAT TATCCAGAAAA CAGAAT	G	T				SILENT- NONCODI NG	dynein	Human Gene SWISSPROT-ID:Q90828 DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A) - GALLUS GALLUS (CHICKEN), 515 aa.	3.70E-214	3
1469	cg43972836	644	GGAGCTGCTGA GTTCTGGACACA GCAGTTCCTTT CCCAGATGAGA CTGGCT	G	A				SILENT- NONCODI NG	dynein	Human Gene Homologous to SPTREMBL-ID:Q12019 SIMILARITY NEAR N-TERMINUS TO S. CEREVISIAE DYNEIN HEAVY CHAIN - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 4910 aa.	1.20E-132	6
1470	cg43932150	78	ACCGCCTCTCA TCGCTCCTGGAA GCGGATCCCGA GCGGACACCAT GTCGGAG	G	gap				SILENT- NONCODI NG	dynein	Human Gene Similar to SWISSPROT- ID:P38650 DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C) - RATTUS NORVEGICUS (RAT), 4644 aa.	1.10E-89	

1471	cg43923118	1830	GCTGCTCCATGG TGAAAACCGACA G[G/gap]CCGCCG AGGCACGCTCC GGGCTCCG	gap			SILENT- NONCODI NG	elastase1 nhib	Human Gene SWISSPROT-ID:P30740 LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI) - HOMO SAPIENS (HUMAN), 379 aa.	9.40E-200	6
1472	cg43923118	1840	GGTGAAAACCGA CAGGCCCGCCGA GG[C/gap]JACGCT CCGGGCTCCGA GCTGGGGGC	gap			SILENT- NONCODI NG	elastase1 nhib	Human Gene SWISSPROT-ID:P30740 LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI) - HOMO SAPIENS (HUMAN), 379 aa.	9.40E-200	6
1473	cg43923118	1863	GGCACGCTCCG GGCTCCGAGCT GGG[G/T]GCGAG GTCAGGAAGGA GGA	T			SILENT- NONCODI NG	elastase1 nhib	Human Gene SWISSPROT-ID:P30740 LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI) - HOMO SAPIENS (HUMAN), 379 aa.	9.40E-200	6
1474	cg42184167	207	CAGGTGCAGCAA C GGACCGGCTCC CT[C/gap]TCACT GGGGAACGAAA CAGGCCATC	gap			SILENT- NONCODI NG	elastase1 nhib	Human Gene Similar to SWISSPROT- ID:P19957 ELAFIN PRECURSOR (ELASTASE-SPECIFIC INHIBITOR) (ESI) (SKIN-DERIVED ANTILEUKOPROTEINASE) (SKALP) - HOMO SAPIENS (HUMAN), 117 aa.	1.60E-60	20
1475	cg43958656	2602	TTTTTTGGTGAA gap GTACTGAACCTG C[gap/C]TTTTTT CCGGTTTCTACA TGCAGA	C			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
1476	cg43958656	521	CGTTTCCAGCCC G CCAATCTCAGAG C[G/C]GAGCCGA CAGAGAGCAGG GAACCGG	C			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6

1477	cg4398656	546	GGAGCCGACAG AGAGCAGGGAA CCG[<i>gap</i>]CATG GCCAAGCCGC GGCGATCGGC	G	<i>gap</i>			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
1478	cg4401749	14845	CGTTTTAATAATT TTTGCTGAATTC[C[<i>gap</i>]TTTACAAC TAAATAACACAG ATATT	C	<i>gap</i>			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2- MACROGLOBULIN RECEPTOR) (A2MR) (APOE) (CD91) - HOMO SAPIENS (HUMAN), 454 aa.	0.00E+00	12
1479	cg43982507	3293	ACAAATAATACC CCGTCGGAATG GT[<i>gap</i>]AACCGA GCCAGCAGCTG AAGTCTCT	T	<i>gap</i>			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00 9 (9p24)	
1480	cg43982507	533	CCTCCCAGCCCC CACCTTCTTCCT C[<i>gap</i>]TTTCGG AAGGCTGGTAA CTTGTCG	C	<i>gap</i>			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00 9 (9p24)	
1481	cg43982507	594	CGGCGGCGGGC GCGGCGGGCGC GGC[<i>gap</i>]GJACCA TCCAGCGGGC ACCATGGGCA	<i>gap</i>	G			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00 9 (9p24)	
1482	cg43982507	594	CGGCGGCGGGC GCGGCGGGCGC GGC[<i>gap</i>]GJACCA TCCAGCGGGC ACCATGGGCA	<i>gap</i>	G			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00 9 (9p24)	

1483	cg43965833	3513	GTTTGGTTGCTG GGGGGCTTTT TGA/GGGTTTGG GGCATTGTTTT TTGTA	A	G			SILENT- NONCODI NG	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	
1484	cg43965833	3763	GTTTATATGTGT ATGTGTGTGACA G/A/GJAAATCTG TAGAGAAGAGGC ACATC	A	G			SILENT- NONCODI NG	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	
1485	cg43965833	3890	AAAGCCCTTTGG AAATCTGGATCA G/A/GJAAATAGAT ACCATGGTTGT GCAAT	A	G			SILENT- NONCODI NG	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	
1486	cg43965833	4483	TGGCTTAAGTC AGAACAACCTGGC C/A/CJAAATTGAA GTCATATTTGAG GGGGG	A	C			SILENT- NONCODI NG	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	
1487	cg43965833	4484	TGGCTTAAGTC GAACAACCTGGC A/A/CJAAATTGAA TCATATTTGAGG GGGGA	A	C			SILENT- NONCODI NG	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	
1488	cg43965833	4502	CTGGCCAAAATT GAAGTCATATTT G/A/TJGGGGGA AATGGCATACGC AATATT	A	T			SILENT- NONCODI NG	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	
1489	cg43965833	4514	GAAGTCATATTT GAGGGGGGAAA TG[G/gap]CATAC GCAATATTATATT ATATTGG	G	gap			SILENT- NONCODI NG	eph	Human Gene SPTREMBL-ID:Q14114 APOLIPOPROTEIN E RECEPTOR 2 PRECURSOR - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	

1490	cg44007516	377	TAATAAAATAAC TGGAGCAGAGAA [A/gap]GCTTTAG GAGTTATACCAT TAGTTC	A	gap			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:Q03933 HEAT SHOCK FACTOR PROTEIN 2 (HSF 2) (HEAT SHOCK TRANSCRIPTION FACTOR 2) (HSTF 2) HOMO SAPIENS (HUMAN), 536 aa.	6.20E-283	
1491	cg43945212	2872	TGTCCTGTGTCT ATGTACCTCTAG C[A/gap]TGTCTT TTTTGTACTTTTC TGGTT	A	gap			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P43135 APOLIPOPROTEIN A1 REGULATORY PROTEIN-1 (ARP-1) (COUP-TF II) - MUS MUSCULUS (MOUSE), 414 aa.	5.80E-232	7
1492	cg43945212	926	GTCCCCCTCCCC TCCCCTCCCGGC G[G/C]AAAGCCC CCCGAAACCAAC AAAGCT	G	C			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P43135 APOLIPOPROTEIN A1 REGULATORY PROTEIN-1 (ARP-1) (COUP-TF II) - MUS MUSCULUS (MOUSE), 414 aa.	5.80E-232	7
1493	cg43945167	405	TGCTACCCACCAC CAAGCCCTGTGT C[G/A]CGACGGC AGCGGCTGCAG TCACCAG	G	A			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P30533 ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR- RELATED PROTEIN- ASSOCIATED PROTEIN 1) (RAP) - HOMO SAPIENS (HUMAN), 357 aa.	9.60E-191 (4p16.3)	4
1494	cg43945167	475	GACACCCGTGC CAGCCCCAGCC ACC[C/gap]TGAC GGCGGGCTGTC CACGGAAATG	C	gap			SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P30533 ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR- RELATED PROTEIN- ASSOCIATED PROTEIN 1) (RAP) - HOMO SAPIENS (HUMAN), 357 aa.	9.60E-191 (4p16.3)	4

1495	cg43945167	561	CTTCCCTGCCGG GCTGGGCTCCC CA/GJTGCCCTC AGAGTTCGTTGT GCCGAG	A	G				SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:P30533 ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR- RELATED PROTEIN- ASSOCIATED PROTEIN 1) (RAP) - HOMO SAPIENS (HUMAN), 357 aa.	9.60E-191	4 (4p16.3)
1496	cg38775224	1064	TGGTAACCCACAG AATTAATAACTGT [A/gap]CTACCCCT GACAAGCTATAT ACATGT	A	gap				SILENT- NONCODI NG	eph	Human Gene SWISSPROT-ID:Q13790 APOLOPROTEIN F PRECURSOR (APO-F) - HOMO SAPIENS (HUMAN), 308 aa.	1.30E-161	12
1497	cg43262939	524	CCTTCAATAGCA TGTCAGTGGAG T[G/A]AAAAAGA ATTGGCCATGA ATTG	G	A				SILENT- NONCODI NG	eph	Human Gene Homologous to SWISSPROT-ID:P08519 APOLOPROTEIN(A) PRECURSOR (EC 3.4.21.-) (APO(A)) (LP(A)) - HOMO SAPIENS (HUMAN), 4548 aa.	4.60E-108	
1498	cg43918531	1635	GAATGATTTTGA AGATTGATGACA TTT/CJCGTAAGCC TGGAGAATCTGA AGAA	T	C				SILENT- NONCODI NG	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa. Jpcls:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5
1499	cg43918531	1729	TAAGTAAATGGA TGTCCTCGTGATG C[G/A]TCTACAGT TATTTATTGTTAC ATCC	G	A				SILENT- NONCODI NG	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa. Jpcls:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5

1500	cg43918531	1843	CAAAGCTGTGTA ATCGTGGGGTA CTT/CATCTCAAC TGCTTTGTATTC ATTG	T	C				SILENT- NONCODI NG	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa.lpcis:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5
1501	cg43944783	38	TTTTTTTTTTT TTTTTTTTTTT TTTAACACGCC CAACTGGCTTGT TTT	A	T				SILENT- NONCODI NG	eph	Human Gene Similar to SWISSPROT- ID:P15705 HEAT SHOCK PROTEIN ST11 - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 589 aa.	2.80E-74	11
1502	cg43984905	2387	CTAGGCTGGAG GAAGCCAGTGG GGT[C/gap]CCCC CTGAGTGGGCT GGGCCCTCTG	C	gap				SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
1503	cg43984905	2392	TGGAGGAAGCC AGTGGGTCCC CCC[gap/C]TGAG TGGGCTGGGCC CTCTGTCCAC	gap	C				SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
1504	cg43984905	2440	CACATGTGGGA CAGGGCTGGTG TG[gap]CTGCT CCGAGCCTCTTG CTCAGAGC	G	gap				SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3

1505	cg43984905	2575	GTCCTTCATTCC GTTAGGAATAAC A[C/A]TGCAGCC CTCTCCAACCTC CGGCCA	C	A			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
1506	cg43984905	2599	ACTGCAGCCCTC TCCAACCTCCGG C[C/gap]AGCGAG TGGTCAAGGATT TTTATAA	C	gap			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
1507	cg43274299	2011	CTGCTCAGACCT GTGACCCCGGC GG[G/gap]ACCCC CATGTCCTCCGC TCCGCCCCG	G	gap			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1508	cg43274299	2149	GTCCCCCGGGG CTCCCGGTCTCTC TG[gap]/GICATGT CTCAGGCTGAGC TCCCTCCC	gap	G			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1509	cg43274299	2156	GGGGCTCCCCG TCCTCTGCATGT CT[gap]/TTCAGGC TGAGCTCCCTCC CCCGCGGT	gap	T			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1510	cg43274299	2170	CTCTGCATGTCT CAGGCTGAGCTC C[C/gap]TCCCCC GCGGTGCCTTC GCCCTCTG	C	gap			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7

1511	cg43274299	2176	ATGTCCTCAGGCT GAGCTCCCTCCC C[C/gap]GCGGTG CCCTCGCCCTCT GGCTGCA	C	gap			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1512	cg43274299	2180	CTCAGGCTGAGC TCCCTCCCCCGC G[G/gap]TGCCTT CGCCCTCTGGCT GCAAATA	G	gap			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P22303 ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	7
1513	cg43972012	102	CAGGGTTCCTGG CTGGGCAGCAC AG[G/gap]CCTGG GGCGACACTCCT GTCCTGTC	G	gap			SILENT- NONCODI NG	esterase	Human Gene SPTREMBL-ID:Q16837 ACID SPHINGOMYELINASE (EC 3.1.4.12) (SPHINGOMYELIN PHOSPHODIESTERASE) (NEUTRAL SPHINGOMYELINASE) - HOMO SAPIENS (HUMAN), 629 aa.	0.00E+00	11 (11p15.4)
1514	cg44011461	172	ATTATCAAGGT TTTCATTGCTTTT [gap/T]ATTCAATG AGGTTTGAACA TGAGA	gap	T			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1515	cg44011461	188	CATTGCTTTTATT CAATGAGGTTTG G/C/AACATGAGA GGCCAAAATGA GGAG	G	C			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)

1516	cg44011461	241	CATTTGGGAA TCCTCTATAAG A[A/gap]TATAAGT TAAGAAAGTTGT CCAAGA	A	gap				SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1517	cg44011461	251	AATCCTCTATAA AGAAATATAAGTT A[A/gap]GAAAGT TGTCCTCAAGATGA AAATAAT	A	gap				SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1518	cg44011461	255	CTCTATAAAGAA TATAAGTTAAGA A[A/gap]GTTGTC CAAGATGAAAT AATAGGA	A	gap				SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1519	cg44011461	524	TGCATTTCCTCT GGTACAGCTGGA G[C/gap]TGGTTC TCATTAACTG AACTCTT	C	gap				SILENT- NONCODI NG	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
1520	cg43984524	860	TATCACCCTGAA CGGCCTGATCT C[A/G]TCTGATCT CGGAAGCTAAGC AGGGT	A	G				SILENT- NONCODI NG	esterase	Human Gene Similar to SPTREMBL- ID:P70665 SIALIC ACID-SPECIFIC 9-O- ACETYLESTERASE - MUS MUSCULUS (MOUSE), 541 aa.	3.20E-99	

1521	cg43319420	1886	CTGCAGTTCTGG ACGGGCTGGCC GA[G/gap]TGGC GGGATCCTTGTC CAGGGAAG	G	gap			SILENT- NONCODI NG	esterase	Human Gene Similar to SWISSNEW- ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.lpcis:SWISSPROT- ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.	3.30E-60	21
1522	cg43319420	1916	CGGGATCCTTGT GCAGGGAAGAG CT[G/gap]CCCTG GGACCTGGCA CCACAAGAC	G	gap			SILENT- NONCODI NG	esterase	Human Gene Similar to SWISSNEW- ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.lpcis:SWISSPROT- ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.	3.30E-60	21
1523	cg43934722	737	GGGATTTTGTGG ACGTCTCCGTGC A[G/T]GAACTGCT GGACTGTGGCC GCTGTG	G	T			SILENT- NONCODI NG	fgf	Human Gene TREMBLNEW- ID:G2738520 FGF-1 INTRACELLULAR BINDING PROTEIN - HOMO SAPIENS (HUMAN), 372 aa.lpcis:TREMBLNEW- ID:G2738522 FGF-1 INTRACELLULAR BINDING PROTEIN - CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRVET), 372 aa.	9.80E-184	
1524	cg43281831	2016	TCCCTTTAACCAC TGCCCTCTCCTT CTT/gapTTCTCCT TCAAGGTTCTTT CCCCCT	T	gap			SILENT- NONCODI NG	fgf	Human Gene Similar to TREMBLNEW- ID:G2827284 NOVEL ANTAGONIST OF FGF SIGNALING - HOMO SAPIENS (HUMAN), 139 aa (fragment).	9.20E-83	4

1525	cg43281831	2017	CCTTTAACCACT GCCCTCTCCTTC TTT/gapJTGCTCTT CAAGGTTCTTTC CCCCTC	T	gap			SILENT- NONCODI NG	fgf	Human Gene Similar to TREMBLNEW- ID:G2827284 NOVEL ANTAGONIST OF FGF SIGNALING - HOMO SAPIENS (HUMAN), 139 aa (fragment).	9.20E-83	4
1526	cg43919380	1038	CGAGGGGTCTCCT CACCTGGTTGAC CC[C/gap]AAAAA TGTTCCCTTGAC CATTGGCT	C	gap			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1527	cg43919380	1257	TGCTCTCTTGCA GGCTGAGTCCCT C[A/C]ATGCAAAA GTGGGGCTAAAT GAAGT	A	C			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1528	cg43919380	2230	TGTAATAAGGAG CATGATTTTAAG A[G/T]GCTTTGGC CCAATGCCATATA AAATG	G	T			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1529	cg43919380	2240	AGCATGATTTTA AGAGGCTTTGGC C[C/gap]AATGCC TATAAAATGCC ATTTCGA	C	gap			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)

1530	cg43919380	3274	TTAAGGTGCCTA CTGTGTGCTAGG C[A/gap]CTGTAC TGGATACTGGGG ACCTTGT	A	gap			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN). 155 aa.	8.40E-82	5 (5q31)
1531	cg43919380	3702	AAGTCTCATAGC CAGCTCCTGTCA C[G/A]TGACTCTC ATATGGATTTCAT TTTCG	G	A			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN). 155 aa.	8.40E-82	5 (5q31)
1532	cg43919380	395	GGGCTACTCTGA GAAGAAGACACC A[G/A]GGGGATT CCTCTTCCCTG GGACAG	G	A			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN). 155 aa.	8.40E-82	5 (5q31)
1533	cg43919380	404	TGAGAAGAAGAC ACCAGGGGGATT C[C/T]TCTTCCCC TGGGACAGCACT GAGCG	C	T			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN). 155 aa.	8.40E-82	5 (5q31)

1534	cg43919380	406	AGAAGAAGACAC CAGGGGGATTG CTC/TJTTCCCT GGGACAGCACT GAGCGAG	C	T			SILENT- NONCODI NG	fgf	Human Gene Similar to SWISSPROT- ID:P05230 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) (BETA- ENDOTHELIAL CELL GROWTH FACTOR) (ECGF- BETA) - HOMO SAPIENS (HUMAN), 155 aa.	8.40E-82	5 (5q31)
1535	cg43918792	691	ACCGCAAACAGC AAAGACTATCCC A/A/CJCTTTCTAT TAACAGTGCCAA GATTA	A	C			SILENT- NONCODI NG	fgf	Human Gene Similar to TREMBLNEW- ID:G2827284 NOVEL ANTAGONIST OF FGF SIGNALING - HOMO SAPIENS (HUMAN), 139 aa (fragment).	1.70E-56	13
1536	cg43918792	697	AACAGCAAAGAC TATCCCAACTTT C/T/GJATTAACAG TGCCAAAGATTAT AACTG	T	G			SILENT- NONCODI NG	fgf	Human Gene Similar to TREMBLNEW- ID:G2827284 NOVEL ANTAGONIST OF FGF SIGNALING - HOMO SAPIENS (HUMAN), 139 aa (fragment).	1.70E-56	13
1537	cg43937658	1026	CAAAGGCAGTAA CCCCAGCGACC AG[C/gap]TGCTG CTGCTGCACGGT GAGGAGGA	C	gap			SILENT- NONCODI NG	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16
1538	cg43937658	353	AGCCTCAGCAG GGCCGGTCCAG ACA/T/CJGGCTGA GTCCCTGTGCTGC CCTGGAG	T	C			SILENT- NONCODI NG	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16
1539	cg43937658	561	CCACAGAAATAC CCATGGCTGTGG G[G/gap]CTGTGA CCAGCAGTGGCT GATTAGG	G	gap			SILENT- NONCODI NG	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16
1540	cg43937658	898	TTTTTTTGGTGG TTTTCTTAAAAA [gap/A]GCCCTTTG AGTGCAGGTCA GGTGA	gap	A			SILENT- NONCODI NG	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16

1541	cg43937658	950	TGGTTCCTGGAAG TACCGGAAGTTC T[G/T]TTGGTATG AGAGAGACTTGT CTACA	G	T			SILENT- NONCODI NG	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16
1542	cg43284508	306	CTCTATCCCAT CCTTTGCAAAAG A[G/A]GGGAGGG GTCTACAAGCCA GAACCT	G	A			SILENT- NONCODI NG	fgfrecept or	Human Gene Similar to SPTREMBL- ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1543	cg43284508	443	ACATCAGAACCA CTGACTGGTAGA G[C/T]CCTTGGAA ATCATACAGTCC ACCCA	C	T			SILENT- NONCODI NG	fgfrecept or	Human Gene Similar to SPTREMBL- ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1544	cg43284508	475	AAATCATACAGT CCACCCATCCCC C[G/A]CCAGACA CATGGACACACC GAGGCT	G	A			SILENT- NONCODI NG	fgfrecept or	Human Gene Similar to SPTREMBL- ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1545	cg43284508	881	CCACGCCCATAT GAGGGGTGGAG AG[G/gap]AGAAG CCAGCAGCACTG GGTGAGC	G	gap			SILENT- NONCODI NG	fgfrecept or	Human Gene Similar to SPTREMBL- ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1546	cg43284508	883	ACGCCCATATGA GGGGTGGAGAG GA[G/gap]AAGCC AGCAGCAC.TGG GGTGAGCCT	G	gap			SILENT- NONCODI NG	fgfrecept or	Human Gene Similar to SPTREMBL- ID:P70561 FGF RECEPTOR ACTIVATING PROTEIN FRAG1 - RATTUS NORVEGICUS (RAT), 254 aa.	8.30E-66	
1547	cg43320667	576	ATTAAAAAGGTC ACCAGCCCGCC AG[G/gap]TGCCA GAAGCCACCGG GTATCCTTG	G	gap			SILENT- NONCODI NG	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00	3 (3p25)

1548	cg43320667	674	TCCTGCGTGGT GATGGTGTCTGG A[C/gap]TCGCCA CTCGAGGTAGGT TGAGATG	C	gap				SILENT- NONCODI NG	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00	3 (3p25)
1549	cg43975899	1613	TTTTACTCACATT CTGTTGTTTCAGT gap/TTCCTCTGCA CTGGGAATTAT TTATG	gap	T				SILENT- NONCODI NG	gaba	Human Gene SWISSPROT-ID:P14867 GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-1 SUBUNIT PRECURSOR (GABA(A) RECEPTOR) - HOMO SAPIENS (HUMAN), 456 aa.	1.30E-248	5 (5q34)
1550	cg43975899	1664	TCTCAACGCAGT AATCCCATCTG C[gap/C]TTTATTG CCTCTGTCTTAA AGAAAT	gap	C				SILENT- NONCODI NG	gaba	Human Gene SWISSPROT-ID:P14867 GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-1 SUBUNIT PRECURSOR (GABA(A) RECEPTOR) - HOMO SAPIENS (HUMAN), 456 aa.	1.30E-248	5 (5q34)
1551	cg43299024	3522	TTTCTCCCTAGA TCGCACTGTGGG C[C/T]GGGGCCC TGGAGGGCTGC TCTGTGT	C	T				SILENT- NONCODI NG	glucoamy lase	Human Gene TREMBLNEW- ID:G2826521 MALTASE- GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)
1552	cg43299024	3529	CTAGATCGCACT GTGGGCCCGGG CC[C/gap]TGGAG GGCTGCTCTGTG TTAATAAG	C	gap				SILENT- NONCODI NG	glucoamy lase	Human Gene TREMBLNEW- ID:G2826521 MALTASE- GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)
1553	cg43299024	3718	GCTGCTCTGCCC CAACGCGACCG CT[G/T]CCCCGGC TGCCAGAGGG CTGGATGC	G	T				SILENT- NONCODI NG	glucoamy lase	Human Gene TREMBLNEW- ID:G2826521 MALTASE- GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)
1554	cg43299024	3744	CCCGGCTGCCC AGAGGGCTGGA TGC[C/gap]TGCC GGTCCCCGAGC AAGCCTGGGA	C	gap				SILENT- NONCODI NG	glucoamy lase	Human Gene TREMBLNEW- ID:G2826521 MALTASE- GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)

1555	cg43892811	387	CTTCTTCCAAGA TTTCACGTCTTG GIC/TGGCCGTT CCAAGGAGCGC GAGGTCG	C	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P08183 MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 1280 aa.	0.00E+00	7
1556	cg43943531	2247	TAAATGTCACGT CCAGCTCTGATA TIGgapICTTCGC ACTGAGCACATC ACATTTA	G	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	11 (11q23.3)
1557	cg43943531	2343	TGTAAGAACAAA ACTGGATGGCAT CIA/CJGAATTGTC TGGAAGTTTTGT CTTGG	A	C				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	11 (11q23.3)
1558	cg43943531	2372	TTGTCTGGAAGT TTTGTCTTGGGC AIG/TJATGGGCT GGCCAAATGAA ATGAT	G	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	11 (11q23.3)
1559	cg43943531	2373	TGTCTGGAAGTT TTGTCTTGGCA G/T/GJATGGGCT GGCCAAATGAA ATGAT	T	G				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	11 (11q23.3)
1560	cg44021330	3335	AACACACATGAT GACTGAGGCATT C/G/AJGGAACCC CTTCATCCAAAA GAATAA	G	A				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q12860 CONTACTIN PRECURSOR (GLYCOPROTEIN GP135) - HOMO SAPIENS (HUMAN), 1018 aa.	0.00E+00	12 (12q11)
1561	cg43997653	2551	GAGCTATTTTAA CCTCCCGCCTCC C/C/TJTGCTGGTC CCCCCACCTGAC GTCTT	C	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P50895 LUTHERAN BLOOD GROUP GLYCOPROTEIN PRECURSOR (B-CAM CELL SURFACE GLYCOPROTEIN) (AUBERGER B ANTIGEN) (F8/G253 ANTIGEN) - HOMO SAPIENS (HUMAN), 628 aa.	0.00E+00	

1562	cg44003301	1920	TGAGATAAAAGA TGACTTGTGAC C[A/G]TTGTAACA ATAGCACAAATA AAGCA	A	G				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P16671 PLATELET GLYCOPROTEIN IV (GP1B) (GPIIB) (CD36 ANTIGEN) (PAS IV) (PAS-4 PROTEIN) - HOMO SAPIENS (HUMAN), 471 aa.	2.00E-254	7 (7q11.2)
1563	cg43957605	150	TTATAGAAAGTT GCAGTTAAAC G[C/T]TTTCTCCA AAATAAAAGAC AAATG	C	T				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q00013 55 KD ERYTHROCYTE MEMBRANE PROTEIN (P55) - HOMO SAPIENS (HUMAN), 466 aa.	3.10E-249	X (Xq28)
1564	cg43957605	510	CAAAATGCTGGAG AGGGGCATACA GT[G/gap]GGTTC CCCCATTCTACA AGCTTAGT	G	gap				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q00013 55 KD ERYTHROCYTE MEMBRANE PROTEIN (P55) - HOMO SAPIENS (HUMAN), 466 aa.	3.10E-249	X (Xq28)
1565	cg43926590	415	TTCAGACAATTC AGCCTTTATTTTA [G/A]AAAAATAATT CTGTAGCTTCCA CTTT	G	A				SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P26572 ALPHA-1,3-MANNOSYL- GLYCOPROTEIN BETA-1,2-N- ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL- OLIGOSACCHARIDE-GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERASE E1) (GNT-1) (GLCNAC-T1) - HOMO SAPIENS (HUMAN), 445 aa. Jpts: SWISSPROT-ID: P26572 ALPHA 1,3-MANNOSYL-GLYCOPROTEIN BETA 1,2-N- ACETYLGLUCOSAMINYLTRANSFERASE E (EC 2.4.1.101) (N-GLYCOSYL- OLIGOSACCHARIDE-GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERASE E1) (GNT-1) (GLCNAC-T1) - HOMO SAPIENS (HUMAN), 445 aa.	4.20E-245	5 (5q35)

1586	cg44003218	158	GATTCCTTCTGT GACTCATCAGTT C/A/CJTTCCTGT AAATTCATGTC TTGCT	A	C				SILENT- NONCODING NG	glycoprotein	Human Gene SWISSPROT-ID: P16671 PLATELET GLYCOPROTEIN IV (GP1B) (GPIIB) (CD36 ANTIGEN) (PAS IV) (PAS-4 PROTEIN) - HOMO SAPIENS (HUMAN), 471 aa.	2.40E-242	7 (7q11.2)
1587	cg42360892	1557	AGAAAGAGGATA CACAAAACGTAC C/C/gapJTATCT GTTCCCTTCC TTGTCAG	C	gap				SILENT- NONCODING NG	glycoprotein	Human Gene SWISSPROT-ID: Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL- GLYCOPROTEIN BETA-1,6-N- ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC- TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)
1588	cg42360892	1584	TATCTGTTTCCC CTTCCTTGTCAG C/G/AJTCGGGAA GATGGTATGAAG TCCTCT	G	A				SILENT- NONCODING NG	glycoprotein	Human Gene SWISSPROT-ID: Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL- GLYCOPROTEIN BETA-1,6-N- ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC- TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)
1589	cg42360892	1826	GCCGATGCATAA AGTCAGCCTGTT C/A/CJAAGTGCTC AGGGACTTAGCA AAATG	A	C				SILENT- NONCODING NG	glycoprotein	Human Gene SWISSPROT-ID: Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL- GLYCOPROTEIN BETA-1,6-N- ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC- TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)

1570	cg42360692	1914	TAAATGTGACCA TTTTTCTGGTAT Ggap/CJAATAAA CTTACAGCAACA AATAATC	gap	C			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL- GLYCOPROTEIN BETA-1,6-N- ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC- TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)
1571	cg42360692	1914	TAAATGTGACCA TTTTTCTGGTAT Ggap/CJAATAAA CTTACAGCAACA AATAATC	gap	C			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q02742 BETA-1,3-GALACTOSYL-O-GLYCOSYL- GLYCOPROTEIN BETA-1,6-N- ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.102) (CORE 2 BRANCHING ENZYME) (CORE2-GLCNAC- TRANSFERASE) (C2GNT) (CORE 2 GNT) - HOMO SAPIENS (HUMAN), 428 aa.	2.10E-234	9 (9q21)
1572	cg43924995	1830	GGCCAAATTTTG ATCCTAACCTTG A/A/CJGTATGCCT TGAACCTATTAA CATGG	A	C			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P13473 LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2) (CD107B ANTIGEN) - HOMO SAPIENS (HUMAN), 410 aa.	1.20E-222	X (Xq24)
1573	cg43987514	76	TTTTTTTTTTT TTGCAGGTAAA [A/G]GAAAAAGACT TTATTAATAATCA GTG	A	G			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa.	3.20E-215	

1574	cg43301245	232	TTCTTAAGTGAA GGTTTCAAGCTG G[G/gap]CTTTGC AGGGGGTATAAT TAGTATG	G	gap			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcds:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383.aa	3.00E-210	1
1575	cg43301245	334	ATGGTGTCCTTT GATAAGGAGGG CT[G/A]GGGGC AGGGAGTTGAAG AAATTCC	G	A			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcds:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383.aa	3.00E-210	1
1576	cg43301245	399	GATCTGTAAACA TTTCCATTAAATCA [gap]/TACAAAGTG TGTAATAATCCC GAGTCT	gap	T			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcds:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383.aa	3.00E-210	1
1577	cg43958670	1152	CATACGGAGTTTC TCCTTTGGGAAA C[G/A]ACAAGACT ACAGTGTTCACT TCGCA	G	A			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377.aa	9.60E-207	1 (1q32)

1578	cg43958670	15	TTTTTTTTTTT TTT/AJTTTTTCC AAATGTACAATTT TAT	T	A			SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1579	cg43958670	16	TTTTTTTTTTT TTT/AJTTTTTCC AAATGTACAATTT TATT	T	A			SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1580	cg43958670	174	GAATTCATATAC GCTTCTGTCATT TACJACAAACT TCCAGAGAAAC TGGTC	A	C			SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1581	cg43958670	1953	AATCTATTACG CTCTCTGCTCTG CJA/TGGAGTGG TTGATTTAGTCT GGTAAG	A	T			SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1582	cg43958670	3091	CTCGCGGCGGC CGGAGGCTCC ATG/C/GJCGGC GCGGGAAGACG CTGTTATT	C	G			SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1583	cg43958670	3092	TCGCGGCGGCC GGGAGGCTCCA TGC/G/CJCGCG CGGGAAGACGC TGTTATTT	G	C			SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)

1584	cg43958670	3099	GGCCGGGAGGC TCCATGCGCGG CGC[G/gap]GGAA GACGCTGTTATT TCGCCGAG	G	gap			SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPBBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1585	cg43958670	3101	CCGGGAGGCTC CATGCGCGCGG CGG[G/gap]AAGA CGCTGTTATTTC TCCGGAGGA	G	gap			SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPBBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.60E-207	1 (1q32)
1586	cg44034752	1702	TAGGTTGACAAC TTGTCATGATTTT [G/A]ACGGTAAG CCACCATGATTG TGTTG	G	A			SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.90E-203	3 (3q27)
1587	cg44034752	1763	TTGACCTTACAA AAACCATGGAA C[gap/C]GTGAC TTTGAAAGGTGC ICTTGCT	gap	C			SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.90E-203	3 (3q27)
1588	cg44034752	1801	GGTGCTCTTGCT AAGCTTATATGT G[gap/G]CCTGTT AATGAAAGTGCC TGAAAGA	gap	G			SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.90E-203	3 (3q27)
1589	cg44034752	1815	GCTTATATGTGC CTGTTAATGAAA G[gap/G]TGCCTG AAAGACCTTCCT TAATAAA	gap	G			SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.90E-203	3 (3q27)
1590	cg34243197	2123	GCTTTCCTGGGC CTCTCAGTTGAA C[gap/C]AAAGCA GCAAAACAAAGG CAGTTT	gap	C			SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSNEW-ID:Q61207 SULFATED GLYCOPROTEIN 1 PRECURSOR (SGP-1) (PROSAPOSIN) - MUS MUSCULUS (MOUSE), 557 aa.	5.00E-202	10 (10q22.1)

1591	cg43059879	106	GAACAAGAAACA AGTGTGACATTT TTAGTGTGGAAT CTGAAAACCACC TTAGC	A	G			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C- BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:SWISSPROT-ID:P02749 BETA- 2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:TREMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa	6.60E-199	17 (17q23)
1592	cg43932434	606	CTTTAAAGAAACA AAACACAAAAA CTTATTAAGAGT AGAAAAATTTAT GCTAA	T	A			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP80 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.80E-195	11 (11pter)

1593	cg43982434	607	TTTAAAGAACAA AACACAAAAAC TTTAAAGAGTA GAAAAATTTATG CTAAA	T	A			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.80E-195	11 (11pter)
1594	cg43982434	608	TTTAAAGAACAA AACACAAAAAC TTTAAAGAGTAG AAAAATTTATGCT AAAA	T	A			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.80E-195	11 (11pter)
1595	cg43988092	636	AATGCTTTTATG AGCCTTTCTGTA GICAAAGATACAAA TATATATATATAT ATTT	C	A			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DÖG), 373 aa.	4.00E-192	8
1596	cg43988092	775	GTAAGACTATTT ATCCACCTGAAT TTCATCAATTC TTTAAAGTTAGT GCATT	C	T			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DÖG), 373 aa.	4.00E-192	8

1597	cg43115790	122	GGTGGTCTGAC TACAAGGCTAG G[C/gap]CCTAGG ACATCTGGTTTT CTTCTT	C	gap			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:Q03395 ROD OUTER SEGMENT MEMBRANE PROTEIN 1 (ROSP1) - HOMO SAPIENS (HUMAN), 351 aa.	1.40E-191	11 (11q13)
1598	cg43918166	985	AAATTCCTTTT TTTTTTTTTTTTT gapTTTTTTTTTGCA TGTTTTTAACA ATC	T	gap			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1599	cg43918166	986	AAATTCCTTTT TTTTTTTTTTTTT gapTTTTTTTTGCA GTGTTTTAACA TCC	T	gap			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1600	cg43918166	987	AAATTCCTTTT TTTTTTTTTTTTT gapTTTTTTTTGCA GTGTTTTAACA TCCC	T	gap			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1601	cg43918166	992	TTTTTTTTTTTTT TTTTTTTTTTTTT ap/TGCATGTGTT TTAACAATCCCC CACC	gap	T			SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5

1602	cg43918166	992	TTTTTTTTTTTT TTTTTTTTTTTTTg ap/TGCATGTGT TTAACAAATCCCC CACC	gap	T				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1603	cg43918166	199	AAATAGAAACC TACTAGATCAAC A/C/AAGTGTGT TCTGTGCTCTAA AATAC	C	A				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1604	cg43918166	274	AACAACCAAGGG AACCTGCTTAA C/A/GTACTGTGT ATTATTGTAGCT AGAGT	A	G				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1605	cg43918166	310	TATTGTAGCTAG AGTCATTCCCTC T/A/TAGCCAAAG GAGGTTTTATAA AAAAG	A	T				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1606	cg43918166	334	AAGCCAAAGGAG GTTTATAAAAAA [gap/A]GAATCAA TATTGGGCCAAT CCCTTT	gap	A				SILENT- NONCODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5

1607	cg43918166	3444	ATTCCTCAGTTG ATGGTTTGAAG T[C/T]GCITCAAT ATTACATGAATT TCCT	C	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1608	cg43918166	968	AAAATGGTTATA TATACAAAATTTTC [T/gap]TTTTTTTTT TTTTTTTTTTTTT TTTG	T	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.50E-190	5
1609	cg44022653	246	TATAACCCCTTTC ATACTAGTTGAA C[gap/T]TTTTTTT TTATAATGTACAT GTACT	gap	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188 3 (3p25)	
1610	cg44022653	247	TATAACCCCTTTC ATACTAGTTGAA C[T/gap]TTTTTTT TATAATGTACAT GTACTA	T	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188 3 (3p25)	
1611	cg44022653	255	TTTCATAC TAGTT GAAC TTTTTTTT T/gap]ATAATGTA CATGTACTACTT TATAA	T	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188 3 (3p25)	
1612	cg44022653	258	ATACTAGTTGAA CTTTTTTTTATA gap/T]ATGTACAT GTACTACTTTATA ATTA	gap	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188 3 (3p25)	
1613	cg44022653	280	TATAATGTACAT GTACTACTTTATA [A/G]TTAAACAAA AAAC TTTAAAT GATT	A	G				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188 3 (3p25)	

1614	cg44022653	323	AATGATTTTAA AAAAGAAAAGAA[gap/GJTAAATCAC AGTGAACATGA AATGG	gap	G				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1615	cg44022653	357	GTGGAACATGAA ATGGAATGTCAA C[gap/GJT]TTGG GACGGGTCATCC AGAGGAG	gap	G				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1616	cg44022653	367	GAAATGGAATGT CAACTTTGGGA C[G]A[GG]TCATC CAGAGGAGTCCA AGAGCC	G	A				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1617	cg44022653	401	AGAGGAGTCCAA GAGCCCCAACAT G[G]TTCGCGTG TCTCTGGTCCTC AGGTCA	G	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1618	cg44022653	414	AGCCCCAACATG GTCGCGTGTCTC T[G]TGTCTCAG GTCATCACCCAG CCTCA	G	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1619	cg44022653	421	ACATGGTCGCGT GTCTCTGGTCCT C[AT]GGTCATCA CCAGCCCTCACC CAACAG	A	T				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1620	cg44022653	496	CCGTGCAAGCTT CCACTGGTGCC T[G]A[CG]TGGGA ACGCACCACTG CCGTGG	G	A				SILENT- NONCODI NG	glycoprot ein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)

1621	cg44022653	498	GTGCAAGCTTCC ACTTGGTGCCTG C[G/AT]GGGAAC GCACCACCTGCC GTGGAA	G	A				SILENT- NONCODING NG	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1622	cg44022653	654	CCCTCCCACGCA GTGTGAGCCCTG G[G/gap]CTGCGC CACACCCGCAG GTGGCCCG	G	gap				SILENT- NONCODING NG	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)
1623	cg43318219	1858	TTTTCAAGAAAA CTGGAAATCTGG [A/T]TTTTCAGCG AACATGCCTGAT TTTA	A	T				SILENT- NONCODING NG	glycoprotein	Human Gene SWISSPROT-ID:P15813 T- CELL SURFACE GLYCOPROTEIN CD1D PRECURSOR (CD1D ANTIGEN) (R3G1) - HOMO SAPIENS (HUMAN), 335 aa. pcis:SWISSPROT-ID:P15813 T- CELL SURFACE GLYCOPROTEIN CD1D PRECURSOR (CD1D ANTIGEN) (R3G1) - HOMO SAPIENS (HUMAN), 335 aa.	3.10E-185	1 (1q21)
1624	cg40915005	1796	GGTCCTAGCAAC CTCCACATGTTT A[A/C]CTATTAA GGATCATCAGGC CTGTT	A	C				SILENT- NONCODING NG	glycoprotein	Human Gene SWISSPROT-ID:P06126 T- CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T-CELL SURFACE ANTIGEN T6/LEU-6) (HTA1 THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa. pcis:SWISSPROT-ID:P06126 T-CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T- CELL SURFACE ANTIGEN T6/LEU-6) (HTA1 THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa.	2.00E-183	1 (1q21)

1625	cg43958915	205	GTAGATTTAACC ACAGAACTGTCT C[G/A]ATTTTAT AAAAATTGATCC CAAGA	G	A			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P18484 ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa. pcis:SWISSPROT-ID:P18484 ALPHA ADAPTIN (C) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.	2.80E-173	11
1626	cg43958915	331	CCCAAAGGGGA GAGGTGTGGG CGG[C/T]GGGC GGGAGGCGCC TTGTGCTGT	C	T			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P18484 ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa. pcis:SWISSPROT-ID:P18484 ALPHA ADAPTIN (C) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.	2.80E-173	11

1627	cg43958915	346	TGTGGGCGGC GGGCGGGGAG GCG[C/gap]CTTG TGCTGTGGCACT GGACACGGT	C	gap			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P18484 ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa. pcls:SWISSPROT-ID:P18484 ALPHA ADAPTIN (C) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.	2.80E-173	11
1628	cg43958915	387	TGGACACGGTG CTCATCTGCAGG AT[G/A]GCCACG AAGACAAACGGC ACAGACG	G	A			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P18484 ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa. pcls:SWISSPROT-ID:P18484 ALPHA ADAPTIN (C) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) - RATTUS NORVEGICUS (RAT), 937 aa.	2.80E-173	11

1628	cg43977071	1845	TGCAGGTTAGGT TCCAGACCACTT A[G/T]GAGTCTGC GAAACGCCCCAC GCTCCA	G	T			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:P28328 PEROXISOME ASSEMBLY FACTOR-1 (PAF-1) (PEROXIN-2) (35 KD PEROXISOMAL MEMBRANE PROTEIN) - HOMO SAPIENS (HUMAN), 305 aa.pcds:SWISSPROT-ID:P28328 PEROXISOME ASSEMBLY FACTOR-1 (PAF-1) (PEROXIN-2) (35 KD PEROXISOMAL MEMBRANE PROTEIN) - HOMO SAPIENS (HUMAN), 305 aa.	1.20E-169	8 (8q21.1)
1630	cg43124001	1942	CAGGGGATTTTA TCCCCCACCAAA A[A/G]CACAGTGA AAGGCCTGCTTT TGTGT	A	G			SILENT- NONCODING	glycoprotein	Human Gene SWISSNEW-ID:O42281 PERIPHERIN (RETINAL DEGENERATION SLOW PROTEIN) (PHOTORECEPTOR OUTER SEGMENT MEMBRANE GLYCOPROTEIN 1) (CRDS1) - GALLUS GALLUS (CHICKEN), 354 aa.pcds:SWISSPROT- ID:O42281 PERIPHERIN (RETINAL DEGENERATION SLOW PROTEIN) (PHOTORECEPTOR OUTER SEGMENT MEMBRANE GLYCOPROTEIN 1) (CRDS1) - GALLUS GALLUS (CHICKEN), 354 aa.	5.50E-156	6 (6p21.1)
1631	cg43248459	577	CACAGAGAGGAT GAGAAACAAAA A[A/gap]GAGAAA AGGAAAAGTAGG TTGAAGA	A	gap			SILENT- NONCODING	glycoprotein	Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	7.10E-155	20
1632	cg43248459	85	AACAGAGAGCAC ACGCATACAGCA C[G/A]GAGCACT GAGGTGGGGGA GCATGGG	G	A			SILENT- NONCODING	glycoprotein	Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	7.10E-155	20

1633	cg43953517	2391	AATAAAAAATTTAT TGAGTGAAACAA A/TJAAAAATACAA TGACTAGTCATG CAT	A	T				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.90E-150	4
1634	cg43953517	2396	AAATTTATTGAGT GAAACAAAAAA A/GJTACAATGAC TAGTCATGCATC ATCA	A	G				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.90E-150	4
1635	cg43922980	3766	TTATTATTACAA AATTATATTCAC C/GJTAATGCCA ACCATCTACAAA AACA	C	G				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P97449 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (CD13) (P161 MEMBRANE PROTEIN) - MUS MUSCULUS (MOUSE), 965 aa.	2.00E-135	5
1636	cg43922980	3957	AGGCCGCTGTT TGTCAGCCATCT G/T/CJTGCTTCT ATTGATAGATGG CATTG	T	C				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P97449 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (CD13) (P161 MEMBRANE PROTEIN) - MUS MUSCULUS (MOUSE), 965 aa.	2.00E-135	5
1637	cg43951991	152	TTACGCACCGCA TGAGAACCGTTA Ggap/GJTTATAA AATCTATCATCA ACCACTA	gap	G				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SPTREMBL-ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	7.60E-132	
1638	cg43951991	27	TTTTTTTTTTT TTTTTTTTTTTC /TTTTTATCAATG TTTTATTTTAA A	C	T				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SPTREMBL-ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	7.60E-132	
1639	cg43951991	836	ATATTTTAAACAA GGAAAAA gap/AJGCAACATT CACAGCACATCA AGCCC	gap	A				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SPTREMBL-ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	7.60E-132	

1840	cg43951991	881	AAGCCCAAAATA GTTTACACCTTC TATTCACCTGAAG CATTGTTTAAAT GTAC	A	T				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SPTREMBL-ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	7.60E-132	
1841	cg43948148	88	GTTTCTTTAAAA TAAAAACCCAC gap/AJAAAAAAGC CAGAACACCCCTA CCCAA	gap	A				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01650 INTEGRAL MEMBRANE PROTEIN E16 - HOMO SAPIENS (HUMAN), 241 aa.	2.00E-128	16
1842	cg44004667	2076	AAAGAAAATCTC TGTGAAACCCCT ATTCTGTGGAGG CGGAATTGCTCT CCCAGC	T	C				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T- LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU-2) - HOMO SAPIENS (HUMAN), 235 aa. pcds:SWISSPROT- ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T-LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU- 2) - HOMO SAPIENS (HUMAN), 235 aa.	7.60E-127	
1843	cg44004667	2296	GAGCCCTCACA CAGCCCTGGCCT CTTCGCTCAACT AGCAGATACAGG GATGA	T	C				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T- LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU-2) - HOMO SAPIENS (HUMAN), 235 aa. pcds:SWISSPROT- ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T-LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU- 2) - HOMO SAPIENS (HUMAN), 235 aa.	7.60E-127	

1644	cg43301424	1194	TGCCCCACCTCC TAACCTAATCCC C/C/AJCGCCCG CTGCCTTTCCCA GGCTCC	A			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW:ID:P11912 B-CELL ANTIGEN RECEPTOR COMPLEX ASSOCIATED PROTEIN ALPHA-CHAIN PRECURSOR (IG-ALPHA) (MB-1 MEMBRANE GLYCOPROTEIN) (SURFACE-IGM- ASSOCIATED PROTEIN) (MEMBRANE-BOUND IMMUNOGLOBULIN ASSOCIATED PROTEIN) (CD79A) - HOMO SAPIENS (HUMAN), 226 aa. cds:SWISSPROT- ID:P11912 B-CELL ANTIGEN RECEPTOR COMPLEX ASSOCIATED PROTEIN ALPHA-CHAIN PRECURSOR (IG-ALPHA) (MB-1 MEMBRANE GLYCOPROTEIN) (SURFACE-IGM- ASSOCIATED PROTEIN) (MEMBRANE- BOUND IMMUNOGLOBULIN ASSOCIATED PROTEIN) (CD79A) - HOMO SAPIENS (HUMAN), 226 aa.	2.30E-125	19 (19q13.2)
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1645	cg43301424	1228	TGCCCTTCCCAG GCTCCCTCACC C[C/gap]AGCGGG TAATGAGCCCTT AATCGCT	gap			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P11912 B-CELL ANTIGEN RECEPTOR COMPLEX ASSOCIATED PROTEIN ALPHA-CHAIN PRECURSOR (IG-ALPHA) (MB-1 MEMBRANE GLYCOPROTEIN) (SURFACE-IGM- ASSOCIATED PROTEIN) (MEMBRANE-BOUND IMMUNOGLOBULIN ASSOCIATED PROTEIN) (CD79A) - HOMO SAPIENS (HUMAN), 226 aa. Jcds:SWISSPROT- ID:P11912 B-CELL ANTIGEN RECEPTOR COMPLEX ASSOCIATED PROTEIN ALPHA-CHAIN PRECURSOR (IG-ALPHA) (MB-1 MEMBRANE GLYCOPROTEIN) (SURFACE-IGM- ASSOCIATED PROTEIN) (MEMBRANE- BOUND IMMUNOGLOBULIN ASSOCIATED PROTEIN) (CD79A) - HOMO SAPIENS (HUMAN), 226 aa.	2.30E-125	19 (19q13.2)
1646	cg42852276	1537	AAAGGCATTATT CTCCAGCCTTAA G[gap]/TATCTTA GGACGTTTCCTT TGCTATG	gap	T		SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P26718 NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 216 aa. Jcds:SWISSPROT-ID:P26718 NKG2- D TYPE II INTEGRAL MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 216 aa.	5.70E-122	12
1647	cg43068999	874	TGGATACTAGAT CTTACATCTGCA G[C/gap]TCTTTCT TCTTTGAATTCC TATCT	gap			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P02743 SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.5S ALPHA-1- GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 223 aa.	1.60E-119	1 (1q21)

1648	cg43986150	1655	ATAAACAGTTT ATTATCTCAATCA A/C]AACATTCTCT ATATATCAAACA CTCC	A	C				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P19397 LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53) - HOMO SAPIENS (HUMAN), 219 aa.	2.60E-117	1 (1p21)
1649	cg43986150	206	CTCGGCCACCTC AAGGATAATCAC T[G/A]AATTCTGC CGAAAGGACTGA GGAAC	G	A				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P19397 LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53) - HOMO SAPIENS (HUMAN), 219 aa.	2.60E-117	1 (1p21)
1650	cg44018623	203	TATTTTATAATAG TATTACAGGAAG[C/A]AAAAATATCAT TTAATACAACCTT GAG	C	A				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	1.90E-114	6
1651	cg43051796	1421	TGGCCAGAGAGT CCTTGTAATTGT C[C/T]CCAATTCA ATCAGTATTTTG GGGCT	C	T				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.]pcis:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL- TMP - HOMO SAPIENS (HUMAN), 202 aa.	4.00E-114	3
1652	cg43051796	259	ACAACAAATAAC AATACTTAGGAT A[C/A]ATCAATCA TTCTTTTCTCTCT TAAA	C	A				SILENT- NONCODI NG	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.]pcis:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL- TMP - HOMO SAPIENS (HUMAN), 202 aa.	4.00E-114	3

1653	cg43051798	286	TCAATCATCTTT TTCCTCTTAAAI ATJCAGAAATTG GTCTTAGTTTCT CATT	A	T				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.lpcds:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL- TMP - HOMO SAPIENS (HUMAN), 202 aa.	4.00E-114	3
1654	cg43287997	1244	CCCTCCCTTTCT TGCATGTAAGTT G[gap/G]TCCCCC ATCCCAAAGTAT TCCATCT	gap	G				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.lpcds:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1655	cg43287997	1430	ACCCCTAATCC CCTACTCCCTCC A[gap/A]CCCCC CTCCACTGTAGG CCACTGG	gap	A				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.lpcds:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)

1656	cg43287997	1440	CCCCCTACTCCCTC CCACCCCCCCTC Cigap/CJACTGTA GGCCACTGGAT GGTCATTT	gap	C				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.jpds:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1657	cg43287997	1466	CTGTAGGCCACT GGATGGTCATTT Gigap/GJCATCTC CGTAAATGTGCT CTGCTCC	gap	G				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.jpds:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1658	cg43287997	1477	CTGGATGGTCAT A TTGCATCTCCGT A/A/TATGTGCTC TGCTCCTCAGCT GAGAG	A	T				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.jpds:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)

1659	cg43287997	1487	TTTGCATCTCCG TAAATGTGCTCT G[gap/G]CTCCTC AGCTGAGAGAGA AAAAAAT	gap	G				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.[pcds:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1660	cg43287997	903	GCCTGAATCAGA GACGCATCTGAC C[C/gap]TCTGGA GAACACTGCCTC CCGCTGG	C	gap				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.[pcds:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)
1661	cg43287997	906	GAATCAGAGACG CATCTGACCCCTC T[gap/T]GGAGAA CACTGCCTCCCG CTGGCCCC	gap	T				SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.[pcds:SWISSPROT- ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)

1662	cg43924574	155	GGCTTGGAAGA GAGATCCAAAGG CC[A/G]GCCTGG CAAGGGGAATCC CACATGA	A	G			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP- 39) (39 KD SYNOVIAL PROTEIN) (YKL- 40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa. pcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	1.00E-106	1
1663	cg41598396	225	CAAAGCTGGGAC TGGAGGGCTTT A[G/gap]CGACTC AATCCAGGTGC AGCATTT	G	gap			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP- 39) (39 KD SYNOVIAL PROTEIN) (YKL- 40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa. pcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	4.50E-106	1
1664	cg43917157	1386	GGTGAAACTGTC ACAATCCGTGTC C[C/A]TTTATAT ATAACTATACTG AGGTA	C	A			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.40E-102	6
1665	cg43917157	1545	CACGCAATCTGC TTGGGACAAAA G[C/T]CTACAGG GGTGCCCAAGCA CGAAAG	C	T			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.40E-102	6

1666	cg43917157	1650	GGAACCTCCATAA AAGAATGAGGCA G/C/T/T/T/C/ACTG GGGAGAACTGG TCTTCA	C	T			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.40E-102	6
1667	cg43917157	21	TTTTTTTTTTTT TTTTTTTT/G/TTA ATTTCTGCCTT TATTGTTAT	T	G			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.40E-102	6
1668	cg43917157	222	TTTTTACATGAA AGCATAAATACG G/A/CAGGTACAA ATTTCTTGAG TTCC	G	A			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1669	cg43917157	3218	GGGAAGCAGAG CCTAAGCTGACC CC[G/A]GCCACT GGCTGGTGGG ACCACATC	G	A			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1670	cg43917157	3305	AGAGACAGGGA CATGAAGTTGTG GC[G/A]TCTCTG GCACGCAAGTGT CCTGGGA	G	A			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1671	cg43917157	3322	GTTGTGGCGTCT CTGGCAGGCAA GT[G/gap]TCCTG GGACAGAGCAAT GGAAACCT	G	gap			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6

1672	cg43917157	4330	TGCCTGCCACTA CACCTAATTTT [T/gap]GTATTTT AGTAGAGATGGG GTTTC	T	gap			SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1673	cg43917157	776	TGGCTATTCTT GTGTAAGGGATG A[C/T]GACTCCCC CTCCCATGGGTC CCATT	C	T			SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4.4E-102	6
1674	cg43255952	160	AACGGGCTGAG AAGGCCCGTCA GGG[gap/G]CCCA GGTCCACACAGA GAGGCCTGGG	gap	G			SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa. pcds:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.	2.6E-101	1 (1p36.1)
1675	cg43255952	226	GAGGGGCAGAC TGGGCAGTGGG GAG[C/gap]CCCC ATCGTGCCCCCAG AGGTGGCCA	C	gap			SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa. pcds:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.	2.6E-101	1 (1p36.1)

1676	cg43255852	373	AAAAAGCACCAG GTCAGGCAGGG CC[C]gap[GAGGG CCCCAGATCCCA GGAGGGCC	C	gap			SILENT- NONCODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa. pcds:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.	2.6E-101	1 (1p36.1)
1677	cg43084350	507	ACCAAAATACC CCTCTCTCCCA C[AT]CCTCTTCT CCGACCCCTCG GGAGGC	A	T			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P21754 ZONA PELLUCIDA SPERM- BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	5.4E-95	7
1678	cg43084350	715	CAGGATGGTGTG TAGCCCAAGTGAC T[C/G]TGAGGATC GCCCTCCTGAC AGAAG	C	G			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P21754 ZONA PELLUCIDA SPERM- BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	5.4E-95	7
1679	cg38834323	24	CAGGGAAGCTC CAGCTGTCCCTC [G/C]CGCAGTTG GCCCTGTGGTGT TCCGA	G	C			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P38159 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HNRNP G) (GLYCOPROTEIN P43) - HOMO SAPIENS (HUMAN), 437 aa.	6.4E-91	
1680	cg43054805	341	ATCCAATGATCA GCGTGAGATGAT C[AT]TTGATTAA ACTTGCTTGAGA TGGCT	A	T			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P55261 CARBOXYPEPTIDASE B PRECURSOR (EC 3.4.17.2) (47 KD ZYMOGEN GRANULE MEMBRANE ASSOCIATED PROTEIN) (ZAP47) - CANIS FAMILIARIS (DOG), 416 aa.	2.6E-85 (13q14.1 1)	13

1681	cg43054905	382	TGAGATGGCTAG TCAAACGTCGAA A[G/C]TTGCTTGA GATGGCTAGTCA AACGT	G	C			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P55261 CARBOXYPEPTIDASE B PRECURSOR (EC 3.4.17.2) (47 KD ZYMOGEN GRANULE MEMBRANE ASSOCIATED PROTEIN) (ZAP47) - CANIS FAMILIARIS (DOG), 416 aa.	2.6E-85	13 (13q14.1 1)
1682	cg43054905	454	TAAC TAGACTTTT ACAA TTTTTTTT ap/TJAAAGGGTAA AAAGACATGAAC CCTA	gap	T			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P55261 CARBOXYPEPTIDASE B PRECURSOR (EC 3.4.17.2) (47 KD ZYMOGEN GRANULE MEMBRANE ASSOCIATED PROTEIN) (ZAP47) - CANIS FAMILIARIS (DOG), 416 aa.	2.6E-85	13 (13q14.1 1)
1683	cg43949899	236	TCCCA TTTTATT TTTTTTTTTTTTT TJAGTATTCAATG AATGGAATTTAA TG	G	T			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P20172 CLATHRIN COAT ASSEMBLY PROTEIN AP50 (CLATHRIN COAT ASSOCIATED PROTEIN AP50) (PLASMA MEMBRANE ADAPTOR AP-2 50 KD PROTEIN) (HA2 50 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 MEDIUM CHAIN) (KIAA0109) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS, 435 aa.	1.1E-84	19
1684	cg44021513	202	GTCCGCTGGGC AGTTATAGGTCC CAJATJGTGTGG GTCTTCCTGCGA GGCCTT	A	T			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P20963 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa.	8E-84	1 (1q22)
1685	cg44021513	209	GGGCAGTTATAG GTCCCAAGTGT G[G/C]GTCCTCCT GCGAGGCCCTTCA CAAAG	G	C			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P20963 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa.	8E-84	1 (1q22)

1686	cg44021513	319	ACTTTATTACACA CTGTGTAACAC A[gap/C]TGTTTT TATGCCACTTTG TGCACA	gap	C				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P20863 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa.	8E-84	1 (1q22)
1687	cg44019290	969	GTGCCCTCACAT CTGGGGTCTTCA G[G/gap]CACACG CCATGCCCTGCCG AGGAGTG	G	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11
1688	cg44019280	1029	CAGACCATGTCC GTGCTAGGCCCA G[G/gap]CACAGC CCAACCACTCCT CATCCAA	G	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11
1689	cg44019290	1380	CTTCTCCTCAAG GTTTGAGGGATT G[C/G]GGGGAGG GGGTCAGCTGA CTCAGAG	C	G				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11
1690	cg44019290	411	TCCTGGGTCTCA CTCCATGGCTTG C[C/gap]TCAGGC CCCGCAGAAATC CCTGAGA	C	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11
1691	cg44019290	773	TACCTCCTTCTC CAACCTCCACT A[G/gap]CGCTGC TTTCCTGGTCAA ACCTGCA	G	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.5E-80	11

1692	cg42876034	122	CTGGGGCAGCA CCACCTGAAGGC AGTCGACTGC CTTTTAAAGA CAGGGT	T	C			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:Q07066 22 KD PEROXISOMAL MEMBRANE PROTEIN - RATTUS NORVEGICUS (RAT), 193 aa.	2.6E-78	
1693	cg41672027	1002	GCATCATTTAATT GCGACATACCAG [G/T]GGAAATTGT ATGTATGTTAGT GACA	G	T			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:Q03401 SPERM-COATING GLYCOPROTEIN 1 PRECURSOR (SCP 1) (ACIDIC EPIDIDYMAL GLYCOPROTEIN 1) (CYSTEINE-RICH SECRETORY PROTEIN-1) (CRISP-1) - MUS MUSCULUS (MOUSE), 244 aa.	3E-77	6 (6p21)
1694	cg43919735	302	AATTCTCACTCT ATCCAAAGCCCC G[G/gap]ATGAGG TCACTGCTTTTAT GAGCCT	G	gap			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P08962 CD63 ANTIGEN (MELANOMA-ASSOCIATED ANTIGEN ME491) (LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 3) (LAMP 3) (OCULAR MELANOMA-ASSOCIATED ANTIGEN) (OMA81H) (GRANULOPHYSIN) - HOMO SAPIENS (HUMAN), 237 aa. pcds:SWISSPROT- ID:P08962 CD63 ANTIGEN (MELANOMA-ASSOCIATED ANTIGEN ME491) (LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 3) (LAMP 3) (OCULAR MELANOMA-ASSOCIATED ANTIGEN) (OMA81H) - HOMO SAPIENS (HUMAN), 237 aa.	2.2E-76	11 (11q12)

1695	cg43981337	1111	GATTGAATCAGC CCACTGCGAGCA C[G/A]GATCTTGA TTGAATCAGCCT ATTGG	A				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) -HOMO SAPIENS (HUMAN), 244 aa.lpcis:SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T- CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.9E-75	X
1696	cg43981337	1146	TGAATCAGCCTA TTGGTGAGTTT T[A/G]GGTCTACA TACATCTTGATT GAATC	G				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) -HOMO SAPIENS (HUMAN), 244 aa.lpcis:SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T- CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.90E-75	X

1697	cg43981337	1256	GCAACTTCTCTAA TTCACAGGGGG GAC[<i>gap</i>]CCTAA ATGTCCTTAAAG GTAGAGAG	C	gap			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.[<i>pcis</i> :SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T- CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.90E-75	X
1698	cg43981337	1258	AACTTTCTAATTC ACAGGGGGGAC C[C/ <i>gap</i>]TAAATG TCCCTTAAAGGTA GAGAGGA	C	gap			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.[<i>pcis</i> :SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T- CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.90E-75	X

1699	cg43981337	567	CTCAATTGGAG GCAAAGAAATGT A[A/G]GTTGTGTG CTGAAACCTGAT GTATC	A	G				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) -HOMO SAPIENS (HUMAN), 244 aa.[pcis:SWISSPROT-ID:P41732 CELL SURFACE GLYCOPROTEIN A15 (T- CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1) - HOMO SAPIENS (HUMAN), 244 aa.	1.90E-75	X
1700	cg43983795	1810	CGCCGCTCTCCA GATCGCTTGGGT C[G/gap]CGCCAG TCGCCACCCACAT CCTCGGC	G	gap				SILENT- NONCODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q95250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa.	1.20E-74	X
1701	cg43983795	1810	GCCGCTCTCCAG ATCGCTTGGTC G[gap]GCGCCAG TCGCCACCCACAT CCTCGGC	gap	G				SILENT- NONCODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q95250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa.	1.20E-74	X
1702	cg43983795	45	TTTTTTTTTTT TTTTTTTTTTT TTGTGGGTAAAA CCATTTTATTAA CT	A	T				SILENT- NONCODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q95250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa.	1.20E-74	X

1703	cg41602760	1820	GCCCACTGAGAA GAGCTTCCAGGA C[G/gap]CACCCA GGACGCTGAGC CCAGGAGC	G	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	3.40E-73	15 (15q26.1)
1704	cg41568631	143	GATGTGGGCCG TTGGGGTGGCAA CC[C/gap]CTTGC AGCCCCCTACCA CGCCATCT	C	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
1705	cg41568631	144	ATGTGGGCCGT GGGTGGGCAAC CC[C/gap]TTGCA GCCCCCTACCA GCCATCTC	C	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
1706	cg41568631	70	TCCATCTCAGCC CCAGGACTCAGT A[C/T]TGCGGTTG CCAACACTGCTG CCAGG	C	T				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
1707	cg41568631	71	CCATCTCAGCCC CAGGACTCAGTA C[T/C]GCGGTTG CCAACACTGCTG CCAGGC	T	C				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
1708	cg43918233	1667	TTATGCTGGTGG CTTCCATCCGTT C[C/gap]TCCTCT GAGGGTGAGTG GAGAGGTA	C	gap				SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.60E-67	2

1709	cg43918233	1675	GTGGCTTCATC CGTTCTCCTCT G[A/gap]GGGTGA GTGGAGAGGTAT ATGGAAA	A	gap				SILENT- NONCODING NG	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.60E-67	2
1710	cg43918233	1688	GTTCTCCTCTCTG AGGGTGAGTGG AG[A/G]GGTATAT GGAAACACGGCT GTGACC	A	G				SILENT- NONCODING NG	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.60E-67	2
1711	cg43918233	1708	TGGAGAGGTATA TGGAAACACGGC T[G/A]TGACCAAA GGGAGATCCCA GCCTGG	G	A				SILENT- NONCODING NG	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1712	cg43918233	1738	CAAAGGGAGATC CCAGCCTGGGC AG[G/C]CTGCGC TGCTGACCAACC TCCCTGG	G	C				SILENT- NONCODING NG	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1713	cg43918233	1988	TCTTCAAAGACT TCAGCAGCAAAAC C[A/T]AAACAGCA GGTTAAAAAAA AGATG	A	T				SILENT- NONCODING NG	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1714	cg43918233	319	GAAGACACCCCC AACAAGTCGGGT G[C/G]GGAGGCA AAGACCCCAAAA GACAGC	C	G				SILENT- NONCODING NG	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.8E-67	2

1715	cg43918233	334	AAGTCGGGTGC GGAGGCCAAAGA CCCA/TJAAAAGA CAGCTCCAACAA GTCGGGT	A	T			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1716	cg43918233	369	CTCCAACAAGTC GGGTGCGGAGG CA/A/CJAGACCCA AAAAGGCAGCAC TAGCAA	A	C			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1717	cg43918233	377	AGTCGGGTGCG GAGGCCAAAGAC CCA/A/CJAAAGG CAGCACTAGCAA GTCGGGT	A	C			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
1718	cg43927045	1406	TAAAAAACGCGG CTGTGGAGACAG G/T/AJGAGCTGCT GGGAAGCCATGT TTTTG	T	A			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.7E-66	13
1719	cg43927045	1420	GTGGAGACAGG TGAGCTGCTGG GAA[G/gap]CCAT GTTTTTGATTTTC AGACAGGT	G	gap			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.7E-66	13
1720	cg43927045	1556	ATCAATACACAA GAGACTCTTTGT G[G/A]CTCAACAC GTGGGTGCGG AGGCAG	G	A			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.7E-66	13
1721	cg43927045	2176	GAAGTGGCGG CACGATGATGGA CT[G/gap]CCGCT GGCCCCGGAGG GTCAGGCAG	G	gap			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.7E-66	13

1722	cg43927045	2184	GGCCACGATGATC GGACTGCCGCT GG[C/gap]CCCCG AGGTCAGGCA GTGGGGCAC	C	gap			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13
1723	cg43927045	2203	CGCTGGCCCCCG GAGGTCAGGC AGT[G/gap]GGGC ACCCCCCACTCG TCCTCGCTC	G	gap			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13
1724	cg43927045	234	TTTGCAAGTTGC TGTTTGTTTCCA G[C/G]TACACCA GTCAGAGCTCCA CAGAGA	C	G			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13
1725	cg43927045	448	ACGTTTCCCGAG TAGGGGCCAAA GC[C/gap]ACTGG AAACCGTGTTCC CTGTGCAG	C	gap			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13
1726	cg43927045	520	CCTGGGGGGAA TGAGTATAAAA GG[G/T]AAATGTT TTTGAAGACAGG CACGAT	G	T			SILENT- NONCODI NG	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	6.70E-66	13

1727	cg44014928	1879	GAGTGGAGCTTT AAGTAAATATGC C[A/gap]AAAAAA ATATTCTTAGCA CAAAAGC	gap			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.lpcis:SWISSPROT-ID:Q10567 BETA- ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.	1.00E-63	5
1728	cg44014928	1886	GCTTTAAGTAAA TATGCCAAAAAA A[A/gap]TATTCTT AGCACAAAAGCC TGCACC	gap			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.lpcis:SWISSPROT-ID:Q10567 BETA- ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.	1.00E-63	5

1729	cg44014928	2113	GAAAAGCAAAGC AAGAGAAATTCTG CT/CJAAAGAGTT TTATTCTGAATCT GAGG	C			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa. lpcis:SWISSPROT-ID:Q10567 BETA- ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.	1.00E-63	5
1730	cg44024345	797	AGCTTTACTGCC TTCCTCCTTATC CT/CJACAGTACA ATCAGCAGTCTA GTTCT	C			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P01215 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 116 aa. lpcis:SWISSPROT- ID:P01215 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 116 aa.	7.70E-63	6
1731	cg44024345	848	TTTCATTGGAAT GAATACAGCATT T/AAGCTTGTTT CACTGCAAATAA AGCC	A			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P01215 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 116 aa. lpcis:SWISSPROT- ID:P01215 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 116 aa.	7.7E-63	6
1732	cg43965368	773	CACCTAACTAAAG AGATAAATCTT C/gap/CJACTTTA CTTCCTAGTATT GCATCCC	C	gap		SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - MUS MUSCULUS (MOUSE), 690 aa.	8.9E-61	6 (6p25)

1733	cg43965366	828	AGGGTTAAAGTA AGGATATTGGC TTC/TCTGCTGAT CAGGCCACAGT GTGACA	C	T			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - MUS MUSCULUS (MOUSE), 690 aa.	8.9E-61	6 (6p25)
1734	cg43279524	926	CTCCCCGCCCC CGTGTGAGACA GGT/GTCTCAAG GCTCAGGGGAA GATGCAT	T	G			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSNEW- ID:P17426 ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT) MUS MUSCULUS (MOUSE), 977 aa. pcis: SWISSPROT-ID: P17426 ALPHA ADAPTIN (A) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT) - MUS MUSCULUS (MOUSE), 977 aa.	2.8E-60	14
1735	cg43252235	1172	TTAAAGGATGGG GTCTTGCTATAT T[gap/A]GCCCCAG GCTGGAGTGCA GTGGCTAT	gap	A			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P23231 MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70) - NEUROSPORA CRASSA, 619 aa.	5.8E-60	

1736	cg43252235	1172	TTAAAGGATGGG GTCTTGCTATAT T[<i>gap</i>]/AJGCCCAG GCTGGAGTGCA GTGGCTAT	gap	A			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P23231 MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70) - NEUROSPORA CRASSA, 619 aa.	5.80E-60	
1737	cg43252235	68	TTTTTTGAATGTA ATATTTATTGG[T/G]GAATTACAT GTGAGGTCATTT ACA	T	G			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P23231 MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70) - NEUROSPORA CRASSA, 619 aa.	5.80E-60	
1738	cg43252235	848	AGACCTGGACCT GGGTAGTTAGTC C[C]/T]TAGAGATG AAGGTGAGCTCA CTACA	C	T			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P23231 MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70) - NEUROSPORA CRASSA, 619 aa.	5.80E-60	
1739	cg44965847	200	CAGTAGGCTCCC CCAGGCTGAGC CC[C]/ <i>gap</i>]/AGCC[C TAACACTGATGC TTGGCAGC	C	gap			SILENT- NONCODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q27127 P-GLYCOPROTEIN - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 302 aa (fragment).	2.60E-58	

1740	cg43322513	1069	GCTGTCCGATGG CGTGAACACAA G[G/C]CCCCCA CACGGAACATGT GCAGCC	G	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1741	cg43322513	11318	TTCTGCAAGTA AGCAGGGAACAT G[T/C]CCTCCAGT TTGCTCTTCTTG CGCCC	T	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1742	cg43322513	11333	AGGGAACATGCT CTCCAGTTTGCT CT[C/T]CTTGCGC CCTCGCCGCTGT TGCTT	T	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1743	cg43322513	11379	TGCTTCTTCTTCT CATCCCTTCAGT G[C]CAAGCTCTG CTCCACGGCGC CCTCT	T	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1744	cg43322513	1268	CATGCACCTTGGC ACGGATGGCACA A[G/C]CAAAATGG TAGACATTGGGG CAACG	G	C				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
1745	cg43322513	1390	GGGCAACCTCCA CATTATCAGTG C[C/T]CCGCCCT GGGTCTCATACA CCTCCG	C	T				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.3E-54	12

1746	cg43322513	8482	AGCTGCCTGGA GGCCCCACTGCT CC[T]CIGCAGCT GCTGCAGCTGTT TCCTTCT	T	C			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.3E-54	12
1747	cg43982558	1399	CAACTGAATGTG CCCTTAGAGCGC AT[C]CAGTTTAA AAGTCATTAAAGA ACATG	T	C			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.1E-53	5 (5q13)
1748	cg43982558	1400	AACTGAATGTG CCCTTAGAGCGCA TTC/TAGTTTAA AGTCATTAAAGAA CATGT	C	T			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.1E-53	5 (5q13)
1749	cg43982558	1443	GAACATGTGAAA GGTGTTTTTTTT [T/gap]CCAATAT GAACATCATGCAA GTTACC	T	gap			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)
1750	cg43982558	1653	AGCTGTATCATC CCAACAAAAGTAT C[C/T]TTTCATGA ACGGGGCATGC AATAGC	C	T			SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)

1751	cg43982558	218	CTTAAGGTGAGG AGAAAGAGCGCT A[G/C]CTTCACATT GATCTCCAGCTT CCAAC	G				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)
1752	cg43982558	219	TTAAGGTGAGGA GAAAGAGCGCTA G[C/G]TTCACATTG ATCTCCAGCTTC CAACT	G				SILENT- NONCODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)
1753	cg43937369	378	GGCCAAGAAGG GCTCTAACAGCA GT[A/G]TCCAG CAGTGTGTTTCC AGATTGA	A	G			SILENT- NONCODING	Guanylyl	Human Gene SWISSNEW-ID:Q02153 GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN) (BETA-3 CHAIN) - HOMO SAPIENS (HUMAN), 619 aa.[pds:SWISSPROT-ID:Q02153 GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN) (BETA-3 CHAIN) - HOMO SAPIENS (HUMAN), 619 aa.	0.00E+00	4
1754	cg43937369	424	ATTATTCTTGGG TGTGGTTGGAGC [G/T]CCCCAACATT TAGCCTGAACCTA ATGT	G	T			SILENT- NONCODING	Guanylyl	Human Gene SWISSNEW-ID:Q02153 GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN) (BETA-3 CHAIN) - HOMO SAPIENS (HUMAN), 619 aa.[pds:SWISSPROT-ID:Q02153 GUANYLATE CYCLASE SOLUBLE, BETA-1 CHAIN (EC 4.6.1.2) (70 KD CHAIN) (BETA-3 CHAIN) - HOMO SAPIENS (HUMAN), 619 aa.	0.00E+00	4

1755	cg42716105	484	GAGTCCTTATAC CTCATTTAGGTT T[<u>gap</u>]/A/AAAATAG GTGCTCTCCTTG TCTGTG	gap	A				SILENT- NONCODI NG	Guanylyl	Human Gene SWISSPROT-ID:P25092 HEAT-STABLE ENTEROTOXIN RECEPTOR PRECURSOR (GC-C) (INTESTINAL GUANYLATE CYCLASE) (EC 4.6.1.2) (STA RECEPTOR) - HOMO SAPIENS (HUMAN), 1073 aa.	0.00E+00	12
1756	cg43089304	129	TCTAGCATTAGT ACATAGTAGGCG C[<u>gap</u>]/CTCAGTA AATGCTTGTTGA AGGAGG	gap	C				SILENT- NONCODI NG	Guanylyl	Human Gene Homologous to SWISSPROT-ID:P43080 GUANYLATE CYCLASE ACTIVATING PROTEIN 1 (GCAP 1) - HOMO SAPIENS (HUMAN), 200 aa.	8.40E-105	6
1757	cg42905276	2266	AAGGAAGCCCC CCACTTTTTTTTT T[<u>gap</u>]/TCTGCCT GAGATTCTTTAA GGAGATA	gap	T				SILENT- NONCODI NG	Guanylyl	Human Gene Similar to SWISSPROT- ID:P16066 ATRIAL NATRIURETIC PEPTIDE RECEPTOR A PRECURSOR (ANP-A) (ANPRA) (GC-A) (GUANYLATE CYCLASE) (EC 4.6.1.2) - HOMO SAPIENS (HUMAN), 1061 aa.	1.20E-51	
1758	cg44913214	2375	GATTCGGACTAG TTTTCTGTTCT G[<u>gap</u>]/CTTTTTT TTTTTATTAAAT TTGCA	T	gap				SILENT- NONCODI NG	helicase	Human Gene TREMBLNEW- ID:G2801555 PUTATIVE ATP- DEPENDENT MITOCHONDRIAL RNA HELICASE - HOMO SAPIENS (HUMAN), 786 aa.	0.00E+00	10
1759	cg44913214	2387	TTTTCTGTTCT GTCTTTTTTTTT T[<u>gap</u>]/ATTTAATTT TGCAAAATAAAAA TTTA	T	gap				SILENT- NONCODI NG	helicase	Human Gene TREMBLNEW- ID:G2801555 PUTATIVE ATP- DEPENDENT MITOCHONDRIAL RNA HELICASE - HOMO SAPIENS (HUMAN), 786 aa.	0.00E+00	10
1760	cg43956596	4029	AGGATGGCAGC AGGTATTGGGTC CT[G/C]AGCCTTC TGGCGGGAGCC CTGAGGC	G	C				SILENT- NONCODI NG	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa. [pcis:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0.00E+00	16

1761	cg43956596	4158	CTCTCTGGCAGAT GGAGGTGGAGT TCT/CJTCCATGC AGGAGCACGGC ATGGCGG	C			SILENT- NONCODI NG	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.lpcis:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0.00E+00	16
1762	cg43931763	105	TTGAGCTGTGGG GAGGTTCCAGCA GTT/CJAGCTACAG TGACGACTAAGA CTCCA	C			SILENT- NONCODI NG	helicase	Human Gene TREMBLNEW- ID:G2306766 ZINC FINGER HELICASE - HOMO SAPIENS (HUMAN), 2492 aa.	0.00E+00	X
1763	cg43937443	306	TCAACAAACAAA CTACACGTCTTT TTATTTTCGGTGT AATACITTTATTTT CTAT	T			SILENT- NONCODI NG	helicase	Human Gene SWISSNEW-ID:Q08211 ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) - HOMO SAPIENS (HUMAN), 1270 aa.lpcis:SPTREMBL-ID:Q99556 NUCLEAR DNA HELICASE II - HOMO SAPIENS (HUMAN), 1270 aa (fragment).	1.90E-189	1
1764	cg43937443	399	AAATCTTTACTC CTTAAAGAAAAA A[gap]/AJTACAAA CTGTGGTATTTT TAAGAGA	A	gap		SILENT- NONCODI NG	helicase	Human Gene SWISSNEW-ID:Q08211 ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) - HOMO SAPIENS (HUMAN), 1270 aa.lpcis:SPTREMBL-ID:Q99556 NUCLEAR DNA HELICASE II - HOMO SAPIENS (HUMAN), 1270 aa (fragment).	1.90E-189	1
1765	cg43924685	497	CTTTTATACCCA CCCCAACAGTCT A[A/G]CTCTAAAG AGGATAAAGCCA ATGAC	G	A		SILENT- NONCODI NG	helicase	Human Gene Homologous to SWISSPROT-ID:Q12099 PROBABLE ATP-DEPENDENT RNA HELICASE FAL1 - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 399 aa.	9.40E-121	3 (18p11.2)

1766	cg43329991	20	TGCGGCCGCCG TGCTGCCG[C/ga p]GCACTCTGGG CTGCTCTGGGC GCTG	C	gap			SILENT- NONCODI NG	helicase	Human Gene Homologous to SWISSPROT-ID:Q14147 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0134 - HOMO SAPIENS (HUMAN), 576 aa.	6.10E-102	19
1767	cg43958815	437	ATTCTGTTGTCA AGGGGCAAGAT GC[C/gap]AGCTT GGAAGTGCCAA GGAGCTAAA	C	gap			SILENT- NONCODI NG	helicase	Human Gene Similar to SWISSPROT- ID:Q06218 PROBABLE ATP- DEPENDENT RNA HELICASE DBP9 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 594 aa.	3.90E-100	
1768	cg43869985	1608	TACTAAATAAAA CCCATCAGTTT TT[G/j]TTATGTA GAAAAGCAATT ATTCC	T	G			SILENT- NONCODI NG	histone	Human Gene SWISSNEW-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) (RETINOBLASTOMA- BINDING PROTEIN 7) - HOMO SAPIENS (HUMAN), 425 aa.lpcds:SWISSPROT-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) - HOMO SAPIENS (HUMAN), 425 aa.	2.90E-214	
1769	cg43969985	1607	ACTAAATAAAC CCATCAGTTTTT TT[G/j]TTATGTA AAAGCAATTTATT CCA	T	G			SILENT- NONCODI NG	histone	Human Gene SWISSNEW-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) (RETINOBLASTOMA- BINDING PROTEIN 7) - HOMO SAPIENS (HUMAN), 425 aa.lpcds:SWISSPROT-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) - HOMO SAPIENS (HUMAN), 425 aa.	2.90E-214	

1770	cg43969995	1903	CCAAGTTAAAAA AAAAAAAAAAAA A[A]gap]CCAACA ACAAAAA ACACCAT	gap		SILENT- NONCODI NG	histone	Human Gene SWISSNEW-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) (RETINOBLASTOMA- BINDING PROTEIN 7) - HOMO SAPIENS (HUMAN), 425 aa.lpcis:SWISSPROT-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) - HOMO SAPIENS (HUMAN), 425.aa	2.9E-214	
1771	cg43969995	3855	CCATGGCGGGC AGGCGAGCCGG GGG[A]gap]ATCC TGGGGTCGAGC GTTGCGGGAG	gap		SILENT- NONCODI NG	histone	Human Gene SWISSNEW-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) (RETINOBLASTOMA- BINDING PROTEIN 7) - HOMO SAPIENS (HUMAN), 425 aa.lpcis:SWISSPROT-ID:Q16576 HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2 (RETINOBLASTOMA BINDING PROTEIN P46) - HOMO SAPIENS (HUMAN), 425.aa	2.9E-214	
1772	cg44026400	225	TTGGGTTTGA AGTAGGCGTTCC C[C]gap]TATTTCT TCTTGGGCGCC GCCTTCT	gap		SILENT- NONCODI NG	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
1773	cg43948414	725	CCCCCTCCGCA GCTACAACTACT T[A]T]TAATAAAG GACTCAAAAAGA GATCG	T		SILENT- NONCODI NG	histone	Human Gene Similar to SWISSPROT- ID:P07305 HISTONE H1' (H1.0) (H1(0)) - HOMO SAPIENS (HUMAN), 193 aa.	1.8E-95	

1774	cg43948414	726	CCCTCCCGCA GCTACAACTACT TA/TAAATAAAG GACTCAAAAAGA GATCGG	T	A			SILENT- NONCODI NG	histone	Human Gene Similar to SWISSPROT- ID:P07305 HISTONE H1' (H1.0) (H1(0)) - HOMO SAPIENS (HUMAN), 193 aa.	1.8E-95	
1775	cg43948414	729	CTCCGCGAGCTA CAACTACTTATA A/TAAAGGACT CAAAAAGAGATC GGGAG	T	A			SILENT- NONCODI NG	histone	Human Gene Similar to SWISSPROT- ID:P07305 HISTONE H1' (H1.0) (H1(0)) - HOMO SAPIENS (HUMAN), 193 aa.	1.8E-95	
1776	cg43948414	772	ATCGGAGGTTT TAAGTGGCCGCA G/C/gap]CCCACC AAACCAAGCAAA GACACCT	C	gap			SILENT- NONCODI NG	histone	Human Gene Similar to SWISSPROT- ID:P07305 HISTONE H1' (H1.0) (H1(0)) - HOMO SAPIENS (HUMAN), 193 aa.	1.8E-95	
1777	cg43250123	8190	AGCGAGCGCG CCGCGCCCTCACT GGC/TCTTGTA CGGTTTATTCTG ATTGAG	C	T			SILENT- NONCODI NG	histone	Human Gene Similar to SWISSPROT- ID:P53973 HISTONE DEACETYLASE HDA1 - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 706 aa.	2.4E-57	
1778	cg43918434	147	TAATTCAGTTAT GGTAAAAA A/A/gap]CTATGTA CATCTCAATCAG ATCACC	A	gap			SILENT- NONCODI NG	homeobo x	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21
1779	cg43918434	434	ACAGAAATCATT TTAAAAAGGGGA A/G/gap]GAGTTT TGTGTTGGAATC AATGTG	G	gap			SILENT- NONCODI NG	homeobo x	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21
1780	cg43918434	435	CAGAAATCATT TAAAAAGGGGAA G/G/gap]AGTTTT GTGTTGGAATCA ATTGTG	G	gap			SILENT- NONCODI NG	homeobo x	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21

1781	cg43918434	437	GAAATCATTTTAA AAAGGGAAGG A[G/gap]TTTTGT GTTGGAATCAAT TGTGCTA	G	gap			SILENT- NONCODING	homeobo x	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21
1782	cg43918434	454	GGGAAGGAGTTT TGTGTTGGAATC A[A/G]TTGTGCTA CCTCTGTAAAAA TGAAG	A	G			SILENT- NONCODING	homeobo x	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0	21
1783	cg43918434	592	TCTGCGGCAAG GCACCTGGTCTG CC[C/gap]TCCGG ACAGCCTTTCGC CCAGTCTT	C	gap			SILENT- NONCODING	homeobo x	Human Gene SPTREMBL-ID:Q12924 ZINC FINGER HOMEODOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 1124 aa.	0.00E+00	21
1784	cg42341753	2020	TGGAGCCTACCT CCCGACATTAC G[C/gap]TTCGCC CCACGCTGCTCC GACTGGC	C	gap			SILENT- NONCODING	homeobo x	Human Gene SWISSPROT-ID:Q14774 HOMEBOX PROTEIN HLX1 (HOMEBOX PROTEIN HB24) - HOMO SAPIENS (HUMAN), 488 aa.	5.20E-263	1
1785	cg43918574	415	TCACTCAGAGGC CAAAGTCTGGGG G[T/G]TAGAAAGA AGGAAGCTTGAC CCAAA	T	G			SILENT- NONCODING	homeobo x	Human Gene SWISSNEW-ID:Q06710 PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa. pcis:SWISSPROT- ID:Q06710 PAIRED BOX PROTEIN PAX- 8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa.	4.20E-245	2
1786	cg43918574	453	AGCTTGACCCAA ACAAAGTTTCAT TTT/GACAGTATA TACAGTCAGGCC TTGGG	T	G			SILENT- NONCODING	homeobo x	Human Gene SWISSNEW-ID:Q06710 PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa. pcis:SWISSPROT- ID:Q06710 PAIRED BOX PROTEIN PAX- 8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa.	4.20E-245	2

1787	cg43918574	459	ACCCAAACAAAG TTTCATTACAGT TAGTATACAGTC AGGCCTTGGG GCAGG	A	G				SILENT- NONCODING	homeobox	Human Gene SWISSNEW-ID:Q06710 PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa. pcis:SWISSPROT- ID:Q06710 PAIRED BOX PROTEIN PAX- 8, ISOFORMS 8A/8B - HOMO SAPIENS (HUMAN), 450 aa.	4.20E-245	2
1788	cg43988803	2504	ACAAAAA ACCCCTCTTTT T[gap]CCTTCGT CAGACTTGGCAG CAAAG	T	gap				SILENT- NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.20E-242 (13q14.1)	13
1789	cg43988803	3493	ATGTATGTATTT AAAGAAATTTCA T[gap]CTGCTTCT ACTGAACATATGC GTACT	T	gap				SILENT- NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.20E-242 (13q14.1)	13
1790	cg43988803	3502	TTTAAAGAAAT TCATCTGCTTCT A[gap]CTGAACATA TGGGTACTGCAT AGCAT	A	gap				SILENT- NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.20E-242 (13q14.1)	13
1791	cg43988803	3590	CTCATAATGTTT GTAGATACAGAA A[gap]GGGAGA TCTGCATCTAAA GCAATGG	A	gap				SILENT- NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.2E-242 (13q14.1)	13
1792	cg43988803	3597	TGTTTGTAGATA CAGAAAAGGGA GA[gap]CTGCA TCTAAAGCAATG GICCTTIG	T	gap				SILENT- NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.2E-242 (13q14.1)	13
1793	cg43988803	780	CACCGCAGCCC CCGCCGCCCGG GCC[G/C]CTGTC GCAGCACCCGC CGGTGCCCC	G	C				SILENT- NONCODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.2E-242 (13q14.1)	13

1794	cg43988803	781	ACCGCAGCCCC CGCCGCCCGGG CCG[C/G]TGTCG CAGCACCCGCC GGTGCCCCC	C	G				SILENT- NONCODI NG	homeobo	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.20E-242	13 (13q14.1)
1795	cg43986910	2486	GCCTTGAACAAA AAGTTTTTTTTT T/gap]GTTTGTTT TTGCTTTCTGAA ATTCA	T	gap				SILENT- NONCODI NG	homeobo	Human Gene TREMBLNEW- ID:G2822167 HOMEBOX PROTEIN HOX-A10 - HOMO SAPIENS (HUMAN), 415 aa.	1.40E-230	7
1796	cg44931625	1329	ACGGTAGCTAAC TTTGGGCAGGT C[G/A]TTAAATT GGTCAATTCAGA ACATT	G	A				SILENT- NONCODI NG	homeobo	Human Gene SWISSPROT-ID:P55347 HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1) - HOMO SAPIENS (HUMAN), 435 aa.	7.60E-230	21
1797	cg43027377	222	TGGCTTCTACCC AGAAAAAAGG G[A/G]AGAGAGT ATAAAGAAAGTG CCAGAT	A	G				SILENT- NONCODI NG	homeobo	Human Gene SWISSPROT-ID:P40424 PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-1 (HOMEBOX PROTEIN PBX1) (HOMEBOX PROTEIN PRL) - HOMO SAPIENS (HUMAN), 430 aa.	5.70E-225	1 (1q23)
1798	cg43983917	1208	GTGCGGATCTG GCGGCCTACACA CG[C/gap]TGCGC TAAGCTGCAACG AAAACGAC	C	gap				SILENT- NONCODI NG	homeobo	Human Gene SWISSPROT-ID:P50458 HOMEBOX PROTEIN LH-2 - HOMO SAPIENS (HUMAN), 423 aa.	4.30E-216	
1799	cg43927965	1412	TTCAAGCAGGTA ACAATACTACTG G[A/gap]AAAAAA AAATAGGAAGCT TAAATG	A	gap				SILENT- NONCODI NG	homeobo	Human Gene SPTREMBL-ID:Q62947 ZINC FINGER HOMEODOMAIN ENHANCER-BINDING PROTEIN-1 - RATTUS NORVEGICUS (RAT), 1104 aa (fragment).	1.50E-207	
1800	cg43980506	1041	GCATGGAAAAGT TTTTATCTCTTCT [G/C]TTTCCTCTC CTGTAAGTAAAG ATT	G	C				SILENT- NONCODI NG	homeobo	Human Gene TREMBLNEW- ID:G2896172 LIM HOMEBOX PROTEIN COFACTOR - HOMO SAPIENS (HUMAN), 373 aa.	1.60E-206	

1801	cg43923014	1901	TGGCAGGGGTG AGGGGTGACGG GGGAGACAAAC TTCAGCAGCTCA TGTCCEGA	A	G			SILENT- NONCODING	homeobox	Human Gene TREMBLNEW- ID:G2738116 LIM HOMEBOX PROTEIN COFACTOR CLIM-2 - MUS MUSCULUS (MOUSE), 375 aa.	1.10E-203	
1802	cg43923014	457	CTGGGGGGGCA AATCTTGGCACC TG[C/gap]CCCCA GAGAGTCCAGTT CCTCCCTG	C	gap			SILENT- NONCODING	homeobox	Human Gene TREMBLNEW- ID:G2738116 LIM HOMEBOX PROTEIN COFACTOR CLIM-2 - MUS MUSCULUS (MOUSE), 375 aa.	1.10E-203	
1803	cg42730678	692	AAGCACCAAAACA CCACAAAAGGAA A[A/gap]CAGCAA CAACAACAAATC CGCTGCC	A	gap			SILENT- NONCODING	homeobox	Human Gene SWISSPROT-ID:P28356 HOMEBOX PROTEIN HOX-D9 (HOX- 4C) (HOX-5.2) - HOMO SAPIENS (HUMAN), 342 aa.	2.60E-188	2
1804	cg43971816	518	CTCAGGGGGCA GTGGCCTGCTG CAG[C/gap]CTCT TGGCTTTTCCAC ATCTCCAC	C	gap			SILENT- NONCODING	homeobox	Human Gene TREMBLNEW- ID:G2822168 HXAB_HUMAN HOMEBOX PROTEIN HOX-A11 - HOMO SAPIENS (HUMAN), 313 aa;pcis:TREMBLNEW-ID:G2745851 HOMEBOX A11 - HOMO SAPIENS (HUMAN), 313 aa.	1.50E-169	7
1805	cg43928691	262	CAGAGGGTGGT GGCCTTTGGAAC CG[C/T]CGTGAA GTCTTCTGCCTG GAACCCG	C	T			SILENT- NONCODING	homeobox	Human Gene SWISSPROT-ID:P50222 HOMEBOX PROTEIN MOX-2 (GROWTH ARREST-SPECIFIC HOMEBOX) - HOMO SAPIENS (HUMAN), 303 aa.	2.00E-167	7
1806	cg43928699	1040	GGAGACCTTAAT TTTGACTTAACA A[A/gap]TAGTTTA TGTAAGTCTCTT AGGTTC	A	gap			SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1807	cg43928699	1075	TACTGCTCTTAG GTTGTTTGTATA A[A/gap]GTGACA TTATAGTGATTAA ATTCTT	A	gap			SILENT- NONCODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10

1808	cg43928699	1080	TCCTAGGTTGTT TTGATAAAGTGA C/gap/GIATTATA GTGATTAATTC TTCCCC	gap	G			SILENT- NONCODI NG	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1809	cg43928699	1492	ACCTGTTTGACC AAGGTGTTAAGG GIG/gap/ATAGTA CCTCCCAATTCA AGCAGAG	G gap	gap			SILENT- NONCODI NG	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1810	cg43928699	1506	GGTGTTAAGGG GATAGTACCTCC CA/A/gap/JTCAA GCAGAGAAACTG ACCTGACT	A gap	gap			SILENT- NONCODI NG	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1811	cg43928699	1511	TAAGGGGATAGT ACCTCCCAATTC A/A/gap/GCAGAG AAACTGACCTGA CTAAAGT	A gap	gap			SILENT- NONCODI NG	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1812	cg43928699	1564	ATCGCAGATGAA CTAGAAGTCACA GIG/gap/JTTAATTA AATGTAAGTAGA TTGTAG	G gap	gap			SILENT- NONCODI NG	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1813	cg43928699	1585	ACAGGTTAATTA AATGTAAGTAGA TTT/gap/GTAGATA CTGTTTATATCA AACAA	T gap	gap			SILENT- NONCODI NG	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEBOX PROTEIN PRH (HOMEBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.80E-148	10
1814	cg43971192	191	GTATTGCACAGT CTGAAAAAATAA C/A/gap/JAAAAA GGGAAGGGGAG GAAAAAA	A gap	gap			SILENT- NONCODI NG	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.90E-144	18

1815	cg43971192	210	AATAACAAAAA AGGGAAGGGA GG[A/gap]AAAAA AAATCACAATGA TATTGGGA	A	gap			SILENT- NONCODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.90E-144	18
1816	cg43971192	219	AAAAGGGAAGG GGAGGAAAAA AA[A/gap]TCACAT GATATTGGGAAC CATCTCA	A	gap			SILENT- NONCODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.90E-144	18
1817	cg43971192	50	ATACITTTATTATG TCATGAAAAA A[gap]GGCATCAA CCAAC TAGATTC ATACT	A	gap			SILENT- NONCODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.90E-144	18
1818	cg43988027	16	CTTATTTTTTTT TTT/GGCTTTT ATTGATTTATTT CTCCG	T	G			SILENT- NONCODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:P50221 HOMEBOX PROTEIN MOX-1 - HOMO SAPIENS (HUMAN), 254 aa.	5.50E-140	17
1819	cg42808326	1284	GAGCTGGAGA GAGACTGGACA GGG/GTAGTGC TGGAACCGCGG AGTTGGCT	G	T			SILENT- NONCODING	homeobo x	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.80E-136	3
1820	cg42808326	1341	AAAGCTACAACG ATGGACTCTTGC A/C/TAGAAAAA AAATCTTGTTAA CAATG	C	T			SILENT- NONCODING	homeobo x	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.80E-136	3
1821	cg42808326	1422	CAAAACGGGAGA GAAAAAGAGGAA GG[A/C]AACTTAT TTCTTAAC TGCT ATTGG	A	C			SILENT- NONCODING	homeobo x	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.80E-136	3

1822	cg42908326	2357	ATTCCCCCTTTTCT TGTTGTTCCCTTCT C/TGTGTTGGTTTC CTGAAAGTCCTAT TTGA	C	T			SILENT- NONCODING	homeobo x	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.80E-136	3
1823	cg42714160	874	GAGGAGGAAGA AAAACAGGCCGA GT[G]gap/AAGGT GCTGGAAAGGG AGGGAGGAC	G	gap			SILENT- NONCODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:P17509 HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX-2.2) (HU-2) - HOMO SAPIENS (HUMAN), 224 aa.	1.10E-123	
1824	cg43983244	2635	AGGAGAGGAAG GCCAAAAA AA[gap/A]TTGGA AAAGAGGGCGG GGGACCCCT	gap	A			SILENT- NONCODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:P43271 PAIRED MESODERM HOMEBOX PROTEIN 1 (HOMEBOX PROTEIN MHOX) (HOMEBOX PROTEIN K-2) (RHOX) - MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT), 217 aa.	2.20E-113	
1825	cg43917865	274	AGCGCGCGCGG GGAGGGTCCGC CCG[G]gap]CCAG GGCCCCGGCGG CTCGCAGAGG	G	gap			SILENT- NONCODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:P28360 HOMEBOX PROTEIN MSX-1 (HOX-7) - HOMO SAPIENS (HUMAN), 297 aa.	1.10E-111 (4p16.1)	4
1826	cg42714182	94	TATTATCATCATC ATCATCATCATC A/gap]TCATCGAA GTATTTACGTC CAGAG	A	gap			SILENT- NONCODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:P17509 HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX-2.2) (HU-2) - HOMO SAPIENS (HUMAN), 224 aa.	1.10E-108	
1827	cg43988025	1278	TTCTGAGAACTG ACTAGAGAAAGAC A[G/A]AAAAATAG CCCGATGTAGGT TTCGG	G	A			SILENT- NONCODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:P50221 HOMEBOX PROTEIN MOX-1 - HOMO SAPIENS (HUMAN), 254 aa.	1.50E-107	17
1828	cg43988025	1279	CTGAGAACTGA CTAGAGAAAGACA G[A/G]AAAAATAGC CCGATGTAGGTT TCGGT	A	G			SILENT- NONCODING	homeobo x	Human Gene Homologous to SWISSPROT-ID:P50221 HOMEBOX PROTEIN MOX-1 - HOMO SAPIENS (HUMAN), 254 aa.	1.50E-107	17

1829	cg43988025	1320	GGTTTCGGTGTC CCCATATAGGCC C[gap]C[GTCCAC ACAGGCTTGACT GGTGGA	gap	C			SILENT- NONCODING NG	homeobo x	Human Gene Homologous to SWISSPROT-ID:P50221 HOMEBOX PROTEIN MOX-1 - HOMO SAPIENS (HUMAN), 254 aa.	1.50E-107	17
1830	cg43268289	1110	TTCTTCCCTCTC TCCCTTTCTCCT CTT[C]CCCTGCTT TCTTGAAAAGGA CTGAA	T	C			SILENT- NONCODING NG	homeobo x	Human Gene Similar to SWISSPROT- ID:Q92988 HOMEBOX PROTEIN DLX- 4 (DLX-7) (DLX-8) - HOMO SAPIENS (HUMAN), 347 aa (fragment).	2.40E-90	17 (17q21.3)
1831	cg43268289	1218	TGTATGCCCTTG GCCTTGACAAAC C[C]TATTGTGA GCAAAAGCAGAA GTGGA	C	T			SILENT- NONCODING NG	homeobo x	Human Gene Similar to SWISSPROT- ID:Q92988 HOMEBOX PROTEIN DLX- 4 (DLX-7) (DLX-8) - HOMO SAPIENS (HUMAN), 347 aa (fragment).	2.40E-90	17 (17q21.3)
1832	cg43988195	2818	TTTTTTGGCTTT TAGTCCAGAAAG [A]gap[CCTCATC TCTGCACCTCTT ACTGA	A	gap			SILENT- NONCODING NG	homeobo x	Human Gene Similar to SPTREMBL- ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12
1833	cg43988195	2902	GGAATAAGAGGA TGTTGGGCACT GC[C]gap]AAGGG CAAGGTCAAAAA ICAGGGT	C	gap			SILENT- NONCODING NG	homeobo x	Human Gene Similar to SPTREMBL- ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12
1834	cg43988195	333	GAAGATGAATAC ACAGAGTCTTT GTTATTTCTCTAT CAAATGTGGTTT TTTAA	T	A			SILENT- NONCODING NG	homeobo x	Human Gene Similar to SPTREMBL- ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12
1835	cg43988195	334	AAGATGAATACA CAGAGTCTTTTG TTTATCTCTATC AAATGTGGTTT TTTAT	T	A			SILENT- NONCODING NG	homeobo x	Human Gene Similar to SPTREMBL- ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12

1836	cg43988195	744	ATGAAGAGAAAA TCCACCTAGCTC AATJGGGGCA GTGAAGATGAGG AAAGAA	A	T				SILENT- NONCODI NG	homeobo	Human Gene Similar to SPTREMBL- ID:Q23590 SIMILARITY TO VARIOUS HOMEOTIC PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.60E-53	12
1837	cg43922794	199	GGGGAAGCAGC ATTGCAGCCGG AG[gap]/GATCGC GGAGTCCCAATG AAACGGGC	gap	G				SILENT- NONCODI NG	hydrolas	Human Gene SWISSPROT-ID:Q14694 PROBABLE UBIQUITIN CARBOXYL- TERMINAL HYDROLASE (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME) (KIAA0190) - HOMO SAPIENS (HUMAN), 798 aa.	0.00E+00	14
1838	cg43298921	110	GCACAATGGCTT TATTGTCACGTG AAGJTGCGGA CCAGGCCTACAG CCCGAG	A	G				SILENT- NONCODI NG	hydrolas	Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa.	3.30E-238	15 (15q23)
1839	cg43298921	153	AGCCCGAGGGA GGACCCCAAGTCA CA[G/gap]GGTTG AAAGGGGTGCTT GAGCCCTT	G	gap				SILENT- NONCODI NG	hydrolas	Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa.	3.30E-238	15 (15q23)
1840	cg43298921	180	GTTGAAAGGGGT GCTTGAGCCCTT T[G/T]TTCCAGA AGAGCAGAGAAA ATCTC	G	T				SILENT- NONCODI NG	hydrolas	Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa.	3.30E-238	15 (15q23)

1841	cg43927025	2499	TATAATTACITTA GCTGCACTAACA [G/gap]TACAATG CTTGTTAATGGT TAATAT	G	gap			SILENT- NONCODING	hydrolase	Human Gene SWISSPROT-ID:P38571 LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR (EC 3.1.1.13) (LAL) (ACID CHOLESTERYL ESTER HYDROLASE) (STEROL ESTERASE) (LIPASE A) (CHOLESTERYL ESTERASE) - HOMO SAPIENS (HUMAN), 399 aa.	5.10E-224	10 (10q24)
1842	cg43923662	111	GATTCATCAAC ATACAAGCCAAA C[AG]AAGATCCC ATTCAATTAGAT ATAC	A	G			SILENT- NONCODING	hydrolase	Human Gene SPTREMBL-ID:Q92931 3- HYDROXYISOBUTYRYL-COENZYME A HYDROLASE - HOMO SAPIENS (HUMAN), 381 aa.	3.70E-158	
1843	cg43923662	153	TAGATATACCAC TCAAGAGAATCT C[CT]AAAGATCT TCACATTTTCCCA TCTT	C	T			SILENT- NONCODING	hydrolase	Human Gene SPTREMBL-ID:Q92931 3- HYDROXYISOBUTYRYL-COENZYME A HYDROLASE - HOMO SAPIENS (HUMAN), 381 aa.	3.70E-158	
1844	cg43923662	366	ATTCTGATAATT TCACGTCATGAAL A/TTATTAGTCTT TGATTTCTTTTCC CA	A	T			SILENT- NONCODING	hydrolase	Human Gene SPTREMBL-ID:Q92931 3- HYDROXYISOBUTYRYL-COENZYME A HYDROLASE - HOMO SAPIENS (HUMAN), 381 aa.	3.70E-158	
1845	cg43305744	955	GGAAGCTGTGGT CCGATAAAGCCT G[CG/gap]CGCAGC CTGTTTGTGGT GACAACC	G	gap			SILENT- NONCODING	hydrolase	Human Gene Similar to SWISSPROT- ID:Q81068 UBIQUITIN CARBOXYL- TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1) - MUS MUSCULUS (MOUSE), 526 aa.	1.10E-61	

1846	cg43951711	737	TATAATCAAAGG TACTATTATTGAT [C/T]ACAATTTAT TTTAAAGTCAGG AAAA	C	T				SILENT- NONCODING	hydrolase	Human Gene Similar to SWISSPROT- ID:Q92353 PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C6G9.08 (EC 3.1.2.15) (UBIQUITIN- THIOLESTERASE) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME) - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 467 aa.	5.00E-58	18
1847	cg43969804	166	CCACTTCCCTG GGGTATTGCTTT G[C/gap]CCCTGT GCCTCCACCCCG AGGAAGC	C	gap				SILENT- NONCODING	hydrolase	Human Gene Similar to SWISSPROT- ID:P09960 LEUKOTRIENE A-4 HYDROLASE (EC 3.3.2.6) (LTA-4 HYDROLASE) (LEUKOTRIENE A(4) HYDROLASE) - HOMO SAPIENS (HUMAN), 610 aa.	1.40E-54	2
1848	cg43969804	307	TTCCCCAGGGAC AACCATCCTCTC C[C/gap]TGTGTC CCCTGCCCCCA CACTGAG	C	gap				SILENT- NONCODING	hydrolase	Human Gene Similar to SWISSPROT- ID:P09960 LEUKOTRIENE A-4 HYDROLASE (EC 3.3.2.6) (LTA-4 HYDROLASE) (LEUKOTRIENE A(4) HYDROLASE) - HOMO SAPIENS (HUMAN), 610 aa.	1.40E-54	2
1849	cg43969804	53	GTTTAATGGGAC CATCACCCTGAT A[C/G]CCCATCAC AGCAGTCCCG GCTGGA	C	G				SILENT- NONCODING	hydrolase	Human Gene Similar to SWISSPROT- ID:P09960 LEUKOTRIENE A-4 HYDROLASE (EC 3.3.2.6) (LTA-4 HYDROLASE) (LEUKOTRIENE A(4) HYDROLASE) - HOMO SAPIENS (HUMAN), 610 aa.	1.40E-54	2
1850	cg43929210	169	CTAAGGAAACAG GAC TTGGGCAAA A[gap/T]TTTTTTA TTATGAAGATAC AGATCT	gap	T				SILENT- NONCODING	hydroxysteroid	Human Gene SWISSPROT-ID:P51659 ESTRADIOL 17 BETA- DEHYDROGENASE 4 (EC 1.1.1.62) (17- BETA-HSD 4) (17-BETA- HYDROXYSTEROID DEHYDROGENASE 4) - HOMO SAPIENS (HUMAN), 736 aa.	0.00E+00	5

1851	cg43928210	175	AAACAGGACTTG GGCAAAATTTT T(gap)/TATTATGA AGATACAGATCT AAGAAC	gap	T			SILENT- NONCODING NG	hydroxysteroid	Human Gene SWISSPROT-ID:P51659 ESTRADIOL 17 BETA- DEHYDROGENASE 4 (EC 1.1.1.62) (17- BETA-HSD 4) (17-BETA- HYDROXYSTEROID DEHYDROGENASE 4) - HOMO SAPIENS (HUMAN), 736 aa.	0.00E+00	5
1852	cg43998672	1777	CGGCCAAGGCC AGCGCTCCATGG CG[G/gap]CCCAG CGGCTGGGGC GGGCGGGG	G	gap			SILENT- NONCODING NG	hydroxysteroid	Human Gene SPTREMBL-ID:Q13194 11- BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220 (16q22)	16
1853	cg43998672	281	CAGTGAAGTCTT GCATGAGACTCC C[G/gap]ATCCAG CGGAGTTCTCCA AGCTGCA	C	gap			SILENT- NONCODING NG	hydroxysteroid	Human Gene SPTREMBL-ID:Q13194 11- BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220 (16q22)	16
1854	cg43998672	384	CGCAGAGGCTC ACTGGGAACCT TG[G/gap]CCTCA CCGGCCTGGA TTGGGCATC	G	gap			SILENT- NONCODING NG	hydroxysteroid	Human Gene SPTREMBL-ID:Q13194 11- BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220 (16q22)	16
1855	cg43998672	553	AGTGGCTGGGC CATAGGTGCACA TG[G/gap]CTCAC CGAGCCACTGCT GGGGAAGG	G	gap			SILENT- NONCODING NG	hydroxysteroid	Human Gene SPTREMBL-ID:Q13194 11- BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220 (16q22)	16
1856	cg42886248	195	TTAATATAACTAT CTGGTAATTATA C/TCTATGTTTAC TAACAATTTTACA AC	C	T			SILENT- NONCODING NG	hydroxysteroid	Human Gene SWISSPROT-ID:P28845 CORTICOSTEROID 11-BETA- DEHYDROGENASE, ISOZYME 1 (EC 1.1.1.146) (11-DH) (11-BETA- HYDROXYSTEROID DEHYDROGENASE 1) (11-BETA-HSD1) - HOMO SAPIENS (HUMAN), 292 aa.	8.50E-151	1

1857	cg43955809	938	TTCCCCCCCCGCT TTTTTTTTTTTTTT T/gap]TGACTTTG CCTGGAGAGGCC AGAGC	T	gap				SILENT- NONCODING	immunoglob	Human Gene Similar to SWISSPROT- ID:P01591 IMMUNOGLOBULIN J CHAIN - HOMO SAPIENS (HUMAN), 137 aa.	5.90E-72	4
1858	cg43955809	939	TCCCCCCCCGCTT TTTTTTTTTTTTTT T/gap]GACTTTGC CTTGAGAGGCCA GAGCT	T	gap				SILENT- NONCODING	immunoglob	Human Gene Similar to SWISSPROT- ID:P01591 IMMUNOGLOBULIN J CHAIN - HOMO SAPIENS (HUMAN), 137 aa.	5.90E-72	4
1859	cg43955809	697	GATGTAAACCA ACTCCCCGCCCC C/C/A/AAAAAATT AAATAGTCACA TTGGT	C	A				SILENT- NONCODING	immunoglob	Human Gene Similar to SWISSPROT- ID:P01591 IMMUNOGLOBULIN J CHAIN - HOMO SAPIENS (HUMAN), 137 aa.	5.9E-72	4
1860	cg43955809	892	AACTCAAGGAGT GAAAATCAGGAG G/G/T]GTAATAAA ATGTCCTCGCA TTCCC	G	T				SILENT- NONCODING	immunoglob	Human Gene Similar to SWISSPROT- ID:P01591 IMMUNOGLOBULIN J CHAIN - HOMO SAPIENS (HUMAN), 137 aa.	5.9E-72	4
1861	cg41382080	146	ACACAATCATTG ACTATTAGAGGC C/A/C]GAGGAGA ATGAGGCCTGG CCTGGGA	A	C				SILENT- NONCODING	immunoglob_recept	Human Gene Similar to SWISSPROT- ID:P08118 PROSTATE SECRETED SEMINAL PLASMA PROTEIN PRECURSOR (PSP-94) (BETA- MICROSEMINOPROTEIN) (SEMINAL PLASMA BETA-INHIBIN) (IMMUNOGLOBULIN BINDING FACTOR) (IGBF) (PROSTATE SECRETORY PROTEIN PSP94) (PN44) HOMO SAPIENS (HUMAN), 114 aa.	2.6E-60 (10q11.2)	10

1862	cg41382080	179	ATGAGGCCTGG CCTGGGAGCCC TGT[G/A]CCTACT AGAAGCACATTA GATTATC	G	A				SILENT- NONCODING	Immunoglobulin receptor	Human Gene Similar to SWISSPROT-ID:P08118 PROSTATE SECRETED SEMINAL PLASMA PROTEIN PRECURSOR (PSP-94) (BETA-MICROSEMINOPROTEIN) (SEMINAL PLASMA BETA-INHIBIN) (IMMUNOGLOBULIN BINDING FACTOR) (IGBF) (PROSTATE SECRETORY PROTEIN PSP94) (PN44) HOMO SAPIENS (HUMAN), 114 aa.	2.6E-60	10 (10q11.2)
1863	cg43925670	155	ATTAAAAAAGCA CTCCCAATACCC C[ga]p/CjATTCCA TAGGATTAAACAG CTAGTAT	gap	C				SILENT- NONCODING	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.[pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)]	0	1
1864	cg43925670	241	CCAGGTATATGT ACATTTTTTTAGG [C/G]ACTTAGACC TTATCTCCATAAA CAT	C	G				SILENT- NONCODING	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.[pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)]	0	1

1865	cg43925670	73	AAAGATAATGTT TATTTATTTTTC[A/T]AATTATAGAA GTTGTAGATGCA AAA	A	T			SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1
1866	cg43925670	74	AAAGATAATGTT ATTTATTTTTC[A/T]ATTATAGAAG TTGTAGATGCAA AAT	A	T			SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1
1867	cg42701070	216	AACCATGGGAAG CAGGGGGCATG GC[C/gap]ACTGG ATCTGAAAGGGA CCGGCTAA	C	gap			SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P20592 INTERFERON-REGULATED RESISTANCE GTP-BINDING PROTEIN MXB (P78-RELATED PROTEIN) - HOMO SAPIENS (HUMAN), 715 aa.	0	21
1868	cg43933380	148	TTTAAAGTCCAAT TTTGAAAAGCTT[G/C]CAGAAATTC TTCTGAAATTACT TAA	G	C			SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1,4E-261	6

1869	cg43933380	149	TTTAAGTCCAATTTC TTGAAAAGCTTG[C/G]AGAAATTTCT TCTGAAAATTACTT AAA	C	G		SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
1870	cg43933380	1521	CCGTTTCATTCTC ACATACACATTG TT[gap]ACACCC TAATGTAACAGG TAGTTTC	T	gap		SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
1871	cg43933380	200	TTACTGTATGCA TAAACTTACAAA A[gap]CIACATAT GCTATACCAAGG CAGAGAA	gap	C		SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
1872	cg43933380	228	ATATGCTATACC AAGGCAGAGAAA A[G/A]AAAAAAG TGAAAGTGGCTAC AAAGG	G	A		SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
1873	cg42489246	610	GTTGCAGTGAGC CAAGATCGTGCC A[C/T]TCCACTCC AGCCTGGGTGAT AGGTG	C	T		SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P48551 INTERFERON-ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA-REC) (TYPE I) INTERFERON RECEPTOR (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR-2) - HOMO SAPIENS (HUMAN), 515 aa.	1.7E-258 (21q22.1)	21
1874	cg43931810	552	CACACCATGAGG AGCGAGGGCTC AG[C/G]TCTCCC CAGGGCCCTGG AAATCCAT	C	G		SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:Q14653 INTERFERON REGULATORY FACTOR 3 (IRF-3) - HOMO SAPIENS (HUMAN), 427 aa.	1.2E-240	19

1875	cg43956260	210	ATGAAAGAGGGC GTATATCTCAAA AT/ATATAAAAAA AAAAAAGGATAA AAAAAT	A			SILENT- NONCODI NG	Interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14
1876	cg43956260	224	ATATCTCAAAATT AAAAAATAAAAAA A/gap]GGATAAAA AATTAGCCTTGA GTTCT	gap			SILENT- NONCODI NG	Interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14
1877	cg43956260	51	TTTTTTTTTTTT TTCCTCTTTTCAA T/A/AAAAATTTTAT TTTAAGTCCTTA GTG	A			SILENT- NONCODI NG	Interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14
1878	cg43956260	89	TAAGTCCTTAGT GAATATCTAAGA G/G/A/AAAAATATA AAGTGCTTGGCT TTAGA	A			SILENT- NONCODI NG	Interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14

1879	cg43082514	1381	TGATTGCTGTGT CCAACTCCAGTA C/gap/CJTGGAGC TTCCTCTTAACTC AGGACT	gap	C			SILENT- NONCODI NG	Interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.5E-188	4 (4q35.1)
1880	cg43082514	2153	GTTGTTATTACAT CCTTGTCGCACA T/gap/JTTTTTTTT TTAATTTTGTA GGTG	T gap	gap			SILENT- NONCODI NG	Interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1881	cg43082514	2162	ACATCCTTGTGG CACATTTTTTTTT T/gap/JTAATTTTG TAAAGGTGAAAA AAGCT	T gap	gap			SILENT- NONCODI NG	Interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1882	cg43082514	2163	CATCCTTGTGGC ACATTTTTTTTTT T/gap/JAATTTTGT AAAGGTGAAAA AGCTT	T gap	gap			SILENT- NONCODI NG	Interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1883	cg43082514	2163	ATCCTTGTGGCA CATTTTTTTTTTT gap/JAATTTTGT AAAGGTGAAAA AGCTT	gap T	T			SILENT- NONCODI NG	Interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1884	cg43082514	2201	GTGAAAAAAGCT TTTATGAGCTCA TIG/CJTAGCAATC AGATTTTCCTGT GGATT	G gap	C			SILENT- NONCODI NG	Interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
1885	cg43083653	135	CAAATGTACATA TTTACACACGTC C/gap/JTATGTGT TCACACATGACT TAATGG	gap T	T			SILENT- NONCODI NG	Interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)

1886	cg43983653	136	AAATGTACATATT TACACACGTCCTT gap/TATGTGTTT ACACATGACTTA ATGGT	gap	T				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)
1887	cg43983653	2064	GAGGTTGCCGG GTTCTTAAGGCA GC[C/gap]GGGCA CGGCCGGCGTG GACTGGGCA	C	gap				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)
1888	cg43983653	261	GGCTTGAGGG GTGGTGGGCGC CGA[G/gap]CAAG GCACTGTATAAA TAAATGCAA	G	gap				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)
1889	cg43983653	432	AGCTCCTCTGAG GCTGAGGGGAGC AT[C/T]GCCCCGA AGGACCCCACTT TCCTTC	C	T				SILENT- NONCODI NG	interferon	Human Gene SWISSPROT-ID:P10914 INTERFERON REGULATORY FACTOR 1 (IRF-1) - HOMO SAPIENS (HUMAN), 325 aa.	5.70E-177	5 (5q31.1)
1890	cg42918267	59	TAAGCTAAAAAC AAAATCAACCGG G[A/T]CCCCAGCT TTTCAGAACTGC AGGGA	A	T				SILENT- NONCODI NG	interferon	Human Gene Homologous to SPTREMBL-ID:Q64112 IFI54=INTERFERON-ALPHA REGULATED GENE - MUS MUSCULUS (MOUSE), 472 aa.	4.00E-105	
1891	cg42918267	72	AAATCAACCGGG ACCCAGCTTTT C[A/G]GAACTGC AGGGAACACAG CATCATG	A	G				SILENT- NONCODI NG	interferon	Human Gene Homologous to SPTREMBL-ID:Q64112 IFI54=INTERFERON-ALPHA REGULATED GENE - MUS MUSCULUS (MOUSE), 472 aa.	4.00E-105	
1892	cg42918267	82	GGACCCAGCTT TTCAGAACTGCA G[G/A]GAAACAG CCATCATGAGTG AGGTCA	G	A				SILENT- NONCODI NG	interferon	Human Gene Homologous to SPTREMBL-ID:Q64112 IFI54=INTERFERON-ALPHA REGULATED GENE - MUS MUSCULUS (MOUSE), 472 aa.	4.00E-105	

1893	cg3000751	184	TCAGCCATCTCA GCAAGCCCAGAA GT/CJATCTGCAA TATCTACGATGG CCTCG	T	C				SILENT- NONCODI NG	Interferon	Human Gene Similar to SWISSPROT- ID:P01562 INTERFERON ALPHA-1/13 PRECURSOR (INTERFERON ALPHA-D) (LEIF D) - HOMO SAPIENS (HUMAN), 189 aa.	8.20E-98	9
1894	cg3000751	199	AGCCAGAGAAGTA TCTGCAATATCT A/C/TJGATGGCCT CGCCCTTTGCTT TACTG	C	T				SILENT- NONCODI NG	Interferon	Human Gene Similar to SWISSPROT- ID:P01562 INTERFERON ALPHA-1/13 PRECURSOR (INTERFERON ALPHA-D) (LEIF D) - HOMO SAPIENS (HUMAN), 189 aa.	8.20E-98	9
1895	cg43510840	187	GATAGAGTACGT GGGATACAGGTC A/C/TJGGGCAGA CTCCTGGCCTCA ATGATG	C	T				SILENT- NONCODI NG	Interferon	Human Gene Similar to SWISSPROT- ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.20E-62	
1898	cg43510840	227	CCTCAATGATGC CTCCTGATCTAT C/G/CJCTAGGCC TGGACGACCAAC ACTGGG	G	C				SILENT- NONCODI NG	Interferon	Human Gene Similar to SWISSPROT- ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.20E-62	
1897	cg44339782	187	GATAGAGTACGT GGGATACAGGTC A/C/TJGGGCAGA CTCCTGGCCTCA ATGATG	C	T				SILENT- NONCODI NG	Interferon	Human Gene Similar to SWISSPROT- ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.20E-62	
1898	cg44339782	227	CCTCAATGATGC CTCCTGATCTAT C/G/CJCTAGGCC TGGACGACCAAC ACTGGG	G	C				SILENT- NONCODI NG	Interferon	Human Gene Similar to SWISSPROT- ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.20E-62	
1899	cg43978774	16	TTTTTTTTTTTT TTTC/TJCTCAT TAAAAATATTTAT TGAGC	C	T				SILENT- NONCODI NG	Interferon	Human Gene Similar to SWISSNEW- ID:Q99873 PROTEIN ARGININE N- METHYLTRANSFERASE 1 (EC 2.1.1.-) (INTERFERON RECEPTOR 1-BOUND PROTEIN 4) - HOMO SAPIENS (HUMAN), 361 aa.	3.50E-50	3

1900	cg43922672	2259	CACCCAGCAAAA GGTTGTTCCCTAA A/G]TAAGGGC AGAGTCACACGG GGGCAG	A	G				SILENT- NONCODING	Interleukin	Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0.00E+00	15
1901	cg43922672	2277	TCCTAAAAATAAG GGCAGAGTCACA C[G]GGGGCAG CTGATACAAATT GCAGAC	G	T				SILENT- NONCODING	Interleukin	Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0.00E+00	15
1902	cg42271251	256	TTGTTCAAGAGT TCCCTATCACTC T[C]gap]TTTAAATC ACTACTCACAGT AACCTC	C	gap				SILENT- NONCODING	Interleukin	Human Gene Homologous to SPTREMBL-ID:Q14629 INTERLEUKIN 2/BCM FUSION PROTEIN - HOMO SAPIENS (HUMAN), 288 aa (fragment).	9.60E-120	4 (4q26)
1903	cg42908571	1039	TTTATGTAAGTC ATATTATATTTT T/gap]AAGAAGTA CCACTTGAAACA TTTTA	T	gap				SILENT- NONCODING	Interleukin	Human Gene Homologous to SWISSPROT-ID:P05231 INTERLEUKIN- 6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR) - HOMO SAPIENS (HUMAN), 212 aa.	3.40E-108	7 (7p21)
1904	cg42908571	155	CTGAGGCTCATT CTGCCCTCGAGC C[C]gap]ACCGGG AACGAAAGAGAA GCTCTAT	C	gap				SILENT- NONCODING	Interleukin	Human Gene Homologous to SWISSPROT-ID:P05231 INTERLEUKIN- 6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR) - HOMO SAPIENS (HUMAN), 212 aa.	3.40E-108	7 (7p21)
1905	cg42887911	900	ACAGTCCTTCCG TGAGGCCTGGG GG[G]A/CATCTGT GCCTTATTATA CTTATT	G	A				SILENT- NONCODING	Interleukin	Human Gene Homologous to SWISSPROT-ID:P20809 INTERLEUKIN- 11 PRECURSOR (IL-11) (ADIPOGENESIS INHIBITORY FACTOR) (AGIF) - HOMO SAPIENS (HUMAN), 199 aa.	2.50E-103	19

1906	cg43994858	323	CAGCAAATTGTC CCTGCTTTAGTC A/C/TAGCAATTT TTCATGTCCTCT GTTC	C	T			SILENT- NONCODING	Interleukin receptor	Human Gene SWISSPROT-ID:P24394 INTERLEUKIN-4 RECEPTOR ALPHA CHAIN PRECURSOR (IL-4R-ALPHA) (CD124 ANTIGEN) - HOMO SAPIENS (HUMAN), 825 aa.	0.00E+00	16 (16p12.1)
1907	cg43987278	710	GAGTTGATCTGA TTGGCTAGTTCA G/G/gap/CCCAGC CTACCTGATTGG ACAGAGC	G	gap			SILENT- NONCODING	Interleukin receptor	Human Gene SWISSPROT-ID:P14784 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (IL-2 RECEPTOR) (P70-75) (HIGH AFFINITY IL-2 RECEPTOR BETA SUBUNIT) (CD122 ANTIGEN) - HOMO SAPIENS (HUMAN), 551 aa.	0.00E+00	22 (22q11.2)
1908	cg43987278	98	ACAGAGTAACAA AGATTTTCTTTA [A/gap]ATAAATGT ATTCAACGAAA ATGAA	A	gap			SILENT- NONCODING	Interleukin receptor	Human Gene SWISSPROT-ID:P14784 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (IL-2 RECEPTOR) (P70-75) (HIGH AFFINITY IL-2 RECEPTOR BETA SUBUNIT) (CD122 ANTIGEN) - HOMO SAPIENS (HUMAN), 551 aa.	0.00E+00	22 (22q11.2)
1909	cg43987278	99	CAGAGTAACAAA GATTTTCTTTAA [A/gap]TAAATGTA TTTCAACGAAA TGAAC	A	gap			SILENT- NONCODING	Interleukin receptor	Human Gene SWISSPROT-ID:P14784 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (IL-2 RECEPTOR) (P70-75) (HIGH AFFINITY IL-2 RECEPTOR BETA SUBUNIT) (CD122 ANTIGEN) - HOMO SAPIENS (HUMAN), 551 aa.	0.00E+00	22 (22q11.2)
1910	cg43091826	1583	CTTCTAACCACC CTGTCTCCAGCT G/C/gap/TCTGCA CACATGGACAGG GACCTGG	C	gap			SILENT- NONCODING	Interleukin receptor	Human Gene Homologous to SPTREMBL-ID:Q13261 INTERLEUKIN- 15 RECEPTOR ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 267 aa.	3.00E-139	10 (10p15)
1911	cg43091826	1621	GACAGGGACCT GGGAAAGGTGG GAG[A/G]GATGC TGAGCCCCAGCG AATCCTCTC	A	G			SILENT- NONCODING	Interleukin receptor	Human Gene Homologous to SPTREMBL-ID:Q13261 INTERLEUKIN- 15 RECEPTOR ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 267 aa.	3.00E-139	10 (10p15)

1912	cg43091826	265	CCTGGGCAGCG CTCGCCCGGG AGT[G/C]CAGCG GTGTCCTGTGGA GCTGCCGC	G	C			SILENT- NONCODI NG	Interleukin receptor	Human Gene Homologous to SPTREMBL-ID:Q13261 INTERLEUKIN- 15 RECEPTOR ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 267 aa.	3.00E-139	10 (10p15)
1913	cg43926168	40	ATTCCGGTTTTT TTTTTTTTTTT[A /TGGCATTTTCA AGATTTTATTGTA AA	A	T			SILENT- NONCODI NG	Interleukin receptor	Human Gene Similar to SWISSPROT- ID:P15510 INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL- 1RA) (IRAP) - HOMO SAPIENS (HUMAN), 177 aa.	8.80E-94	2 (2q14.2)
1914	cg43278750	1578	AGTCTCTAAAT GTTGCTTTTCTC A[G/A]CCTGTGTTA TCCATATTTCAAT CCTT	G	A			SILENT- NONCODI NG	Interleukin receptor	Human Gene Similar to SWISSPROT- ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1915	cg43278750	1583	TCTAAATGTTGC TTTTCTCAGCCT G[T/C]TTATCCAT ATTCAATCCTT GGAAC	T	C			SILENT- NONCODI NG	Interleukin receptor	Human Gene Similar to SWISSPROT- ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1916	cg43278750	1611	ATCCATATTTCAA TCCTTGGAAGT[G T/C]CCAGCTCCC ATGACTCTATGC CCAC	T	C			SILENT- NONCODI NG	Interleukin receptor	Human Gene Similar to SWISSPROT- ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1917	cg43278750	1613	CCATATTTCAAT CCTTGGAAGTGT C[C/T]AGCTCCCA TGACTCTATGCC CACCA	C	T			SILENT- NONCODI NG	Interleukin receptor	Human Gene Similar to SWISSPROT- ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1918	cg43278750	1616	TATTTCAATCCTT GGAAGTGTCCAG [C/T]TCCCATGAC TCTATGCCACC AAGC	C	T			SILENT- NONCODI NG	Interleukin receptor	Human Gene Similar to SWISSPROT- ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	

1919	cg43278750	1617	ATTCAATCCTT GGAAGTGTCCAG CT/CJCCCATGAC TCTATGCCCCACC AAGCT	T	C			SILENT- NONCODING NG	Interleukin-8 receptor	Human Gene Similar to SWISSPROT- ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1920	cg43278750	1627	TGGAACGTGTC AGTCCCATGAC TTCGJTATGCCCA CCAAGCTCTTGA ATTT	C	G			SILENT- NONCODING NG	Interleukin-8 receptor	Human Gene Similar to SWISSPROT- ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1921	cg43278750	1650	CTCTATGCCAC CAAGCTCTTGAA TTTGTTCTCATT TCTTCACTTACA ACCT	T	G			SILENT- NONCODING NG	Interleukin-8 receptor	Human Gene Similar to SWISSPROT- ID:P15533 DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR - MUS MUSCULUS (MOUSE), 353 aa.	5.30E-71	
1922	cg41657511	1553	TTGAGCATTTT TTTAGGATGGG A/gap]GGTGCGT GAGGTTCTCTCA GCCCCAG	A	gap			SILENT- NONCODING NG	Interleukin-8 receptor	Human Gene Similar to SWISSPROT- ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GROMGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11
1923	cg41657511	1560	TTTTTTTTTAGG ATGGGAGGTGC GT/A]GAGGTTCT CTCAGCCCCAGG GGGGTG	T	A			SILENT- NONCODING NG	Interleukin-8 receptor	Human Gene Similar to SWISSPROT- ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GROMGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11
1924	cg41657511	1561	TTTTTTTTTAGG TGAGGAGGTGCG TTGTTAGGTTCTC TCAGCCCCAGG GGGTGC	G	T			SILENT- NONCODING NG	Interleukin-8 receptor	Human Gene Similar to SWISSPROT- ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GROMGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11

1925	cg41657511	1618	GTAAGGACAGCC TTCACGTGCCT TTCCTGAGCTGCT TTCCGCTCCCTG GGCTC	C	T			SILENT- NONCODI NG	interleukin-8 receptor	Human Gene Similar to SWISSPROT- ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GROMGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11
1926	cg41657511	1698	TGGCAGGGATGT TCTAGAAATGGG G[G/gap]TTGGTT CCTCTAGCTACC CCAAATG	G	gap			SILENT- NONCODI NG	interleukin-8 receptor	Human Gene Similar to SWISSPROT- ID:P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GROMGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	4.80E-58	11
1927	cg43929155	1432	AACTGAACATTC CAGAGCGGTAG TTGTTAATCACGT AAAGCTAGAAAT GATCC	G	T			SILENT- NONCODI NG	interleukin-8 receptor	Human Gene Similar to SWISSPROT- ID:P21109 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (CXCR-1) - ORYCTOLAGUS CUNICULUS (RABBIT), 355 aa.	4.20E-55	2
1928	cg43933187	44	TTTTTTTTTTTT TTTTTTTTTTTTG TTCAATGTTTAGA ACATTTTATTAAA G	G	T			SILENT- NONCODI NG	isomerase	Human Gene SWISSNEW-ID:P11388 DNA TOPOISOMERASE II, ALPHA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1531 aa.	0.00E+00 (17q21)	17
1929	cg43933187	458	TAGACACAGCCA AAGTGTTCCTT TC/TGGCCCTCTGA TGATTTGAGAAG ATGA	C	T			SILENT- NONCODI NG	isomerase	Human Gene SWISSNEW-ID:P11388 DNA TOPOISOMERASE II, ALPHA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1531 aa.	0.00E+00 (17q21)	17
1930	cg43951261	5307	CTGTGAGAATTG TTATAGACTGCC GT/gap]GCATTA GCACAGATTTTA ATTGICA	T	gap			SILENT- NONCODI NG	isomerase	Human Gene SWISSPROT-ID:Q02880 DNA TOPOISOMERASE II, BETA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1626 aa.	0.00E+00 3 (3p)	3 (3p)

1931	cg40915009	3857	GACCAGCCAGG GCAACATGGTGA AA[AGap]CCCCA TCTCTACTAAAA AACAAAAA	A	gap			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0.00E+00	
1932	cg40915009	3875	GGTGAAAACCCCA ATCTCTACTAAA AATJACAAAAAA TTAGCCAGGTGT GGCGG	A	T			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0.00E+00	
1933	cg40915009	3944	GCTACTTAGGAG GCTGAGGCAGG AGIAGIATCACCT GAACACAGGAG GTAGAGG	A	G			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0.00E+00	
1934	cg40915009	3950	TAGGAGGCTGA GGCAGGAGAAAT CAC[CT]TGAACA CAGGAGGTAGA GGCTGCAG	C	T			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0.00E+00	
1935	cg40915009	3954	AGGCTGAGGCA GGAGAATCACCT GA[AG]CACAGG AGGTAGAGGCT GCAGIGAG	A	G			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0	
1936	cg40915009	3958	TGAGGCAGGAG AATCACCTGAAC AC[AG]GGAGGT AGAGGCTGCAGT GAGCCG	A	G			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q13472 DNA TOPOISOMERASE III (EC 5.99.1.2) - HOMO SAPIENS (HUMAN), 1001 aa.	0	
1937	cg43993971	78	TTTTACCTCCTCA CGTGGCATCTTT A/GTTTTCTACA TGGGATGTGAAC AAC	A	G			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:P06744 GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) (NEUROLEUKIN) (NLK) - HOMO SAPIENS (HUMAN), 558 aa.	3.6E-305 (19q13.1)	19

1938	cg43930054	587	TGGCTGGCAGA GGAGAGCTGGG GAG[G/gap]CTGC AGCCTTTACAGC AGACAGCAG	G	gap			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:P34949 MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNANOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa.	2E-222	15 (15q22)
1939	cg43969064	581	AGAAACACATTA GGGATCATATTC ATT/CJAGACAAAA ACCTTTACATTTT CTTA	T	C			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q08752 40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PIPIASE) (ROTAMASE) (CYCLOPHILIN-40) (CYP- 40) (CYCLOPHILIN-RELATED PROTEIN) - HOMO SAPIENS (HUMAN), 370 aa.	1.3E-200	4
1940	cg44001328	215	TGTGGAAGATAA GAGTTAGAGACC T[C/A]GGCCTCCT GGTCAGTGGAG CCCTTG	C	A			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa. pcds:TREMBLNEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa.	9.9E-189	1
1941	cg44001328	237	CCTCGGCCTCCT GGTCAGTGGAG CC[C/gap]TTGGC CTCATGCCCTGGT GGGCTAAG	C	gap			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa. pcds:TREMBLNEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa.	9.9E-189	1
1942	cg44001328	308	GGTAGGGGAGG CCTTGGCTTGGC CC[C/gap]AGCAG CTCCAGGGCCCT GAGTTCCT	C	gap			SILENT- NONCODING	isomerase	Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa. pcds:TREMBLNEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa.	9.9E-189	1

1943	cg44001328	334	AGCAGCTCCAG GGCCCTGAGTTC CT[G/gap]CCAGA GGCTGGAGAGC AGGCAGCTG	G	gap			SILENT- NONCODING	Isomerase	Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa.lpcds:TREMBLNEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa.	9.9E-189	1
1944	cg43958501	129	TCACATAGAAAA GCTAAAGACAAA AT/CJACTGGTAC CAACATAGCCC TTAGG	T	C			SILENT- NONCODING	Isomerase	Human Gene SWISSPROT-ID:P46926 PUTATIVE GLUCOSAMINE-6- PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE- 6- PHOSPHATE DEAMINASE) (OSCILLIN) (KIAA0060) - HOMO SAPIENS (HUMAN), 289 aa.	1.6E-156	5
1945	cg43958501	19	TTTTTTTTTTTT TTTTT[A/T]TTTGA AAATACTGGATT TAATAGAA	A	T			SILENT- NONCODING	Isomerase	Human Gene SWISSPROT-ID:P46926 PUTATIVE GLUCOSAMINE-6- PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE- 6- PHOSPHATE DEAMINASE) (OSCILLIN) (KIAA0060) - HOMO SAPIENS (HUMAN), 289 aa.	1.6E-156	5
1946	cg44004587	967	TGTTTATCACAG CCTACTAAAAAC A[C/gap]AGAGTT TCACCTCATTGTT CAAAAT	C	gap			SILENT- NONCODING	Isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	
1947	cg44004587	1036	GCAAAGATTAAA TTAAGTTTATTT [G/gap]CTCGCTC TCATTTTACAATA ATCTC	G	gap			SILENT- NONCODING	Isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	
1948	cg44004587	1262	AAAGTCATTCTA AGTTTGTAAAGC A[G/C]ATAAAATTT TTCTGTAATCATT TACC	G	C			SILENT- NONCODING	Isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	

1949	cg44004587	282	GTACAATTTTAA CATTAAATATACA CTTATTCATAAT CTCATCTATTTAA CA	C	T				SILENT- NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	
1950	cg44004587	378	TTCTGACTCTG TAGGACAGTGGT C[C/gap]TCAGTT GGGGTTGACT CTGTCCTCC	C	gap				SILENT- NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3E-123	
1951	cg44004587	573	ACCGAGTGGGA CTCAATTCCCAT TTT[gap]ATGAAC ACCTCTGTGCTC ACTGJAA	T	gap				SILENT- NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3.00E-123	
1952	cg44004587	783	ATATCATTTAATT TCCCTTGAACCT gap/TGCTCTGCT AGTTTAATCTGC TAATA	gap	T				SILENT- NONCODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3.00E-123	
1953	cg43255138	882	CGTGCCATGGC GGGGTTCTCCA AT/CJACACTCAC ACTGTCCATGTT CTTTT	T	C				SILENT- NONCODING	isomerase	Human Gene Homologous to SWISSPROT-ID:Q00688 RAPAMYCIN- SELECTIVE 25 KD IMMUNOPHILIN (FKBP25) (PEPTIDYL-PROLYL CIS- TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) - HOMO SAPIENS (HUMAN), 224 aa.	1.40E-118	19
1954	cg42711479	676	CTTGAGGAAACT TCGGTTGCAGAT T[G/gap]AAGCAT TTCAGGTTGTGC ATTGTG	G	gap				SILENT- NONCODING	isomerase	Human Gene Similar to SPTREMBL- ID:Q16645 PEPTIDYL-PROLYL CIS- TRANS ISOMERASE - HOMO SAPIENS (HUMAN), 108 aa.	2.90E-54	2
1955	cg42711479	729	GATGCATGTAGT AGCCTTTCCTGA T[G/A]ACAGAACA CAGATCTCTTGT TCGCA	G	A				SILENT- NONCODING	isomerase	Human Gene Similar to SPTREMBL- ID:Q16645 PEPTIDYL-PROLYL CIS- TRANS ISOMERASE - HOMO SAPIENS (HUMAN), 108 aa.	2.90E-54	2

1956	cg43918167	986	CCAACCATGTCA AGATGATAACA ATTCTCGCTTAG TACAAGAGATGG ATGCA	T	C				SILENT- NONCODI NG	isomeras einhibitor	Human Gene Similar to SWISSPROT- ID:P49312 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HELIX-DESTABILIZING PROTEIN) (SINGLE-STRAND BINDING PROTEIN) (HNRNP CORE PROTEIN A1) (HDP-1) (TOPOISOMERASE-INHIBITOR SUPPRESSED) - MUS MUSCULUS (MUSE), 319 aa.	8.80E-78	5
1957	cg43145505	3397	TTAAACAGCATG CATTGAACTGAA A[A/gap]GATAAC TGAGAAAATGAA AGCTCAC	A	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa. pcis:SWISSPROT- ID:P42336 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.	0.00E+00	3
1958	cg43918241	2846	ACCTAGAGAGAG AAAAAATGCTTT [T/gap]CTTTGTGA AAAATCTGAATT CCTGT	T	gap				SILENT- NONCODI NG	kinase	Human Gene SPTRMBL-ID:Q63553 SNF1-RELATED KINASE - RATTUS NORVEGICUS (RAT), 746 aa.	0.00E+00	3
1959	cg43918241	3412	GCACACAAATGT TGCAAAAGTCAA A[A/gap]CCCCAT GAATTAAACCT ACTGGAA	A	gap				SILENT- NONCODI NG	kinase	Human Gene SPTRMBL-ID:Q63553 SNF1-RELATED KINASE - RATTUS NORVEGICUS (RAT), 746 aa.	0.00E+00	3
1960	cg43918241	4823	TTCTGTATGTGT GTATATATATATA [gap/T]ATTATGTA CTTCTGGCAATT CTATC	gap	T				SILENT- NONCODI NG	kinase	Human Gene SPTRMBL-ID:Q63553 SNF1-RELATED KINASE - RATTUS NORVEGICUS (RAT), 746 aa.	0.00E+00	3

1961	cg43983484	2863	GGGACTGTGGT GACTTCTGCTGC TG[G/gap]CCCCG CCCCTGCCCCCA GAGCGTCC	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1962	cg43983484	2959	TGTGTGTGAATC TGCTTTCTCTCT G[C/gap]CTTCGG AGGAAATTGTA AATCCTG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1963	cg43983484	2960	GTGTGTGAATCT GCTTTCTCTCTG C[C/gap]TTCGGA GGGAAATTGTAA ATCCTGT	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1964	cg43983484	359	GGCCGGCGGCGG GCCCGCCGCGG GGC[G/C]GCGGC GGCGGGGCGAC GGTCCCCCG	G	C			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1965	cg43983484	360	GCCGGCGGCGG CCCGCCGCGGG GCG[G/C]GCGCG GCGGGGCGCAG GTCCCCCGC	G	C			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q05655 PROTEIN KINASE C, DELTA TYPE (EC 2.7.1.-) (NPKC-DELTA) - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	3
1966	cg43917863	127	TATACATTGAGA TATGTTTGAAAC A[C/gap]TTCCTAA GGCTACAAAACA GAACAT	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q08881 TYROSINE-PROTEIN KINASE ITK/TSK (EC 2.7.1.112) (T-CELL-SPECIFIC KINASE) (TYROSINE-PROTEIN KINASE LYK) (KINASE EMT) - HOMO SAPIENS (HUMAN), 620 aa.	0.00E+00	4
1967	cg43978564	205	CAAAACAAATGTA CGACAGGTCAGA A[A/G]CTTAAGTT ACAAAATAGAGT CAATA	A	G			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q99683 MITOGEN-ACTIVATED KINASE KINASE KINASE 5 - HOMO SAPIENS (HUMAN), 1374 aa.	0.00E+00	6

1968	cg43976564	307	TAAAAAACATA AATTTATACAG TACJATTGAAAT TACGCATTTCTA CTCAG	A	C			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q99683 MITOGEN-ACTIVATED KINASE KINASE KINASE 5 - HOMO SAPIENS (HUMAN), 1374 aa.	0.00E+00	6
1969	cg43916734	20924	CCTCATTTGGAG GAAAAAAGCAT GIC/TTATTCTAGC ACAACAAGATGA AATTA	C	T			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
1970	cg43916734	20951	TTCTAGCACAAAC AAGATGAAATTA TTG/AJGAATACAA AAGTGGCTCCTT CCCAT	G	A			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
1971	cg43916734	20956	GCACAACAAGAT GAAATTAATGGAA TTAGJCAAAAGTG GCTCCTTCCCAT GTGCA	A	G			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
1972	cg43916734	21059	TTAGCTTTTGTGTT GTTTTTTTTTTTG ap/TTCCTTCTAAC ACTTGTAATTGG AGGC	gap	T			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
1973	cg43090980	2252	CCAGAGACAGG AAAGAATTGGCC TTC/GJCCCTGG GAACTGGTTCAA GAGACA	C	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q04759 PROTEIN KINASE C, THETA TYPE (EC 2.7.1.-) (NPKC-THETA) - HOMO SAPIENS (HUMAN), 706 aa.	0.00E+00	10
1974	cg43090980	2718	ATTCCTATCTGT GGATGTGTAAAT G[G/gap]CTGGGG GGCCAGCCCTG GATAGGTT	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q04759 PROTEIN KINASE C, THETA TYPE (EC 2.7.1.-) (NPKC-THETA) - HOMO SAPIENS (HUMAN), 706 aa.	0.00E+00	10

1975	cg43090980	2726	CTGTGGATGTGT AAATGGCTGGG GG[G/gap]CCAGC CCTGGATAGGTT TTTATGGG	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q04759 PROTEIN KINASE C, THETA TYPE (EC 2.7.1.-) (NPKC-THETA) - HOMO SAPIENS (HUMAN), 706 aa.	0.00E+00	10
1976	cg43956329	2485	GTAACCTACAGTG GCATTAGGACTT A/C/T/CGCTTAGA TGACAAATAGTGC TCCTT	C	T			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P14619 CGMP-DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa. pcis:SWISSPROT-ID:P14619 CGMP- DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa.	0.00E+00	10
1977	cg43956329	3342	TCTGTAATGTC AGTGTCTGAACA G[A/gap]CAACAC AAATTCAAATCAT TATACG	A	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P14619 CGMP-DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa. pcis:SWISSPROT-ID:P14619 CGMP- DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa.	0.00E+00	10
1978	cg43956329	3427	ATTAACCAAAAC TCCTGTCCAATT T/C/G/ACTTATAC AACATAGTCAGT CTAGA	C	G			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P14619 CGMP-DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa. pcis:SWISSPROT-ID:P14619 CGMP- DEPENDENT PROTEIN KINASE, BETA ISOZYME (CGK) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 686 aa.	0.00E+00	10
1979	cg44022982	3348	CAGGAGGAGG GGAGGTGCAGG GAA[G/A/JAGGGG CCGGCCTCAGCT GTCACCAG	G	A			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q16584 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 847 aa.	0.00E+00	11

1980	cg44022882	3469	GTCATCTGGGGC CAGGGCTCTCTG G/A/GTGCCTTCC TGCTGCCCCAGC CAGGG	A	G				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q16584 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 847 aa.	0.00E+00	11
1981	cg42922283	4204	ATGGCTGCCCTC TGGCAGGGCAG GGT/CJAGGGCA GTGACACTGTAG GAGCATA	T	C				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q99558 NIK, SERINE/THREONINE PROTEIN- KINASE - HOMO SAPIENS (HUMAN), 947 aa.	0.00E+00	17
1982	cg43299934	926	CTTCTCAATAG GACTTCTGGAG AGGAC	G	T				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92667 KINASE A ANCHOR PROTEIN - HOMO SAPIENS (HUMAN), 803 aa.	0.00E+00	17
1983	cg43336163	2707	CGTTGGAAGACT GAGTGCCCGGG GC/A/gap/CAGCA CAGAAGCCGCG CCCACCGCC	A	gap				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19
1984	cg43336163	2786	GTCTCCGCCCCAG CTCCAGTCCTGT G/A/TTCGGGC CCGCCCCCTAG CGGCCCGG	A	T				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19
1985	cg43336163	2787	TCTCCGCCCCAGC TCCAGTCCTGTG A/T/AJCCGGGCC CGCCCCCTAGC GGCCCGG	T	A				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19
1986	cg43336163	3208	TCTCGGAGCCCC AGCCGGCTCCG CC/G/GCCTTCG GCGGTTGGATA TTTATTG	C	G				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19

1987	cg43336163	3209	CTCGGAGCCCC AGCCGGGCTCCG CCC[C/G]CTTCG GCGGTTTGGATA TTTATTGA	C	G			SILENT- NONCODI NG	Kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0.00E+00	19
1988	cg44929725	5014	TCACCAAGGTCT CTGTGTCAAACC T[G/A]TGGCCACT CTATATGCACCT TGTTT	G	A			SILENT- NONCODI NG	Kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
1989	cg42859664	338	AGTGTGGATGCT GGTGGCAGGAG TC[C/A]AGGACTG TGAAGAGCTGTC AGCATA	C	A			SILENT- NONCODI NG	Kinase	Human Gene SWISSPROT-ID:P07332 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FES/FPS (EC 2.7.1.112) (C-FES) - HOMO SAPIENS (HUMAN), 822 aa.	0.00E+00	15 (15q26.1)
1990	cg38810367	4136	AGGTTTCACCAT GATGGCCAGGC TG[A/G]TCTCGAA CTCCTAACCTCA AGTGAT	A	G			SILENT- NONCODI NG	Kinase	Human Gene SWISSPROT-ID:P52333 TYROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3) (LEUKOCYTE JANUS KINASE) (L-JAK) - HOMO SAPIENS (HUMAN), 1124 aa.	0.00E+00	19 (19p13.1)
1991	cg43995263	191	AAGATTATAAATA CGAGGGGGTAA G[C/gap]CCCACC TGAGGGGCACAG AACCTTTT	C	gap			SILENT- NONCODI NG	Kinase	Human Gene SWISSPROT-ID:Q16760 PUTATIVE DIACYLGLYCEROL KINASE ETA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK-ETA) (DAG KINASE ETA) (DIACYLGLYCEROL KINASE, DELTA) (KIAA0145) - HOMO SAPIENS (HUMAN), 1169 aa.	0.00E+00	2 (4p16.3)
1992	cg43995263	194	ATTATAAATACG AGGGGGTAAGC CC[C/gap]ACCTG AGGGCACAGAA CCTTTTCTC	C	gap			SILENT- NONCODI NG	Kinase	Human Gene SWISSPROT-ID:Q16760 PUTATIVE DIACYLGLYCEROL KINASE ETA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK-ETA) (DAG KINASE ETA) (DIACYLGLYCEROL KINASE, DELTA) (KIAA0145) - HOMO SAPIENS (HUMAN), 1169 aa.	0.00E+00	2 (4p16.3)

1993	cg43995263	2249	ACGTTTCTGAGA ACTGGCTGGGG GC[C/gap]AGGAG GCGGACCACAC GGTGCGGCC	C	gap			SILENT- NONCODI NG	Kinase	Human Gene SWISSPROT-ID:Q16760 PUTATIVE DIACYLGLYCEROL KINASE ETA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK-ETA) (DAG KINASE ETA) (DIACYLGLYCEROL KINASE, DELTA) (KIAA0145) - HOMO SAPIENS (HUMAN), 1169 aa.	0.00E+00	2 (4p16.3)
1994	cg43969763	6070	TTAAGATATCATA TGGGTCAGGTCA [T/gap]TTTTTTT TCTGTGCTGGTT GCCAC	T	gap			SILENT- NONCODI NG	Kinase	Human Gene SWISSPROT-ID:Q13627 SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	21 (21q22.1)
1995	cg43969763	6078	ATATGGGTCAGG TCATTTTTTTTT gap/TCTGTGCTG GTTGCCACATCT TAGCA	gap	T			SILENT- NONCODI NG	Kinase	Human Gene SWISSPROT-ID:Q13627 SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	21 (21q22.1)
1996	cg43969763	6135	CAAAAAACTAAA GCAGTTTTTAAA C[C/T]GATATTTA CGTAAAGAAAAT CATAA	C	T			SILENT- NONCODI NG	Kinase	Human Gene SWISSPROT-ID:Q13627 SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	21 (21q22.1)
1997	cg43918968	663	CCTGATAGAGGA AGAGGTGGCAG GG[A/G]AAACTG CCCAGCTCAAAG CCCTAGT	A	G			SILENT- NONCODI NG	Kinase	Human Gene SPTREMBL-ID:Q13308 COLON CARCINOMA KINASE-4 PRECURSOR - HOMO SAPIENS (HUMAN), 1070 aa.	0.00E+00	6 (6p21.1)
1998	cg43019995	3241	GCCCGTGGGAC CATGACTTAGGG AG[G/gap]TGGGA CCCACCCACCCC CATCCAGG	G	gap			SILENT- NONCODI NG	Kinase	Human Gene SWISSPROT-ID:P53667 LIM DOMAIN KINASE 1 (EC 2.7.1.-) (LIMK-1) - HOMO SAPIENS (HUMAN), 647 aa.	0.00E+00	7 (7q11.23)

1999	cg44910735	226	GGGGTGCTCTCG GGCAGAGACCC CCG/GC/GCTTG GGCAGCTGAG GCGGCCGGG	G	C				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q13869 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE - HOMO SAPIENS (HUMAN), 1149 aa.	0.00E+00	9 (9q34.1)
2000	cg43257904	116	CGGGGGAGACA CAAAAGGGACCC CC[C/gap]AAAT CCACATGGGT GCTGGGAAC	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2001	cg43257904	141	CAAAATCCACAT GGGGTGCTGGG AA[C/gap]CCCAA AATCCAGTGGAA GGCACATC	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2002	cg43257904	2476	CGGACTCTCGTT ATTGGCTCTGCG G[G/gap]ACTCAG CCTCCACCCCTT ATTGGGT	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2003	cg43257904	267	AATTAGAAGTA TCCCCAAAGCCA A[gap/A]GAGGAA ACCAAATGATGG AGGAGAC	gap	A				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2004	cg43257904	318	AGGGGGCTCAG TCTTTGGCGGG GT[C/gap]CCCCA ATCCAGAAGAA CTGGAAAA	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)

2005	cg43257904	38	TTTTTTTTTTTT TATTTTTTTTTT /GJCCAGCAGAA TTCTGTGCTTCT TGG	T	G				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2006	cg43257904	482	TGAGATTGGCTC CCTGGTGGCTTG G(G/gap)CGGGG CCTAAGGCACAA GGCGGGCT	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	X (Xp11.4)
2007	cg42879455	2335	ATAGTGGCTTCT GAGCAAAGGCC AAJAGJAAATTAT TGTGCTGAAAT TTCCCG	A	G				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q06187 TYROSINE-PROTEIN KINASE BTK (EC 2.7.1.112) (BRUTON'S TYROSINE KINASE) (AGAMMAGLOBULINAEMIA TYROSINE KINASE) (ATK) (B CELL PROGENITOR KINASE) (BPK) - HOMO SAPIENS (HUMAN), 659 aa.	0.00E+00	X (Xq21.3)
2008	cg43016289	6151	TACATCATCTGG CCAGGCATGGTC G(gap/C)TTACGC CTGTAATCCTAG CACCTTG	gap	C				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q28021 RHO-ASSOCIATED KINASE - BOS TAURUS (BOVINE), 1388 aa.	0.00E+00	
2009	cg43931272	1166	TTAGGGATAAAA CACTAACTCTAG T(G/C)CCTTTAAC GGCAATAGCAA CTTT	G	C				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW- ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	
2010	cg43931272	1452	CCTCACTCAGAG CAGCCACACACA GT/GGGCCGTT GACGCTGGAAC CTCGGGC	T	G				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW- ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	

2011	cg43931272	307	GGCTAATTTTAT ATTTTAGTAGA AGIATGGCGTT CACCATGTGGAC CAGA	A	G		SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW- ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	
2012	cg43931272	959	TCTCAGTACTCC CACTCAATTTTT [gap/T]CCCTACT GAGATGAGGGA AGCAATT	gap	T		SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW- ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	
2013	cg44003408	253	GGACTGGAGACT GATGCATGAGG GG[G/C]CTACGG AGCGCAGGAG CGGTGGTG	G	C		SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P53355 DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1) - HOMO SAPIENS (HUMAN), 1431 aa.	0.00E+00	
2014	cg44001122	4440	AGTGTGTTGGGT TTGTTTTTCTTT A/GIAGAAAAAGA AATGTACACCAC TCCT	A	G		SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P31152 EXTRACELLULAR SIGNAL- REGULATED KINASE 4 (EC 2.7.1.-) (ERK4) (MAP KINASE ISOFORM P63) (P63-MAPK) - HOMO SAPIENS (HUMAN), 557 aa.	4.40E-307	18
2015	cg43957153	131	GGACCGGCGG CGCGCGCGCG GCA[G/C]CGCG GCGCGTAGGG TGTTTAAAC	G	C		SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.20E-304	4 (1p36)
2016	cg43957153	132	GGACCGGCGG GGCGCGCGCG CAG[C/G]GGCG CGCGTAGGGT GTTTAACT	C	G		SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.20E-304	4 (1p36)
2017	cg43957153	81	AAGTGACGATAC TTTGGCGCGCG C[C/gap]GGTTGC TGTTCTCTCT GGCTCCG	C	gap		SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.20E-304	4 (1p36)

2018	cg44004766	3864	CAGATTCGAAAT TCTGTGCCATGG C/A/GTATATGTT CAAATTCAAACC ATTTT	A	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07947 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE YES (EC 2.7.1.112) (P61-YES) (C-YES) - HOMO SAPIENS (HUMAN), 543 aa.	1.60E-300	
2019	cg44004766	4255	TGTATAGTAGGG ATAAAACACTAA CTT/gapTTAATGT GTATTCATTTTAA ATTGTT	T	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07947 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE YES (EC 2.7.1.112) (P61-YES) (C-YES) - HOMO SAPIENS (HUMAN), 543 aa.	1.60E-300	
2020	cg44004766	4256	GTATAGTAGGGA TAAACACTAAC TTT/gapTAATGTGT ATTCATTTTAAAT TGTTG	T	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07947 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE YES (EC 2.7.1.112) (P61-YES) (C-YES) - HOMO SAPIENS (HUMAN), 543 aa.	1.60E-300	
2021	cg43952782	322	CGCCGGGCCGG GGACACCCCGG CGC[C/gap]GCCC CCTCGGTGCTCT CGGAAGGCC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2022	cg43952782	351	CCCTCGGTGCTC TCGGAAGGCC AC[C/gap]GGCTC CCGGGCCCGCC GGGACCCCC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2023	cg43952782	367	AAGGCCACCCG GCTCCCGGGCC CGC[C/gap]GGGA CCCCCGGAGC CGCCTCGGCC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2024	cg43952782	377	GGCTCCCGGGC CCGCCGGGACC CCC[C/gap]GGAG CCGCTCGGCC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)

2025	cg43952792	383	CGGGCCCGCCG GGACCCCGCG AGC[Gap]GCCT CGCCCGCGCCG GAGGAGGGCG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2026	cg43952792	388	CGCCCGGACC CCCCGGAGCG CCT[C]gap]GGCC GCGCCGGAGGA GGCGGGGAG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2027	cg43952792	559	TATAAAGTTGT GATCGTTGGCG GA/C]ATTTTGG AATTAGATAAT GGCGTG	A	C			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
2028	cg43971741	2104	TGAGCACAGTTA TGACAGAGAAGT TIT[Gap]CTCCG ACCAGAAATTATC CACAGCA	T	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2028	cg43971741	2108	CACAGTTATGGC AGAGAAGTTTCT C[C]gap]GCACCA GAATTATCCACA GCAACTT	C	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2030	cg43971741	2133	CGCACCGAATT ATCCACAGCAAC TIT[Gap]GGCTGA GCCCCACTACAC ACAGAGA	T	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2031	cg43971741	2161	CTGAGCCCCACT ACACACAGAGAA AIT/C]CATCAACC TGACTTAAGAGT TTTCA	T	C			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9

2032	cg43971741	2162	TGAGCCCCACTA CACACAGAGAAA TTC/TATCAACCT GACTTAAGAGTT TTCAA	C	T			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2033	cg43971741	2196	GACTTAAGAGTT TTCAAGATGTCA AIA/gapJCTTCAG GCTGATCAGCAG ATGGGAT	A	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2034	cg43971741	2234	CAGCAGATGGG ATGTGAAAAATA CTA/gapJCCCTA TTCTATCAATTTGC TGTTGCT	A	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2035	cg43971741	2508	ATTATAGTTTCAT GTCATTGAAAGT TIT/gapJAAATTGG TTTCATTAAAGA TCAAT	T	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2036	cg43971741	2516	ATGTCATTGAAA GTTTAAATTGGT TIT/gapJCATTTAA AGATCAATATAC TAGGTC	T	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2037	cg43971741	2521	ATTGAAAGTTTA AATTGGTTTCATT TIT/gapJAAAGATC AATATACTAGGT CIGCCT	T	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
2038	cg43119489	2360	GGTCTCAGCGG CCGGCAGACGT GAGIG/gapJCGCT TCCGAGCGCAG GCCTCCGCCG	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q00537 SERINE/THREONINE-PROTEIN KINASE PCTAIRE-2 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 523 aa.	2.70E-282	

2039	cg43119489	2376	AGACGTGAGGC GCTTCCGAGCG CAG[G/gap]CCTC CGCCGCCACAG CCGCCTTCG	G	gap			SILENT- NONCODI NG	Kinase	Human Gene SWISSPROT-ID:Q00537 SERINE/THREONINE-PROTEIN KINASE PCTAIRE-2 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 523 aa.	2.70E-282	
2040	cg43123314	2399	TGACATTCTTA GGAAACCCAGA GG[G/gap]TGGAG GTGGGGGCCCC ACGGCTAAA	G	gap			SILENT- NONCODI NG	Kinase	Human Gene SWISSPROT-ID:Q16875 6- PHOSPHOFRUCTO-2-KINASE (EC 2.7.1.105) / FRUCTOSE-2,6- BISPHOSPHATASE (EC 3.1.3.46) BRAIN/PLACENTA-TYPE ISOZYME (6PF-2-KFRU-2,6-P2ASE) - HOMO SAPIENS (HUMAN), 520 aa.jpds:SP TREMBL-ID:Q16875 FRUCTOSE 6-PHOSPHATE,2- KINASE/FRUCTOSE 2,6- BISPHOSPHATASE (EC 3.1.3.46) (FRUCTOSE-2,6-BISPHOSPHATE 2- PHOSPHATASE) (FRUCTOSE-2,6- BISPHOSPHATASE) - HOMO SAPIENS (HUMAN), 520 aa	1.80E-281	
2041	cg43921754	153	CCGGCCACCC CCGGCCCCGCG CCA[gap]G[CAGC CCCTCGCCGCG CGTCCAGCGT	gap	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07948 TYROSINE-PROTEIN KINASE LYN (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 511 aa.	2.40E-281	8 (8q13)
2042	cg43921754	207	CGGCCAGCAGC CTCCCCATACGC AG[G/gap]TCCTG CTGGACCGCCC CGTCGCGCC	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07948 TYROSINE-PROTEIN KINASE LYN (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 511 aa.	2.40E-281	8 (8q13)
2043	cg43921754	285	AGCTCCGCCGC CCCGAACTTTC AC[C/gap]GCGAG CGGGAATATGG GATGTATA	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07948 TYROSINE-PROTEIN KINASE LYN (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 511 aa.	2.40E-281	8 (8q13)

2044	cg43921754	282	CGCCCCCGAAA CTTCCACCGGA GC[G/gap]GGAAA TATGGGATGTAT AAATCAA	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P07948 TYROSINE-PROTEIN KINASE LYN (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 511 aa.	2.40E-281	8 (8q13)
2045	cg43922705	178	GAGAGCCTCTCG GCAGCGGGGG GG[G/gap]TCCTC TCCTCCAGAACA AAAGGCAC	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P27987 1D-MYO-INOSITOL-TRISPHOSPHATE 3 KINASE B (EC 2.7.1.127) (INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE) (IP3K) (IP3 3-KINASE) - HOMO SAPIENS (HUMAN), 505 aa (fragment).	3.80E-279	1 (1q41)
2046	cg44019155	1267	AATCCACGTTTA TTTTCTCTGTGT CT[C/G]GAAGTGT CTATGTAATGAC ATTGA	T	C			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P23443 RIBOSOMAL PROTEIN S6 KINASE (EC 2.7.1.-) (S6K) (P70-S6K) - HOMO SAPIENS (HUMAN), 502 aa.	8.90E-275	17
2047	cg44019155	1317	CTCTCTGAAACT GTCATTTTGAGT C[gap]TGTTC CCTTGCAGGATG CTCACAC	gap	T			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P23443 RIBOSOMAL PROTEIN S6 KINASE (EC 2.7.1.-) (S6K) (P70-S6K) - HOMO SAPIENS (HUMAN), 502 aa.	8.90E-275	17
2048	cg44019155	1317	CTCTCTGAAACT GTCATTTTGAGT C[gap]TGTTC CCTTGCAGGATG CTCACAC	gap	T			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P23443 RIBOSOMAL PROTEIN S6 KINASE (EC 2.7.1.-) (S6K) (P70-S6K) - HOMO SAPIENS (HUMAN), 502 aa.	8.90E-275	17
2049	cg44019155	1363	CACACATCTCCC TCTCCACCTTTT T[gap]GCCCTTA ATTCATTAAAG CATTGC	T	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P23443 RIBOSOMAL PROTEIN S6 KINASE (EC 2.7.1.-) (S6K) (P70-S6K) - HOMO SAPIENS (HUMAN), 502 aa.	8.90E-275	17
2050	cg43241753	1017	CCACAGCCCTTC TCTCTGCTTTTC IC/T]TTTATTCA GCTACCCCATCCA GTGG	C	T			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q16675 PROTEIN-TYROSINE KINASE PRECURSOR - HOMO SAPIENS (HUMAN), 477 aa.	4.20E-268	9

2051	cg43241753	2525	GCTGCACCGGC CGCTTCCCCCA CC[C]gapJGTGCC GGGAGGCCCTTC CCTGCGCTT	C	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q16675 PROTEIN-TYROSINE KINASE PRECURSOR - HOMO SAPIENS (HUMAN), 477 aa.	4.20E-268	9
2052	cg43241753	2530	ACCGGCCGCTTT CCCCACCCGT GC[C]GJGGGAGG CCTTCCCTGCCG TTGCGGC	C	G			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q16675 PROTEIN-TYROSINE KINASE PRECURSOR - HOMO SAPIENS (HUMAN), 477 aa.	4.20E-268	9
2053	cg43947749	1615	CTTCCATCTGGG AGCCCCAAGAG GG[G]CJCTGGGA AGGGGGGCCAT AGCCCATC	G	C			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.60E-267	19
2054	cg43947749	1616	TTCCATCTGGGA GCCCCAAGAGG GG[C]GJTGGA GGGGGGCCATA GCCCATCA	C	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.60E-267	19
2055	cg43947749	2070	AGGTCTACTCCC TCCTCACCCAC C[C]gapJTGAGG GCCAGGGGAGT GGAGAGAG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.60E-267	19
2056	cg43932396	923	CCCAATGCCACA TTGGGCATAGCT G[C]TJAGAAGTCC TTAACATTTCCT ACGT	C	T			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P31749 RAC-ALPHA SERINE/THREONINE KINASE (EC 2.7.1.-) (RAC-PK-ALPHA) (PROTEIN KINASE B) (PKB) (C-AKT) - HOMO SAPIENS (HUMAN), 480 aa.	1.40E-262 (14q32.3)	14

2057	cg43932396	409	ACAGGGAGTCA GGGAGGGCCTG GGG[C/gap]GACA GCGGAAAGGTTA AGCGTCGAA	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P31749 RAC-ALPHA SERINE/THREONINE KINASE (EC 2.7.1.-) (RAC-PK-ALPHA) (PROTEIN KINASE B) (PKB) (C-AKT) - HOMO SAPIENS (HUMAN), 480 aa.	1.40E-262	14 (14q32.3)
2058	cg43932396	480	AGAGATCATCTG AGGGGAGGCT CC[C/gap]GGTGG GACAGTCACCAA GAACTGTG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P31749 RAC-ALPHA SERINE/THREONINE KINASE (EC 2.7.1.-) (RAC-PK-ALPHA) (PROTEIN KINASE B) (PKB) (C-AKT) - HOMO SAPIENS (HUMAN), 480 aa.	1.40E-262	14 (14q32.3)
2059	cg43957447	2146	ATGTTGTCATTG ATATAAACCTGT T[gap/T]GGTTCA GCAAACAACTA AAATGAT	gap	T			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49336 CELL DIVISION PROTEIN KINASE 8 (EC 2.7.1.-) (PROTEIN KINASE K35) - HOMO SAPIENS (HUMAN), 464 aa.	1.80E-260	
2060	cg43930359	1473	GCATGAGGAGAT GGAGGCGGGA CT[G/gap]GGCCG CCCAGCCCCCTG ACTCCAGC	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P49761 PROTEIN KINASE CLK3 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 490 aa. [pcis:SWISSPROT-ID:P49761 PROTEIN KINASE CLK3 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 490 aa.	4E-255	
2061	cg43930359	1511	CCTTGACTCCAG CCTCGACCGCCA G[G/gap]CCCCAG GCCAGAGCCAC CCAATGAA	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P49761 PROTEIN KINASE CLK3 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 490 aa. [pcis:SWISSPROT-ID:P49761 PROTEIN KINASE CLK3 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 490 aa.	4E-255	
2062	cg43965549	1595	CCATGTTTGCTC TAAATTAAAGACA G[gap/G]CATTGA TCTCCTGGAGGC TGGTTCT	gap	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.3E-253	10 (10p11.2)

2063	cg43985549	1803	CAGGTGACGTGAA TTCTAAGGCAGG A[<i>gap</i>]TTTGAG AGTTCACAGAAG GATCGTG	<i>gap</i>			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.3E-253	10 (10p11.2)
2064	cg43985549	2199	AAACATTTTATAC TGACATGCTAT[G/ <i>gap</i>]CTGAAGA CATTCAAAACGT GATGTT	<i>gap</i>			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.3E-253	10 (10p11.2)
2065	cg43985549	2282	ATTTTGTACATC CCAAAGGATGAG [A/C]ATGTGACCT TTAAGAAAAATG AAAA	C			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)
2066	cg43985549	2283	TTTTGTACATCCA CAAAGGATGAGA [A/C]TGTGACCTT TAAGAAAAATGA AAAC	C			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)
2067	cg43985549	2286	TGTACATCCCAA AGGATGAGAATG T[<i>gap</i>]TGACCTTT AAGAAAAATGAA AACTTT	T			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)

2068	cg43985549	2485	AGTAGTCTTATG TAAAGTATGTTTT T/gapJACATTATG CAAATAAAACCC AATAC	T	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253 (10p11.2)	10
2069	cg43926820	475	TCTCAGCATGAA CTCCTGAGTGAA G/C/GJCTCTCCTC AGCGTGACTCAG GAACA	C	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P51956 SERINE/THREONINE-PROTEIN KINASE NEK3 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 3) (HSPK 36) - HOMO SAPIENS (HUMAN), 459 aa (fragment)	1.40E-251	13
2070	cg43328922	119	CTGGCACCTCTG GAGAGGGCAGA GC/C/gapJTCCTC AGAAGAGCTGG CCTGAGGAA	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P23677 1D-MYO-INOSITOL-TRISPHOSPHATE 3 KINASE A (EC 2.7.1.127) (INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE) (IP3K) (IP3 3-KINASE) - HOMO SAPIENS (HUMAN), 461 aa.	1.30E-250 (15q14)	15
2071	cg43292279	1658	CCGAGCCTGAAC TGAGCCCCAGC GG/C/gapJCTGGC GGGCCTTTTCC TGCCTCCC	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41240 TYROSINE-PROTEIN KINASE CSK (EC 2.7.1.112) (C-SRC KINASE) (PROTEIN- TYROSINE KINASE CYL) - HOMO SAPIENS (HUMAN), 450 aa.	8.40E-247	15
2072	cg43292279	1985	CTGTCCTGCCCG TGAGGGTGGGG GG/C/gapJACCGG GCCCTCTCTAG GGACCCCT	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41240 TYROSINE-PROTEIN KINASE CSK (EC 2.7.1.112) (C-SRC KINASE) (PROTEIN- TYROSINE KINASE CYL) - HOMO SAPIENS (HUMAN), 450 aa.	8.40E-247	15
2073	cg43292279	2181	GCCCACCCGCC TTGTGAGATGGA AT/C/TGTAATAA ACCACGCCATGA GGACAC	C	T			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41240 TYROSINE-PROTEIN KINASE CSK (EC 2.7.1.112) (C-SRC KINASE) (PROTEIN- TYROSINE KINASE CYL) - HOMO SAPIENS (HUMAN), 450 aa.	8.40E-247	15

2074	cg43292279	2214	ACCACGCCATGA GGACACCGCCG CC[C/gap]GCCTC GGCGCTTCCTCC ACCGAAAA	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P41240 TYROSINE-PROTEIN KINASE CSK (EC 2.7.1.112) (C-SRC KINASE) (PROTEIN- TYROSINE KINASE CYL) - HOMO SAPIENS (HUMAN), 450 aa.	8.40E-247	15
2075	cg43928793	1815	TTCTGTGCCGAC CAGCCCCCAGG AC[C/gap]TCCGG AGCGCCCTGCA GGGCCGGGC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:Q15831 SERINE/THREONINE-PROTEIN KINASE 11 (SERINE/THREONINE- PROTEIN KINASE LKB1) - HOMO SAPIENS (HUMAN), 433 aa. pcds:SWISSPROT-ID:Q15831 SERINE/THREONINE-PROTEIN KINASE 11 (SERINE/THREONINE- PROTEIN KINASE LKB1) - HOMO SAPIENS (HUMAN), 433 aa. pcds:SPTREMBL-ID:Q15831 SERINE/THREONINE PROTEIN KINASE - HOMO SAPIENS (HUMAN), 433 aa. pcds:TREMBLNEW-ID:G2754827 SERINE THREONINE KINASE 11 - HOMO SAPIENS (HUMAN), 433 aa.	4.70E-237	
2076	cg43069976	120	GGTCCCTGGAG CTCCGCACCTGG CG[G/gap]CGCAA CCTGCGTGAGG CAGCGCGAC	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa. pcds:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1

2077	cg43069976	1592	AAATGCTGTAGT GTTGAATACTTG GTT/CJTCCATGAG CCATGCCCTTTCT GTATA	T	C			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.lpcis:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa	3.00E-235	1
2078	cg43069976	1593	AATGCTGTAGTG TTGAATACTTGG TTT/CJCCATGAGC CATGCCCTTTCTG TATAG	T	C			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.lpcis:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa	3.00E-235	1
2079	cg43069976	1813	TCTAAATCTTGG GAGAAAAAATAA TTG/ATTAGGAAA AAAATATTTATGC AGGA	G	A			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.lpcis:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 2) (NIMA- LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa	3.00E-235	1

2080	cg43957648	211	GAGCAGACACA GTACCTGATCCA AC/A/GCCACAA GGCAAATCTATG GCCATCA	A	G				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2081	cg43957648	413	CCAGGCGTAGCT CATGAGGGCCA CG[C/gap]CGGCG GCTGGAGCCCC CGTGAGCAA	C	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2082	cg43957648	414	CAGGCGTAGCTC ATGAGGGCCAC GC[C/gap]GGCGG CTGGAGCCCCC GTGAGCAAT	C	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2083	cg43957648	418	CGTAGCTCATGA GGCCACGCCG GC[G/T]GCTGGA GCCCCCGTGAG CAATACTG	G	T				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2084	cg43957648	426	ATGAGGGCCAC GCCGGCGGCTG GAG[C/gap]CCCC GTGAGCAATACT GCTGGGCCA	C	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2085	cg43957648	78	AGGCTTTATTG AAAGTGGCAGG GG[C/gap]CTCTC AATGTTCTATGA AAACTAAC	C	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2
2086	cg43957648	79	GGTCTTTATTGA AAGTGGCAGGG GC[C/gap]TCTCA ATGTTCTATGAA AACTAACA	C	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	9.70E-230	2

2087	cg43257603	3364	AACTCCAGGTCT AAACAGCTGACC C[G]gap]AGTGAT GGGGAATTTATC CGTGACC	G	gap		SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2088	cg43257603	3368	CCAGGTCTAAAC AGCTGACCCGA GT[G]gap]ATGGG GAATTTATCCGT GACCAATT	G	gap		SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2089	cg43257603	3384	GACCCGAGTGAT GGGGAATTTATC C[G]TTGACCAAT TTATCCITGACC AATAA	G	T		SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2090	cg43257603	3386	CCCGAGTGATG GGGAAATTTATCC GT[G]TACCAAT TATCCITGACCA ATAACC	G	T		SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2091	cg43257603	3426	GACCAATAACCT AATTGCTATTCC C[G]T]GAGTTATA AAAGTCCCCATC CTTAT	G	T		SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2092	cg43257603	3427	ACCAATAACCTA ATTGCTATTCC GIGT]AGTTATAA AAGTCCCCATCC TTAT	G	T		SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2093	cg43257603	3478	AGCTCTACTGGA ATTTTCATACAC G[G]gap]TAAATG CAGAAAGTTACTA AGTATTA	G	gap		SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)

2094	cg43257603	3627	ATCAAGGTGACT AAGAAATCAGT T[G/C]TGTAATA AAAACAAGCAGC ATAAA	G	C				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	8.10E-224	10 (10q11.2)
2095	cg43984889	1176	TCTAGAAAGTTC TATTAGTCGTGA T[A/C]TCGTCTTG TTTTGCTTTGTAT TTTG	A	C				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q15120 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 3 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 3) - HOMO SAPIENS (HUMAN), 406 aa.[pcis:SPTREMBL-ID:Q15120 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	X
2096	cg43984889	696	CTGGGACTAAAT CATCAGGGCATG G[C/gap]CACCTG ATGTCTTCCACT TTCAGGG	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q15120 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 3 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 3) - HOMO SAPIENS (HUMAN), 406 aa.[pcis:SPTREMBL-ID:Q15120 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	X
2097	cg43984889	697	TGGGACTAAATC ATCAGGGCATGG C[C/gap]ACCTGA TGCTTCCACTT TCAGGGT	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q15120 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 3 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 3) - HOMO SAPIENS (HUMAN), 406 aa.[pcis:SPTREMBL-ID:Q15120 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 406 aa.	9.8E-221	X

2098	cg42508800	132	CATCGCGGACTCT TGCCAGACTCT T[A/C]GAGCCGG GGCACCCTCAAA CCCCAG	A	C			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q16654 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 4 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 4) - HOMO SAPIENS (HUMAN), 411 aa. Jcdls:SPTRMBL-ID:Q16654 PYRUVATE DEHYDROGENASE KINASE ISOFORM 4 - HOMO SAPIENS (HUMAN), 411 aa.	1.6E-220	7 (7q21.3)
2099	cg43947829	389	TCATTCCAACAG CTTTACCAGGCT TTC/GJGCCAACCC CAATAAGTTACA CACTCA	C	G			SILENT- NONCODI NG	kinase	Human Gene TREMBL-NEW- ID:G2978628 AURORA RELATED KINASE 1 - HOMO SAPIENS (HUMAN), 403 aa.	1.5E-217	
2100	cg38438124	1574	GCCTCGGACAG ACATGAACATTG GA/GTTGGACAG AGGTGGCTTCG GTGTAGGA	G	T			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII-ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P-5- KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS.MUSCULUS (MOUSE), 405 aa.	2.8E-216	10
2101	cg43917871	1157	AATCAGCCTATT ATAATTTTTTTTTT T/gapJATGACTGA ACTACTATAAAT CCACA	T	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)
2102	cg43917871	1201	ATCCACAAGCAA CGGTTACAGACAC GIG/TTCCTTCTG AAGTGTTTCACC CCTCC	G	T			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)

2103	cg43917871	1234	GAAGTGTTTCAC CCCTCCCGCCA G[G/gap]CGCAAG CTGCATCAAGGA GAGGGTG	G	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)
2104	cg43917871	1241	TTCACCCCTCCC CGCCAGGCGCA AG[C/gap]TGCAT CAAGGAGAGGG TGGACTCCC	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)
2105	cg43990838	21	TAGATTTTTTTT TTTTTTT[A/T]TG TTGACACAAAT CTTTTATTC	A	T				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q03426 MEVALONATE KINASE (EC 2.7.1.36) (MK) - HOMO SAPIENS (HUMAN), 396 aa.	1.4E-203	12 (12q24)
2106	cg43945404	1579	TAGTAATCATTG GATGCATGATGG G[G/gap]CAGGGC CGGTGATGGTG CCTCCCC	G	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q62922 PROTEIN KINASE C-BINDING PROTEIN ZETA1 - RATTUS NORVEGICUS (RAT), 392 aa (fragment).	2.6E-197	11
2107	cg43945404	1586	CATTGGATGCAT GATGGGCGCAGG GC[C/gap]GGTGA TGGTGCCTCCCC CTTGGCTGG	C	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q62922 PROTEIN KINASE C-BINDING PROTEIN ZETA1 - RATTUS NORVEGICUS (RAT), 392 aa (fragment).	2.6E-197	11
2108	cg43945404	1661	CTTTCACCGCTC ATTATGTAGTCT G[G/gap]CTACAG CCCTCAAAAACA GCTTATA	G	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q62922 PROTEIN KINASE C-BINDING PROTEIN ZETA1 - RATTUS NORVEGICUS (RAT), 392 aa (fragment).	2.6E-197	11
2109	cg43945404	1670	CTCATTATGTAG TCTGGCTACAGC C[C/gap]TCAAAA ACAGCTTATACT CTTAAGA	C	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q62922 PROTEIN KINASE C-BINDING PROTEIN ZETA1 - RATTUS NORVEGICUS (RAT), 392 aa (fragment).	2.6E-197	11

2110	cg43933472	1413	GTGACTAAAGCA ACAGTAAGCAGT A[gap/A]GGTGCA CTGAAGTACATA CTGCCGC	gap	A				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P28482 EXTRACELLULAR SIGNAL- REGULATED KINASE 2 (EC 2.7.1.-) (ERK2) (MITOGEN- ACTIVATED PROTEIN KINASE 2) (MAP KINASE 2) (MAPK 2) (P42-MAPK) (ERT1) - HOMO SAPIENS (HUMAN), 360 aa.	5.4E-197	22
2111	cg43933472	1565	TCCAAACGGCTC AAAGGAGTCAAA G[T/C]GGATAAG CCAAGACGGGC TGGAGAC	T	C				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P28482 EXTRACELLULAR SIGNAL- REGULATED KINASE 2 (EC 2.7.1.-) (ERK2) (MITOGEN- ACTIVATED PROTEIN KINASE 2) (MAP KINASE 2) (MAPK 2) (P42-MAPK) (ERT1) - HOMO SAPIENS (HUMAN), 360 aa.	5.4E-197	22
2112	cg43933472	634	GATGCTGACATG CTGTAGAAGGAA A[A/C]JAGAAATTGT ATACTTTCTCATT TAAA	A	C				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P28482 EXTRACELLULAR SIGNAL- REGULATED KINASE 2 (EC 2.7.1.-) (ERK2) (MITOGEN- ACTIVATED PROTEIN KINASE 2) (MAP KINASE 2) (MAPK 2) (P42-MAPK) (ERT1) - HOMO SAPIENS (HUMAN), 360 aa.	5.4E-197	22
2113	cg42923892	233	CACACATGGGG CTCCCCAGGCAA GG[C/gap]CACCT GCTGACAGAGGT GAAGGCGA	C	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q92961 MAP KINASE KINASE MEK5B - HOMO SAPIENS (HUMAN), 448 aa.	1.8E-196	
2114	cg43929069	149	AATGAACCAAAT TACCCAAACAAA A[T/G]AAACATGG CAATATAAAAAT GTAA	T	G				SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P49759 PROTEIN KINASE CLK1 (EC 2.7.1.-) (CLK) - HOMO SAPIENS (HUMAN), 484 aa. pcis:SWISSPROT-ID:P49759 PROTEIN KINASE CLK1 (EC 2.7.1.-) (CLK) - HOMO SAPIENS (HUMAN), 484 aa.	1.6E-192	
2115	cg44131795	251	CCACAGGAATTA ACGGAAGAAGTG T[A/G]TACAATT TTGAGCTATGCT CTTA	A	G				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW- ID:G2760825 PROTEIN KINASE C- BINDING PROTEIN BETA 15 - RATTUS NORVEGICUS (RAT), 498 aa.	1.1E-191	

2116	cg43917159	2170	CCATAAGCAGAA CAAGAACCAAT C[A/gap]AACGTC TTAACGCGTATA GAGAGAT	A	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.2E-191	16 (16p13.3)
2117	cg43917159	2172	TAAGCAGAACAA GAACCAATCAA A[gap]AICGTCTT AACGCGTATAGA GAGATCA	gap	A				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.2E-191	16 (16p13.3)
2118	cg43917159	2397	TGCAGAAATGTTG TTGGTTACTGTT G[C/gap]TCCCCG AGCCCTCAACT CGTCCCG	C	gap				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.20E-191	16 (16p13.3)
2119	cg43917159	304	AAGCAATTCTAC CTGCCCTGGCCT C[C/T]CAAAGTGC TAGAATTACAGG CATAA	C	T				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.20E-191	16 (16p13.3)
2120	cg43917159	320	CTTGGCCTCCCA AAGTGCTAGAAT TTA/G[CAGGCATA AGCCACCACGC CTGGCC	A	G				SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P19784 CASEIN KINASE II, ALPHA' CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 350 aa.	2.20E-191	16 (16p13.3)
2121	cg42703622	1554	GGAACTTAGTG TGCCTTGGA G[G/gap]CCGCAA GTTGCTTACTCC GAGTAGC	G	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa.	3.00E-187	12
2122	cg44932781	121	AGACCAATGCA GAGAAGCCGGT AG[G/gap]AACCC GAGGCCACGGA GGCTGCTGG	G	gap				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:P78356 PHOSPHATIDYLYNOSITOL-4- PHOSPHATE 5-KINASE TYPE II BETA (EC 2.7.1.68) (1- PHOSPHATIDYLYNOSITOL-4- PHOSPHATE KINASE) (DIPHOSPHOINOSITIDE KINASE) (PTDINS(4)P-5-KINASE) - HOMO SAPIENS (HUMAN), 416 aa.	2.50E-185	17

2123	cg43934426	936	GCACTGGCAGC CTGCTGTGCAGG GGC/AJAGCAGC ATCCACAGGGG GCATCCAG	C	A			SILENT- NONCODI NG	kinase	Human Gene TREMBL-NEW- ID:G1778153 MAP KINASE 3B - HOMO SAPIENS (HUMAN), 347 aa.	3.20E-183	
2124	cg43987006	123	CCATGATTTCAGG GGCACAGCTGC CC[C/gap]AGCAG ACACACACTTTC ATACGCAC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P21425 RIBOSOMAL PROTEIN S6 KINASE I (EC 2.7.1.-) (S6K) (P70-S6K) - RATTUS NORVEGICUS (RAT), AND ORYCTOLAGUS CUNICULUS (RABBIT), 502 aa.	3.10E-176	11
2125	cg43933478	47	TTTTTTTTTTTT TTTTTTTTTTTT[G /TJGAAGAGATT CCTGTCAITTTAA TTA	G	T			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P54619 5'- AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa. pcds:SWISSPROT-ID:P54619 5'- AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	7.80E-173	12
2126	cg44131752	1527	ACATGTTTCAC TTAATACCAGAG A[C/gap]CCCCC CCTTCCCCCTCCC CCTTCCC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	7.80E-173	16
2127	cg44131752	1535	CCACTTAATACC AGAGACCCCCC CC[C/gap]TTCCC CTCCCGCTTCCC CTCCCCCT	C	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	7.80E-173	16
2128	cg44131752	1604	ATTGCAATAAAA CAAACCTTTCTC TIG/TJACAAACA CACCAAAGCTTT ATTCA	G	T			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	7.80E-173	16

2129	cg44000392	245	CTAGACCGATCT CCGGGGAGCCC CG[G/gap]AGTAG GCGAGCGGCGG CCGCCAGCT	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.10E-172	7
2130	cg44000392	265	CCCGGGAGTAG GCGAGCGGCGG CCG[C/gap]CAGC TAGTTGAGCGCA CCCCCGGCC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.1E-172	7
2131	cg44000392	266	CCCGGAGTAGG CGAGCGGCGGC CG[C/gap]AGCT AGTTGAGCGCAC CCCCCGGCC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.1E-172	7
2132	cg44000392	289	GCCAGCTAGTTG AGCGCACCCCG CG[C/G]CCGCC CAGCGCGCCGC GGCGGGCG	C	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.1E-172	7
2133	cg44000392	290	CCAGCTAGTTGA GCGCACCCCGC GC[C/G]CGCCCC AGCGCGCCGCG GCGGGCGC	C	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.1E-172	7
2134	cg43291463	1258	GATCAAGAACAA AAAAAATAGCAG CT[<i>gap</i>]TTTTTT TTCTGTACAGAC GTATAG	T	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q25197 PROTEIN-TYROSINE KINASE - HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS), 1477 aa.	6.5E-172	15 (15q25)

2135	cg43291483	1616	CCTTGACTCCAA GCCTGTCGCCCA G/A/GJCTGCTTC GGGGCCCATGG CCACCAG	A	G				SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q25197 PROTEIN-TYROSINE KINASE - HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS), 1477 aa.	6.5E-172	15 (15q25)
2136	cg43007055	1516	TTTGTTGGAGTG GTGCCAGGTACT G/G/gapJTTTTGG AGAACTTGCTA CAACCAG	G	gap				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2137	cg43007055	1568	GATTGATTTTAAA GATGCTTTTTT T/gapJATTTACT TTTTTTTAAGCAC CAAA	T	gap				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2138	cg43007055	1583	TGTCITTTTTTAT TTTACTTTTTTT /gapJAAGCACCAA ATTTGTTGTTT TTT	T	gap				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2139	cg43007055	1601	TTTTTTTAAGCAC CAAATTTTGTG gap/JTTTTTTTTT TCCTCCCTCCCC ACAG	gap	T				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2140	cg43007055	1611	CACCAAATTTTG TTGTTTTTTTTT gap/JCTCCCTC CCCACAGATCCC ATCTC	gap	T				SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)

2141	cg43007055	1611	CACCAAAATTTTG TTGTTTTTTTTT gap/TCTCCCCTC CCCACAGATCCC ATCTC	gap	T			SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2142	cg43007055	2474	GTCCTTGAGAAAT AAAGGAAAAAAA A[ap/A]TCTTCA GATGCAATGGTT TTGTGTA	gap	A			SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2143	cg43007055	350	GTCCCGCTGCC GCTGTGCGCGCC GC[C/gap]GCTGC TGCTGCTGCTCG CCCCGTCG	C	gap			SILENT- NONCODI NG	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
2144	cg43925513	189	TGAATTATTATT CCTCTCTTCCAT C/gap]AGATGAG GCTTATCGTGTC AAATCC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P51948 CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) - HOMO SAPIENS (HUMAN), 309 aa.lpcis:SWISSPROT- ID:P51948 CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) - HOMO SAPIENS (HUMAN), 309 aa.	1.2E-165	14

2145	cg43925513	346	TGGAAGGACTGT GTTGTGCAGCTG C[A/gap]CATAGC TATAATTTTATAA GTCTGC	A	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P51948 CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) - HOMO SAPIENS (HUMAN), 309 aa. pcids:SWISSPROT- ID:P51948 CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY FACTOR) (P36) (P35) - HOMO SAPIENS (HUMAN), 309 aa.	1.2E-165	14
2146	cg43336176	2028	TGCCCCCTCAGTT GAGTGGGCAGG GC[C/gap]GGGG GTGGTCCAGCC CTCGCCCGGGC	C	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q16205 MYOTONIN PROTEIN KINASE - HOMO SAPIENS (HUMAN), 625 aa.	1.1E-164	19
2147	cg43982923	1494	TCCGACTTCTGT CCGCCCTAGGC CC[C/gap]GGGAC CCCCGGCCTCC AGGCTGGGG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2148	cg43982923	1505	TCCGCCCTAGGC CCCGGGACCCC CG[G/gap]CCTCC AGGCTGGGGCC TGGCCTATT	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19

2149	cg43982923	1519	CGGACCCCG GCCTCCAGGCT GGG[<i>gap</i>]CCTG GCCTATTTAAGC CCCCTCTTG	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2150	cg43982923	1551	CTATTTAAGCCC CCTCTTGAGAGG G[<i>gap</i>]TGAGAC AGTGGGGGTGC CTGGTGCG	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2151	cg43982923	1585	TGGGGGTGCT GGTGGCTGTG CTC[<i>gap</i>]AGCA GTGCTGGGCCC AGCCGGGGTG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2152	cg43982923	1600	CGCTGTGCTCCA GCAGTGCTGGG CC[<i>gap</i>]AGCCG GGGTGGGGTGC CTGAGCCCG	C	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
2153	cg43982923	1605	TGCTCCAGCAGT GCTGGGCCCCAG CC[<i>gap</i>]GGGTGG GGTGCCTGAGC CCGAATTT	G	A			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19

2154	cg43916763	76	ATACTGCGTTCC ATCCCGACCCG GG[G/gap]CCACG GTACTGGGCCCT GTTTCCCC	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSNEW-ID:P24941 CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (P33 PROTEIN KINASE) - HOMO SAPIENS (HUMAN), 298 aa. lpdls:SWISSPROT-ID:P24941 CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (P33 PROTEIN KINASE) - HOMO SAPIENS (HUMAN), 298 aa.	1.2E-158	12 (12q13)
2155	cg43921600	115	CTGGCTCTTGA AATTGAGCGGAG A[G/gap]CGACGC GGTTGTTGTAGC TGCCGTG	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT-ID:P06493 CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1) - HOMO SAPIENS (HUMAN), 297 aa.	2.6E-158	10 (10q21.1)
2156	cg43933460	98	GACGGTTTCTGA GCGTTGGCCTTT G[G/gap]CACGCG CTACCCCTTTT GCTTGG	G	gap			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL-ID:Q63185 EUKARYOTIC INITIATION FACTOR 2A PROTEIN KINASE - RATTUS NORVEGICUS (RAT), 620 aa.	2.3E-155	7
2157	cg43257282	1399	CCCCAGAAAAAG GCCGGGTGACA CC[G/gap]GGGG GCTCCAGCCC GTGCACCCTG	G	gap			SILENT- NONCODI NG	kinase	Human Gene Homologous to SPTREMBL-ID:Q15130 CDC2-RELATED KINASE - HOMO SAPIENS (HUMAN), 316 aa.	2.9E-147	16
2158	cg43958362	161	TTTTGAAAAGTC ACAAAAAAGGT A[C/gap]CCCCAA ACTCAGGTATAC CAAGTAA	C	gap			SILENT- NONCODI NG	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP- ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.1E-147	12
2159	cg43958362	2286	CCCGGAACCGC GGTCCCAAGG AGC[C/gap]TGCG GAAGGAGTCGG AGCACCAGGA	C	gap			SILENT- NONCODI NG	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP- ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.1E-147	12

2160	cg43958362	322	CTCCCGGGAAC TGAGCTGCGTAT A/A/CJAGAAGTCT GCTTTGGTCCAA AGGAC	A	C				SILENT- NONCODI NG	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP- ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.1E-147	12
2161	cg43958362	716	TCTAGACGTGGT GACTTAAAAAAT G[G/gap]CCTTAA GGCTGCAGAGC CAGCCACC	G	gap				SILENT- NONCODI NG	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP- ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.1E-147	12
2162	cg44016530	214	CATGTTTTTTTT TTTTTTTGTGTTT /A/TAGAGTTTTT AACATAAAAGTTTT A	T	A				SILENT- NONCODI NG	kinase	Human Gene Homologous to SPTREMBL-ID:Q92631 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 240 aa (fragment).	1.70E-129	12
2163	cg43265203	982	CAACATCACTGG AAGAAATACCTA T[C/T]GTTAAACC CTGATATACATT CTTAA	C	T				SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP- ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa. pcis:SWISSPROT-ID:P54619 5'- AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	5.50E-124	
2164	cg43265203	54	GGATTATTTTAA TTTTTCAATCTG A/gap]AAAAA AAACCCAAACA AAAA	A	gap				SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP- ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa. pcis:SWISSPROT-ID:P54619 5'- AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	5.50E-124	

2165	cg432865203	65	AATTTTCAATCT GAAAAAAAAAAAAA A/gap]CCCCAAAC AAAAAAAAAACAA ACTAT	gap			SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP- ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.lpcis:SWISSPROT-ID:P54619 5'- AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	5.50E-124	
2166	cg432865203	73	ATCTGAAAAAA AAAAACCCAAAA C/gap/A]AAAAAA AAACAAAGTATC CTCATAT	gap	A		SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSNEW-ID:P54619 5'-AMP- ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.lpcis:SWISSPROT-ID:P54619 5'- AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA CHAIN) - HOMO SAPIENS (HUMAN), 331 aa.	5.50E-124	
2167	cg42866488	1761	AGTCGCTCTCAT GAAGCCCTTAGG G/gap/G]AGAGCA CCTGTTGTGTGC CTGACAC	gap	G		SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.lpcis:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16
2168	cg42866488	2085	TGGGGAGAGCT GGCAGTGTGCG GAC/gap]GCTGA TAACATTTCCC AATATTGA	C	gap		SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.lpcis:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16

2169	cg42866488	2449	TGGAATTACTGA AAGTCTGTGGCC Cgap/TJAAGAGA GAGACACAAGTG GCCTTAA	gap	T			SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.lpcis:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16
2170	cg42866488	2691	TTTGCAATAAAA GGCTCTGGAAG CA/ATJAAAAAAA AAAAAAAAAAAAA AA	A	T			SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.lpcis:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16
2171	cg42866488	2692	TTGCAATAAAG GCTCTGGAAGCA A/ATJAAAAAAA AAAAAAAAAAAAA	A	T			SILENT- NONCODI NG	kinase	Human Gene Homologous to SWISSPROT-ID:O00142 THYMIDINE KINASE 2, MITOCHONDRIAL (EC 2.7.1.21) - HOMO SAPIENS (HUMAN), 234 aa.lpcis:SPTREMBL-ID:O00142 THYMIDINE KINASE 2 - HOMO SAPIENS (HUMAN), 234 aa.	4.50E-122	16
2172	cg42925992	133	GGAGGGAGGCG GGGGGCACCTG GG[C/gap]CCGC CATGAACCCCGG CTTCGATT	C	gap			SILENT- NONCODI NG	kinase	Human Gene Homologous to SPTREMBL-ID:Q12851 GC KINASE - HOMO SAPIENS (HUMAN), 819 aa.	5.10E-105	
2173	cg43918705	1032	CTCACCAACGA AGGGTATCAGCT AT/gap/JTTTTTT TTAAATTCAAAA GAATA	T	gap			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.lpcis:SPTREMBL ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1

2174	cg43918705	1152	CAACATTTTAGG ATTAGGGATAC CTTCGCTTCCTC TTTTCTTGCAA GTTTT	T	C			SILENT- NONCODI NG	Kinase	Human Gene Similar to SWISSPROT- ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.lpcis:SPTREMBL ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1
2175	cg43918705	1728	ATCTAGTTAAATT TCCCATTTGTAT TAJTATTTTCTT GAATACITTTTTC AT	T	A			SILENT- NONCODI NG	Kinase	Human Gene Similar to SWISSPROT- ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.lpcis:SPTREMBL ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1
2176	cg43918705	2392	AGGCCAGCAAAT ACAGAGGTGGTT TIG/AJATCAAAACA GCTCTAGTATGA AGCAA	G	A			SILENT- NONCODI NG	Kinase	Human Gene Similar to SWISSPROT- ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.lpcis:SPTREMBL ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1

2177	cg43918705	2839	ATTGAGTGATGT TGATGTATATC AAGJTTATTTAG TAAATAATCTCAA TAAA	A	G			SILENT- NONCODI NG	Kinase	Human Gene Similar to SWISSPROT- ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.[pcis:SPTREMBL ID:Q29561 UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE) - SUS SCROFA (PIG), 196 aa.	2.40E-100	1
2178	cg43965859	147	GCTGCGCTCAG GCCAGGAGGAC CTCTTGJAATCAG GACGGGGTGGG GCGGGGCT	T	G			SILENT- NONCODI NG	Kinase	Human Gene Similar to SWISSPROT- ID:P00568 ADENYLATE KINASE ISOENZYME 1 (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE) (AK1) (MYOKINASE) - HOMO SAPIENS (HUMAN), 194 aa.	2.40E-98 (9q34.1)	9
2179	cg43965859	73	TTTAGTGCTCAG CTGTCCATGAAA A/C/AJAGGATAAG CGGCTTCCTCCG TCTGT	C	A			SILENT- NONCODI NG	Kinase	Human Gene Similar to SWISSPROT- ID:P00568 ADENYLATE KINASE ISOENZYME 1 (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE) (AK1) (MYOKINASE) - HOMO SAPIENS (HUMAN), 194 aa.	2.40E-98 (9q34.1)	9
2180	cg43952004	165	GGGAGTCTTGA GGCTGAGTGCG TA[gap/G]CTTCA AATCCAGCACTA ATTCTCTCA	gap	G			SILENT- NONCODI NG	Kinase	Human Gene Similar to TREMBLNEW- ID:E1263921 KINASE-BINDING PROTEIN 1 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 645 aa.	6.30E-94	14
2181	cg43952004	229	GGTCTTCATAGA TTGGTGGCTTGA G[C/gap]CCTGCA ATTAATTATAATC CCTTGC	C	gap			SILENT- NONCODI NG	kinase	Human Gene Similar to TREMBLNEW- ID:E1263921 KINASE-BINDING PROTEIN 1 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 645 aa.	6.30E-94	14
2182	cg43952004	231	TCTTCATAGATT GGTGGCTTGAG CC[C/gap]TGCAA TTAATTATAATCC CTTGCCC	C	gap			SILENT- NONCODI NG	kinase	Human Gene Similar to TREMBLNEW- ID:E1263921 KINASE-BINDING PROTEIN 1 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 645 aa.	6.30E-94	14

2183	cg43970923	1814	CCCAGCTATCCC CGCTCTGACCTT Ggap/GJATTTTC ATTCTTATGTTT TCTCTT	gap	G			SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:P97841 GUANYLATE KINASE ASSOCIATED PROTEIN - RATTUS NORVEGICUS (RAT), 666 aa.	1.40E-92	
2184	cg44924345	157	TTTTGTCGTTCC AAAGTACAAAA Ggap/AJAAAAA AAATCAAAGGCA TTTCATC	gap	A			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:P52623 URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) - MUS MUSCULUS (MOUSE), 260 aa (fragment).	7.10E-92	1
2185	cg44924345	166	TCCAAAGTACAA AAAGAAAAA Agap/AITCAAAG GCATTTTCATCTC CATGGTG	gap	A			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:P52623 URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) - MUS MUSCULUS (MOUSE), 260 aa (fragment).	7.10E-92	1
2186	cg43966625	652	CACAGCGGCGG GGAGCGGCGG TGGAG/GGGGG CGGTGCTGGGC CCAGGGCCG	A	G			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa. pcis:SPTREMBL-ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407 aa.	3.20E-89	17
2187	cg43286014	219	ACGTGGAGGATCA ACTCGGTGGATA AATTTAAGGATA AGTTGAGCGAG GGCGG	A	T			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:P23919 THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE) - HOMO SAPIENS (HUMAN), 212 aa.	1.00E-87	
2188	cg43983647	440	AAATTCCTTCTCTC TCTCTGAACTG C/TTGACTTTCAA AAATTCACAGAA TGA	C	T			SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q62920 PROTEIN KINASE C- BINDING PROTEIN ENIGMA - RATTUS NORVEGICUS (RAT), 520 aa (fragment).	1.10E-86	4

2189	cg43919577	1088	ACAAGCAGTGCA CAGTGGCCGG CA[G/gap]GTACT TAAGTACCTTAT CCTAATCC	G	gap			SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q63835 PHOSPHATIDYLINOSITOL 4- KINASE - RATTUS NORVEGICUS (RAT), 697 aa.	4.60E-81	10
2190	cg43919577	1089	CAAGCAGTGCAC AGTGGCCGGC AG[G/gap]TACTT AAGTACCTTATC CTAATCCT	G	gap			SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q63835 PHOSPHATIDYLINOSITOL 4- KINASE - RATTUS NORVEGICUS (RAT), 697 aa.	4.60E-81	10
2191	cg43919577	117	GACCTTACATTTA CAAGTAGAAACAT A/GCATGTGTTA TCTGTGGGTAAG GTAG	A	G			SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q63835 PHOSPHATIDYLINOSITOL 4- KINASE - RATTUS NORVEGICUS (RAT), 697 aa.	4.60E-81	10
2192	cg43919577	416	TTAAGAACAGCA TTCCTTTTGGAC A/GA/TATGTGAT AGACCCCAATTTT TAATA	G	A			SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q63835 PHOSPHATIDYLINOSITOL 4- KINASE - RATTUS NORVEGICUS (RAT), 697 aa.	4.60E-81	10
2193	cg43971367	2030	GAGCGGCAGGA GAACGCTCTGGAG GC[G/gap]GCACT GTTGCCGATCCG GGTCTGGA	G	gap			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:P54352 ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 517 aa.	1.60E-75	
2194	cg43980968	1675	CCCAGTGCCACAC AGGTGCGCAGGA GC[G/gap]TGTC AGGACTCTGCA TTGCTGCC	C	gap			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:P27515 URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 501 aa.	9.50E-75	

2195	cg43984445	247	AGGAGGCCAG ATCACAGCCTGA ACIATTCATGGT ATTGGTTACAGA TTCCTT	A	T				SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:Q16854 DEOXYGUANOSINE KINASE PRECURSOR (EC 2.7.1.113) (DGUOK) - HOMO SAPIENS (HUMAN), 277 aa. lpcis:SPTRMBL-ID:Q16854 DEOXYGUANOSINE KINASE (EC 2.7.1.113) - HOMO SAPIENS (HUMAN), 277 aa.	8.70E-73	2
2196	cg43246312	890	CGTGAATGGCCA GAGCTACTCTTC AIACTTGTCTGAA CAATGTCAAAAA GAATT	A	C				SILENT- NONCODI NG	kinase	Human Gene Similar to SPTRMBL- ID:Q90269 INTRACELLULAR TYROSINE KINASE DOMAINS OF PLATELET-DERIVED GROWTH FACTOR RECEPTOR SUBTYPE ALPHA - BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO), 457 aa (fragment).	4.20E-62	11
2197	cg43246312	839	TGACACTTGCT GAACAAATCTTT AIACTAAGTCAGA ACTTCTGATGGA TTAAA	A	C				SILENT- NONCODI NG	kinase	Human Gene Similar to SPTRMBL- ID:Q90269 INTRACELLULAR TYROSINE KINASE DOMAINS OF PLATELET-DERIVED GROWTH FACTOR RECEPTOR SUBTYPE ALPHA - BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO), 457 aa (fragment).	4.20E-62	11
2198	cg43988142	201	GCCCCGTGACCCA GCCCCCTTAAGC C[A/G]GCCAGGC AGGGTCCCCCG ACACCGCT	A	G				SILENT- NONCODI NG	kinase	Human Gene Similar to SPTRMBL- ID:O09132 A6 PROTEIN TYROSINE KINASE HOMOLOG - MUS MUSCULUS (MOUSE), 350 aa.	3.00E-61	3
2199	cg43988142	386	GTGGCAGGGAG CGGAAGGTGGG CAG[C/gap]CCCA CAGTCCACACGT GGCCGGGCC	C	gap				SILENT- NONCODI NG	kinase	Human Gene Similar to SPTRMBL- ID:O09132 A6 PROTEIN TYROSINE KINASE HOMOLOG - MUS MUSCULUS (MOUSE), 350 aa.	3.00E-61	3

2200	cg43918784	361	AAACGGGTAAC T GTACCTGTTAAA T[C]ATCCTGGTT GGCAACTTTTAA AATCT	C	A				SILENT- NONCODI NG	Kinase	Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	1.80E-57	7
2201	cg43918784	508	TCCATAAATAATA TTAACATTTTCA[AGJGTAGAAAT CTTGAAGTTCTA AAGG	A	G				SILENT- NONCODI NG	Kinase	Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	1.80E-57	7
2202	cg43918784	706	AACCTCTCGGTT ACAATGGATTCC T[C]TGGTTTCTG ATTGTGGGTAT CCGAA	C	T				SILENT- NONCODI NG	Kinase	Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	1.80E-57	7
2203	cg43979971	1998	TAAAAAATAATT TTTTAAACCTTA[A/CJAACACTACG AGATCTGATTTA TTCT	A	C				SILENT- NONCODI NG	Kinase	Human Gene Similar to SPTREMBL- ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	2.80E-56	2
2204	cg43979971	285	GCCGCGACAGC AGCGCCGGCCCC CGG[ap]CJAGCT CCGCGGGCCCC GGCCCCGGGCC	gap	C				SILENT- NONCODI NG	Kinase	Human Gene Similar to SPTREMBL- ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	2.80E-56	2
2205	cg43979971	321	GCCCCGGCCCC GGCCCCGGCCCC CGG[C]gap]CCCCG GCGGCACAGGC TGTCGGCTGG	C	gap				SILENT- NONCODI NG	Kinase	Human Gene Similar to SPTREMBL- ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	2.80E-56	2
2206	cg43979971	324	CCGGCCCCGGC CCCGCCCCCGG CCC[C]gap]GGCG GCACAGGCTGTC GGCTGGCCCC	C	gap				SILENT- NONCODI NG	Kinase	Human Gene Similar to SPTREMBL- ID:Q15522 STE20-LIKE KINASE - HOMO SAPIENS (HUMAN), 426 aa.	2.80E-56	2

2207	cg43928048	1310	CTAAACTATATAT GTATTTTTCCTCA T/CJAGGAAAGCA CAAGGAGAAGAC AGAA	T	C				SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT- ID:P20505 30 KD PROTEIN KINASE HOMOLOG (EC 2.7.1.-) (PROTEIN B1) - VACCINIA VIRUS (STRAIN COPENHAGEN), 300 aa.	5.30E-55	
2208	cg43105476	234	AGATGTTGCTTA AATATATTCATAA [G/A]CCTGTTGTA AGATTTTCACTTA TGC	G	A				SILENT- NONCODI NG	kinase inhibitor	Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
2209	cg42714770	146	GTCATGAAGTCG ACAGCTTCCGGA G[G/gap]CTGCCGA GGCTCGCAAGAA ATGCCCA	G	gap				SILENT- NONCODI NG	kinase inhibitor	Human Gene Similar to SWISSPROT- ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P18- INK4) (P18-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 158 aa.	1.40E-79	9 (9p21)
2210	cg42714770	317	GACATTTACGGT AGTGGGGGAAG GCIA/TTTATATCT ACGTTAAAAGGC AGGACA	A	T				SILENT- NONCODI NG	kinase inhibitor	Human Gene Similar to SWISSPROT- ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P18- INK4) (P18-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 158 aa.	1.40E-79	9 (9p21)
2211	cg42714770	450	TCGGTGACTGAT GATCTAAGTTTC C[G/C]GAGGTTT CTCAGAGCCTCT CTGGTT	G	C				SILENT- NONCODI NG	kinase inhibitor	Human Gene Similar to SWISSPROT- ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P18- INK4) (P18-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 158 aa.	1.40E-79	9 (9p21)
2212	cg42714770	454	TGACTGATGATC TAAGTTTCCGGA G[G/gap]TTTCTC AGAGCCTCTCTG GTTCTTT	G	gap				SILENT- NONCODI NG	kinase inhibitor	Human Gene Similar to SWISSPROT- ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P18- INK4) (P18-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 158 aa.	1.40E-79	9 (9p21)

2213	cg42714751	61	AGATGGGCAGG GGCGGGTGGT GGG[G/T]CCCAG TCTGCAGTTAAG GGGGCAGG	G	T			SILENT- NONCODING	kinasereceptor	Human Gene Similar to SWISSPROT-ID:P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 156 aa.	2.60E+03	9 (9p21)
2214	cg44021336	191	ACACACCTGTGG GGCAGCTGAAC A[G/A]AAAGAAG GATGCCCAGGAT AGCTAT	G	A			SILENT- NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:P35590 TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1138 aa.[pcis:SWISSPROT-ID:P35590 TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1138 aa.	0.00E+00	1
2215	cg43241731	301	GAATCTGCGCCC CAGAGAGTCCC GG[G/gap]AGCGC CGCCGGTCCGT GCCCGGCGC	G	gap			SILENT- NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:Q16620 BDNF / NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKB TYROSINE KINASE) (GP145-TRKB) (TRK-B) - HOMO SAPIENS (HUMAN), 822 aa.	0.00E+00	9
2216	cg43917080	209	GATACACCGGGT GTGGGATTACCA A[A/C]TAGGACCA ACAATGTGTGCG GGGCA	A	C			SILENT- NONCODING	kinasereceptor	Human Gene SPTREMBL-ID:Q01974 PROTEIN-TYROSINE KINASE TRANSMEMBRANE RECEPTOR ROR2 PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 943 aa.	0.00E+00	9
2217	cg43917080	232	AAATAGGACCAA CAATGTGTGCGG G[G/gap]CACAGA CGGCTGCCTGT GGGCTCTGT	G	gap			SILENT- NONCODING	kinasereceptor	Human Gene SPTREMBL-ID:Q01974 PROTEIN-TYROSINE KINASE TRANSMEMBRANE RECEPTOR ROR2 PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 943 aa.	0.00E+00	9
2218	cg44021449	336	CACACAGTAGCT GTTAGCCACACAG G[C/gap]AGAGGG CATCGGGGCCAT TTGGCCG	C	gap			SILENT- NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:Q06418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	15

2219	cg44021449	3359	GGCAGAGGGCA TCGGGGCCATTT GGC/gap/CGGCT CTGGTGGCCACT GAGCTGGC	C	gap			SILENT- NONCODING NG	kinaserec eptor	Human Gene SWISSPROT-ID:Q06418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	15
2220	cg44021449	4345	CTGTTAGGGACA TTTCCAAGCTGT TAAAGTTGCTGT TTAAATAGAAAT AAAA	A	G			SILENT- NONCODING NG	kinaserec eptor	Human Gene SWISSPROT-ID:Q06418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	15
2221	cg43322545	2984	GGGGAAACTCC ACCTCCCACCTT TTC/TCCACCCCA CGCCTTATCCCC ACTTG	C	T			SILENT- NONCODING NG	kinaserec eptor	Human Gene SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa. lpcis:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0.00E+00 (19q13.1)	19
2222	cg44024023	641	CCTGCTCCAGG GATGCTGGGAC GTG/gap/GJCGGT GCCTGCTAAGTG CTCAGCTGT	gap	G			SILENT- NONCODING NG	kinaserec eptor	Human Gene SWISSPROT-ID:P29317 EPHRIIN TYPE-A RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ECK) (EPITHELIAL CELL KINASE) - HOMO SAPIENS (HUMAN), 976 aa.	0.00E+00	
2223	cg44024023	869	GTGCTGCTAAG TGCTCAGCTGTG TIG/gap/CGTCTC GCAGGGAAAGA GGGCCCAAG	G	gap			SILENT- NONCODING NG	kinaserec eptor	Human Gene SWISSPROT-ID:P29317 EPHRIIN TYPE-A RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ECK) (EPITHELIAL CELL KINASE) - HOMO SAPIENS (HUMAN), 976 aa.	0.00E+00	

2224	cg44025829	1915	AGGAAGATTGA CGTGTGTCAT T[G/T]TCCAGCTG GGACCTAATGCT GGCCT	G	T			SILENT- NONCODING	Kinaserec eptor	Human Gene SWISSPROT-ID:Q04771 ACTIVIN RECEPTOR TYPE I PRECURSOR (EC 2.7.1.-) (ACTR-I) (SERINE/THREONINE-PROTEIN KINASE RECEPTOR R1) (SKR1) (ACTIVIN RECEPTOR-LIKE KINASE 2) (ALK-2) (TGF-B SUPERFAMILY RECEPTOR TYPE I) (TSR-I) - HOMO SAPIENS (HUMAN), 509 aa.	7.90E-283	2
2225	cg43263845	277	GAAGACCCAGG GAACCTGGATATC TA[G/T]CGAGAAC TTCCTCCGGATT CCCCGG	G	T			SILENT- NONCODING	Kinaserec eptor	Human Gene TREMBLNEW-ID:G247985 ACTIVIN RECEPTOR, ACTRIIB=TRANSMEMBRANE PROTEIN SERINE KINASE - XENOPUS LAEVIS, 510 aa.	3.30E-204	2
2226	cg43954819	1423	GTGAGCATCCTG GCAGGTGCCCC AG[G/T]ATGCCAC GCCTGGAAGGG CCGGCTT	G	T			SILENT- NONCODING	Kinaserec eptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH- RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2227	cg43954819	1573	GTCTCACTCGTT CTGTTACCCAGG G[C/gap]TCTGCA GCACCTCACCTG AGACCTC	C	gap			SILENT- NONCODING	Kinaserec eptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH- RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2228	cg43954819	1808	CTGGGAAAGG GCTGGCTGCAAT TG[C/gap]AGCTC ACTGCTGCTGCC TCTGAAAC	C	gap			SILENT- NONCODING	Kinaserec eptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH- RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2229	cg43954819	2785	TGCAAAAATAAC CAAGTCCTCCGA A[G/gap]GCATCT CACGGAACCGTA GACTAGG	G	gap			SILENT- NONCODING	Kinaserec eptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH- RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13

2230	cg43954819	2796	GCAAAATAACC AAGTCCTCCGAA G[gap]CATCTC ACGGAACCGTAG ACTAGGA	G	gap			SILENT- NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2231	cg43954819	46	CGGAAGCGCG GAGCTGGGAGT GGC[A/T]CAGCC ATGGCTGTGAGA AGGGACTC	A	T			SILENT- NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2232	cg43954819	48	GAAGCGCGGA GCTGGGAGTGG CAC[A/C]GCCAT GGCTGTGAGAA GGGACTCCG	A	C			SILENT- NONCODING	kinasereceptor	Human Gene SWISSPROT-ID:P52799 EPHRIN-B2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5) (LERK-5) (HTK LIGAND) (HTK-L) - HOMO SAPIENS (HUMAN), 333 aa.	2.60E-181	13
2233	cg43989555	1630	AGGCCAGCTG CCTGGGCTGG GGC[C/gap]TGGG GAGGGGAAGCC CACCCACAAT	C	gap			SILENT- NONCODING	kinasereceptor	Human Gene Similar to SWISSPROT-ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 - HOMO SAPIENS (HUMAN), 822 aa. pcis:SPTRMBL-ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE - HOMO SAPIENS (HUMAN), 822 aa.	1.20E-99	11
2234	cg43980494	897	CTCACAAGTCCC TGGGAAGACAG GG[C/T]ATGGGC TTACAGAGAGGA GAGGGGG	C	T			SILENT- NONCODING	kinesin	Human Gene SPTRMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2235	cg43980494	1446	TGGTCCGAAATA TAAGCCGAGCTC A[G/T]CATCTTGC CACACACGTGAC ATGGC	G	T			SILENT- NONCODING	kinesin	Human Gene SPTRMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16

2236	cg43980494	376	GGGGACACAGG AACACGATGACA TG[G/gap]CCAGG GCCACAACCTCT TCTGTCGT	G	gap			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2237	cg43980494	383	CAGGAACACGAT GACATGGCCAG GG[C/gap]CACAA CTTCTTCTGTCG TGGGGAAG	C	gap			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2238	cg43980494	384	AGGAACACGATG ACATGGCCAGG GC[C/gap]ACAAC TTCCTCTGTCGT GGGGAAGA	C	gap			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2239	cg43980494	481	AGGGGGACACT GGCTGCATTCCC CC[G/C]CCCCCA GGAAGCACCTCT AGGCCCT	G	C			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2240	cg43980494	489	ACTGGCTGCATT CCCCCGCCCCC AG[G/gap]AAGCA CCTCTAGGCCCT GGACCCCT	G	gap			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2241	cg43980494	515	AAGCACCTCTAG GCCCTGGACCC CT[C/G]GCTCAC CCTGGCCCTAA GACTCCA	C	G			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2242	cg43980494	559	GACTCCATCTCT TCTCTGCCCTCTG G[C/gap]CCTCCT GGCTCTTCCTCC TGCTCCC	C	gap			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16

2243	cg43980494	648	GTTCAGGGCCTG ACCCCAACCCCC C[gap]/G[ATACCA CCTTATGAAGGT ACAACCT	gap	G			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2244	cg43980494	768	TCCTTCCTCTCC TCCCTCCCCCTG G[A/gap]AAAAA AAAAAAAGGAAA AGAAAGC	A gap	gap			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2245	cg43980494	781	CCTCCCCCTGGA AAAAAAGGAAA A[gap]/A]GGAAA GAAAGCACCAAC TCCCCGG	gap	A			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0.00E+00	16
2246	cg43925424	232	GCGGGCGGTA GCTCCGGCGCC CCTC/A]GCTGGT GACTGCTGCGC	C	A			SILENT- NONCODI NG	kinesin	Human Gene SWISSPROT-ID:Q07866 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa.	1.90E-304	14
2247	cg43987378	2380	CGTGCCCTC TTTTTTTAAATA AAGGTTTTATTAT G/C]CATTGCCC AAGAAGGCAGAT ACTT	G	C			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL-ID:Q14834 KINESIN-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 519 aa (fragment).	1.50E-254	6
2248	cg43088603	1956	AAAATCCATTTC AAATTTATTGATG IG/C]ATTCATGTT GTTCTTCITTTAT TTT	G	C			SILENT- NONCODI NG	kinesin	Human Gene Similar to SWISSPROT- ID:P33174 KINESIN-LIKE PROTEIN KIF4 - MUS MUSCULUS (MOUSE), 1231 aa.	1.70E-79 4 (4q24)	6
2249	cg44002977	231	GCTAGCTACTCT AGAGGACCACA GG[G/A]TGCAGA GAGGGTGTCCT GAGGGTCC	G	A			SILENT- NONCODI NG	kinesin	Human Gene Similar to SWISSPROT- ID:Q07866 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa.	2.70E-60	6

2250	cg44002977	406	TGTGAGGGCTGT GGGGTGCGGG GA[C/gap]CCAGC AGACCTGGGG CCGGGTTGA	C	gap			SILENT- NONCODI NG	kinesin	Human Gene Similar to SWISSPROT- ID:Q07866 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa.	2.70E-60	6
2251	cg43946310	3902	ACTCCTTGCTTC CTGATGCTGGGC A[A/gap]TGAGGC AGATAGCACTGG GTGTGAG	A	gap			SILENT- NONCODI NG	laminin	Human Gene SWISSPROT-ID:Q13753 LAMININ GAMMA-2 CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1193 aa.	0.00E+00	1
2252	cg43946310	4427	AGATTGCATTTT ATTAAAGCATTI C/GJCTACCGCA AAGCAAATGTTG GGAA	C	G			SILENT- NONCODI NG	laminin	Human Gene SWISSPROT-ID:Q13753 LAMININ GAMMA-2 CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1193 aa.	0.00E+00	1
2253	cg43946310	4440	ATTAAAGCATT CCTACCAGCAA G[C/G]AAATGTTG GGAAAGTATTTA CTTT	C	G			SILENT- NONCODI NG	laminin	Human Gene SWISSPROT-ID:Q13753 LAMININ GAMMA-2 CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1193 aa.	0.00E+00	1
2254	cg43983535	143	GAATTAGCACCA TCTGAATACAGA A[G/A]GAATTCTA TGTACATGCACA AATTA	G	A			SILENT- NONCODI NG	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0.00E+00	6 (6q22)
2255	cg44009224	5282	CTCCCCAGCTCG AGATCATCTTC A[C/A]TCAGGACA CAAACACAGACAG GTTTA	C	A			SILENT- NONCODI NG	laminin	Human Gene SWISSPROT-ID:Q16787 LAMININ ALPHA-3 CHAIN PRECURSOR (EPILIGRIN 170 KD SUBUNIT) (E170) - HOMO SAPIENS (HUMAN), 1713 aa.	0.00E+00	

2256	cg43958558	283	AGGTTTAGATTC TTTTTTTTTTTTT gap/TJAATCTGCC CCTTCAGATTA TATCA	T				SILENT- NONCODI NG	laminin	Human Gene Homologous to SWISSNEW-ID:P17931 GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALECTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.jpcls:SWISSPROT-ID:P17931 GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE- BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALECTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.	3.90E-139	14 (14q21)
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2257	cg43958558	283	AGGTTTAGATTC TTTTTTTTTTTTT gap/TAAATCTGCC CCTTCAGATTA TATCA	gap	T				SILENT- NONCODI NG	lamhin	Human Gene Homologous to SWISSPROT-ID:P17931 GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALECTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa. pcds:SWISSPROT-ID:P17931 GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE- BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALECTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.	3.90E-139	14 (14q21)
2258	cg43970746	127	GGGAGGAGGG AAGTGAGGCC CAG[C/gap]CCCA CAACCCCTCCCC GCCCCACCCC	C gap	gap				SILENT- NONCODI NG	MHC	Human Gene SWISSPROT-ID:P48634 LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) - HOMO SAPIENS (HUMAN), 2142 aa.	0.00E+00	3
2259	cg43921887	335	CATTGAGCATGA TTCCACCTGGGC ATT/CJGAGCTGG AAAAGAGCTCAG TCJTCA	T C	C				SILENT- NONCODI NG	MHC	Human Gene SWISSPROT-ID:P46379 LARGE PROLINE-RICH PROTEIN BAT3 (HLA-B-ASSOCIATED TRANSCRIPT 3) - HOMO SAPIENS (HUMAN), 1132 aa.	0.00E+00	14
2260	cg43298284	1921	TGAGTTGCACAG CTATGAAGGCTG T[G/A]CACTGCAC GAATGGAAGAG GCACCT	G A	A				SILENT- NONCODI NG	MHC	Human Gene SWISSPROT-ID:Q30201 HEREDITARY HAEMOCHROMATOSIS PROTEIN HLA-H PRECURSOR - HOMO SAPIENS (HUMAN), 348 aa.	7.30E-193	6

2261	cg43298284	2363	CGGTGGCTCGC GCCTGTGGTCCC AGC/gapJACTTT GGGAGGCCAAA GCGGTGCTG	C	gap			SILENT- NONCODI NG	MHC	Human Gene SWISSPROT-ID:Q30201 HEREDITARY HAEMOCHROMATOSIS PROTEIN HLA-H PRECURSOR - HOMO SAPIENS (HUMAN), 348 aa.	7.30E-193	6
2262	cg43298284	2394	GGGAGGCCAAA GCGGTGCTGAG ATTG/AJCAGGTG TGAGCCACCCTG CCCAGCC	G	A			SILENT- NONCODI NG	MHC	Human Gene SWISSPROT-ID:Q30201 HEREDITARY HAEMOCHROMATOSIS PROTEIN HLA-H PRECURSOR - HOMO SAPIENS (HUMAN), 348 aa.	7.30E-193	6
2263	cg43298284	2506	ACTTGGCTGCAT AAATGTGGTACA A/G/CJCATTTCTGT CTTGAAGGGCAG GTGCT	G	C			SILENT- NONCODI NG	MHC	Human Gene SWISSPROT-ID:Q30201 HEREDITARY HAEMOCHROMATOSIS PROTEIN HLA-H PRECURSOR - HOMO SAPIENS (HUMAN), 348 aa.	7.30E-193	6
2264	cg42479188	1420	TCCCCTGAGACC TACTCCTTCCA G/C/TCCCAAATC ATTACTTTTCTG TGGT	C	T			SILENT- NONCODI NG	MHC	Human Gene Homologous to SWISSPROT-ID:P13765 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DO BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 273 aa.	3.40E-147 (6p21.3)	6
2265	cg43966144	99	CACTCATTGGG GGGTCAAGGA CC/C/gapJGGCA ATATAGTATTCT GCTCAGTG	C	gap			SILENT- NONCODI NG	MHC	Human Gene Homologous to SWISSPROT-ID:P28068 CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 263 aa.	9.10E-147 (6p21.3)	6
2266	cg39425214	678	GGCAGCGGGAC CCGCCAGACC CTC/C/GJACCCG GGAGAGTCCCA GGCGCCTTT	C	G			SILENT- NONCODI NG	MHC	Human Gene Similar to SWISSPROT- ID:P16215 CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CH28 ALPHA CHAIN PRECURSOR - PAN TROGLÖDYES (CHIMPANZEE), 346 aa.	4.70E-55	
2267	cg42928872	3016	GACAGGGGTTT CTTCTGGGCATT AC/A/GJTCGCATA GAAATCAATAAT TTGTGG	A	G			SILENT- NONCODI NG	misc_cha nnel	Human Gene TREMBLNEW- ID:G2465531 KIDNEY AND CARDIAC VOLTAGE DEPENDENT K+ CHANNEL - HOMO SAPIENS (HUMAN), 676 aa.	0.00E+00	11

2268	cg42928872	3073	GGATCTGTGTTT TAATGAGTTTCA C/A/GJGTGTGATT TTGATTATTAATT GTGC	A	G			SILENT- NONCODI NG	misc_cha nnel	Human Gene TREMBLNEW- ID:G2465531 KIDNEY AND CARDIAC VOLTAGE DEPENDENT K+ CHANNEL - HOMO SAPIENS (HUMAN), 676 aa.	0	11
2269	cg43984759	158	CGTCGAGTGACA GCGGCCCTGGGG GG[G/gap]CAGGG GGGGCGGGGGC GGCCGGGATC	G	gap			SILENT- NONCODI NG	misc_cha nnel	Human Gene SPTREMBL-ID:Q14193 H- DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20
2270	cg43984759	3297	GCTACAGGGAAT GATTGGTCATGG G/G/gapJAAGTCT CTGCGCCATAAG CCACGAT	G	gap			SILENT- NONCODI NG	misc_cha nnel	Human Gene SPTREMBL-ID:Q14193 H- DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20
2271	cg43984759	3324	AGTCTCTGCGCC ATAAGCCACGAT C/C/A/CAGCGCA AAACCCTTACTC AAATGT	C	A			SILENT- NONCODI NG	misc_cha nnel	Human Gene SPTREMBL-ID:Q14193 H- DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20
2272	cg43984759	3378	ATTGACTTCGGT ATTTCATAGTAC C/T/C/GAGATTTT ATTTGAGATAC CATCA	T	C			SILENT- NONCODI NG	misc_cha nnel	Human Gene SPTREMBL-ID:Q14193 H- DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20
2273	cg43984759	3388	GGTATTTTCATAG TACCTGAGATTT TA/TJTTTTTGAGA TACCATCAGGGT GAGTT	A	T			SILENT- NONCODI NG	misc_cha nnel	Human Gene SPTREMBL-ID:Q14193 H- DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20

2274	cg43957213	130	GGCAAGATTGAG TCCCTGACCGCA A[G/gap]GCACTT ACAGTCTAGTTG GGAAGGG	gap		SILENT- NONCODING	misc_cha nnel	Human Gene SWISSNEW-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa.lpcds:SWISSPROT-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa.lpcds:TREMBLNEW-ID:E308262 AMILORIDE-SENSITIVE EPITHELIAL SODIUM CHANNEL ALPHA SUBUNIT - HOMO-SAPIENS (HUMAN), 669-aa	0	1 (1p36.1)
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2275	cg43957213	131	GCAAGATTTCAGT CCCTGACCGCAA G[<i>gap</i>]CACTTA CAGTCTAGTTGG GAAGGGA	G	<i>gap</i>			SILENT- NONCODING	misc_cha nnel	Human Gene SWISSNEW-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa.lpcis:SWISSPROT-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa.lpcis:TREMBLNEW-ID:E308262 AMILORIDE-SENSITIVE EPITHELIAL SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 669 aa	0	1 (1p36.1)
2276	cg42684570	221	AACCTAAAAGCA AAGTTGTGAAAG A[G/A]AAGCAGAA TTCCAAAGTCCC TTATT	G	A			SILENT- NONCODING	misc_cha nnel	HOMO SAPIENS (HUMAN), 669 aa Human Gene SWISSPROT-ID:P46098 5- HYDROXYTRYPTAMINE 3 RECEPTOR PRECURSOR (5-HT-3) (SEROTONIN- GATED ION CHANNEL RECEPTOR) - HOMO SAPIENS (HUMAN), 478 aa.	1.8E-260	11 (11q23.1)
2277	cg40367355	1773	AGGGCAATTGGA ATAATGTCCTGT T[A/G]GATAAACA GACATTTAGCAA TGCTG	A	G			SILENT- NONCODING	misc_cha nnel	Human Gene SPTREMBL-ID:O00564 INWARDLY RECTIFYING K+ CHANNEL HOMO SAPIENS (HUMAN), 375 aa.	4.10E-199	21
2278	cg44963814	1142	GGGGCCAGCCCC CTCCCCGCCCTCC TC[C/T]TGCCCTG GCGGCAGGGGT CGCGATG	C	T			SILENT- NONCODING	misc_cha nnel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.lpcis:TREMBLNEW- ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)

2279	cg44963814	1152	CCTCCCCGCGCTC CTCCCTGCCCTGG C[G/gap]GCAGGG GTCGCGATGATG GGCTGGA	G	gap			SILENT- NONCODING	misc_cha nnel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.lpcis:TREMBLNEW- ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2280	cg44963814	1220	TTCTGGGACCCCA CTCCGACTCCCC C[gap]/CTCCCCG GCATCATTTCCC CTCCCCG	gap	C			SILENT- NONCODING	misc_cha nnel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.lpcis:TREMBLNEW- ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2281	cg44963814	1285	CCTGGGGTCCC CCCTCCCTGTAA TG[C/G]ACTCCTG CCCCGGCCCCAA CCTCGCC	C	G			SILENT- NONCODING	misc_cha nnel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.lpcis:TREMBLNEW- ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2282	cg44963814	797	CCGCCTCAAGGA AGAGCCAGCCG TA[A/gap]TGGGG ACTCTCCAGGCA CCGCCTGC	A	gap			SILENT- NONCODING	misc_cha nnel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.lpcis:TREMBLNEW- ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)

2283	cg44963814	805	AGGAAGAGCCA GCCGTAATGGG GAC[T/C]CTCCAG GCACCGCCTGC CCCCAGCG	T	C			SILENT- NONCODING	misc_cha nnel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.lpcis:TREMBLNEW- ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2284	cg44963814	854	GTGGGGGTGGC CACTCCTGGGCC CC[gap/C]AGAAA GCCTCAGAGTCC TGCCGACG	gap	C			SILENT- NONCODING	misc_cha nnel	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa.lpcis:TREMBLNEW- ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
2285	cg43328088	392	TGCTTGAGGAAG GTCTTGAGAAA C[G/C]CTCACTCC CTCTAAACTTTTA GCTT	G	C			SILENT- NONCODING	misc_cha nnel	Human Gene Similar to SWISSPROT- ID:P35526 CHLORINE CHANNEL PROTEIN P64 - BOS TAURUS (BOVINE), 437 aa.	2.70E-99	1
2286	cg43309398	221	GCTCTTGGTCCA GCTGTCGCGG GG[G/gap]CGCTG CGGTCAGCCG GGCGCGGCG	G	gap			SILENT- NONCODING	misc_cha nnel	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	2.10E-67 (15q24)	15
2287	cg43309398	236	GGTCGCGGGGG CGCTGCGGTCTA GC[C/gap]GGGCG CGCGGGCGGCG GCGCAGAGA	C	gap			SILENT- NONCODING	misc_cha nnel	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	2.10E-67 (15q24)	15
2288	cg43978512	1658	ATCCTTCCCCCG CATGTTTCATAGA C[G/A]GACAGAC TTCTACTTTCAGT CGCTA	G	A			SILENT- NONCODING	misc_cha nnel	Human Gene Similar to SWISSPROT- ID:Q15700 CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN 110) - HOMO SAPIENS (HUMAN), 870 aa.	6.20E-53	10

2289	cg43978512	1702	GTCGCTAGAAAA GAGCTGAGTCTG GTC/TGTCCCTC AGGCGGCCAGC TGCAGT	C	T			SILENT- NONCODI NG	misc_cha nnel	Human Gene Similar to SWISSPROT- ID:Q15700 CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN 110) - HOMO SAPIENS (HUMAN), 870 aa.	6.20E-53	10
2280	cg43013507	1808	TCGCACGCCCG AGGGCCGGCCT CCG[G/gap]TCCC GCTTCCAGTTTC CTTGAAGCG	G	gap			SILENT- NONCODI NG	ngf	Human Gene SWISSPROT-ID:Q00911 EARLY GROWTH RESPONSE PROTEIN 4 (EGR-4) (EARLY RESPONSE PROTEIN NGFI-C) (NERVE GROWTH FACTOR-INDUCED PROTEIN C) - RATTUS NORVEGICUS (RAT), 478 aa.	2.40E-226	2 (2p13)
2281	cg43013507	1987	GATTCAAGACAG TCCTTTGTAAC G[G/gap]CACACG CCCCAGGCCTTC CTCTATA	G	gap			SILENT- NONCODI NG	ngf	Human Gene SWISSPROT-ID:Q00911 EARLY GROWTH RESPONSE PROTEIN 4 (EGR-4) (EARLY RESPONSE PROTEIN NGFI-C) (NERVE GROWTH FACTOR-INDUCED PROTEIN C) - RATTUS NORVEGICUS (RAT), 478 aa.	2.40E-226	2 (2p13)
2282	cg43013507	2037	AACCCCGAGAGA CAGGCTGGGC AG[G/gap]GCCAA GGCGGTCTCGC GCGGGACTT	C	gap			SILENT- NONCODI NG	ngf	Human Gene SWISSPROT-ID:Q00911 EARLY GROWTH RESPONSE PROTEIN 4 (EGR-4) (EARLY RESPONSE PROTEIN NGFI-C) (NERVE GROWTH FACTOR-INDUCED PROTEIN C) - RATTUS NORVEGICUS (RAT), 478 aa.	2.40E-226	2 (2p13)
2283	cg43013507	2089	TACAGCAGTGTC TTATCCAGCAGC C[gap/G]ATTGGA TGTAACGTTTG CTTTGGG	gap	G			SILENT- NONCODI NG	ngf	Human Gene SWISSPROT-ID:Q00911 EARLY GROWTH RESPONSE PROTEIN 4 (EGR-4) (EARLY RESPONSE PROTEIN NGFI-C) (NERVE GROWTH FACTOR-INDUCED PROTEIN C) - RATTUS NORVEGICUS (RAT), 478 aa.	2.40E-226	2 (2p13)
2294	cg44929972	1659	TTAAACTCTAGA CACAGTTTTAT CT/CITGGATTAA CTTAGATAACTTT TGTA	T	C			SILENT- NONCODI NG	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.70E-214	7

2295	cg44929972	2199	GTAACACTGATT TTATCTGCTGTA TIGAJAGACTTTG TGCATTTTACTTT GAAA	G	A			SILENT- NONCODI NG	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.70E-214	7
2296	cg43940300	227	CTTTGCTTTTCT GTCAGAAATAGCT TTCJACAAACATA CTACTACTATTTA TTT	T	C			SILENT- NONCODI NG	ngf	Human Gene Similar to SWISSNEW- ID:P78543 BTG2 PROTEIN PRECURSOR (NGF-INDUCIBLE ANTI- PROLIFERATIVE PROTEIN PC3) - HOMO SAPIENS (HUMAN), 158 aa.jpcls:SWISSPROT-ID:P78543 BTG2 PROTEIN PRECURSOR (NGF- INDUCIBLE ANTI-PROLIFERATIVE PROTEIN PC3) - HOMO SAPIENS (HUMAN), 158 aa.jpcls:SPTREMBL- ID:P78543 NGF-INDUCIBLE PC3 ANTI- PROLIFERATIVE PROTEIN - HOMO SAPIENS (HUMAN), 158 aa	3.10E-82	1
2297	cg44022292	2240	ATGGTTGCCATG ATCTACCGCTTT TIG[gap]CGCCCC TGCTGACTCCGG CGTCGGG	G	gap			SILENT- NONCODI NG	nucl_rec pt	Human Gene SPTREMBL-ID:Q15625 STEROID RECEPTOR (TR2-11) - HOMO SAPIENS (HUMAN), 603 aa.	0.00E+00	12
2298	cg43971768	182	TAAGAAGAAAGA GAAATGGTTAAG TIA/GICTTAACT GTCCACTGACAC CTGCT	A	G			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15
2299	cg43971768	23	TTTTTTTTTTGTT CAGAGCAAAG[IT] TCATTTTATTGT AATGAAATTTTA	G	T			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15
2300	cg43971768	277	TTGTTAGATGAA GCAAGCCGTCCT G[C/IT]TCCGCA CAGCCTGTGAAA CCTCCA	C	T			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15

2301	cg43971768	330	TTGCCACCTTTCA AGGTCAGTGCCC C/G/CAGACCC TGGCCTGTTGTT GACCAT	A	G			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15
2302	cg43971768	343	GGTCAGTGCCC CACAGACCCTGG CCT/CJGTGTTG ACCATAACACTA GCTTTG	T	C			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15
2303	cg43991048	204	TAATATTTTCA GTGCTACTAATG gap/AJAAAAAAA AATTAAAGCCTG CACTG	gap	A			SILENT- NONCODI NG	nucl_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	0.00E+00	17
2304	cg43991048	214	TCAGTGCTACTA ATGAAAAA A/gap/AJTAAAG CCTGCACTGGAA ATTACA	gap	A			SILENT- NONCODI NG	nucl_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	0.00E+00	17
2305	cg43921419	2593	AACCCGGCCAT CCATCACAAGG C/gap/CJAACCTG GGAGAGTAACTA TTTGGG	gap	C			SILENT- NONCODI NG	nucl_rec pt	Human Gene SPTREMBL-ID:Q14452 GLUCOCORTICOID RECEPTOR REPRESSION FACTOR 1 - HOMO SAPIENS (HUMAN), 835 aa.	0.00E+00	19
2306	cg43921419	3208	ACAATCGGCCCA TCACCGAGCCCC C/C/gap/JGGGCC AGGCCAGCTC CCCCTCTG	C	gap			SILENT- NONCODI NG	nucl_rec pt	Human Gene SPTREMBL-ID:Q14452 GLUCOCORTICOID RECEPTOR REPRESSION FACTOR 1 - HOMO SAPIENS (HUMAN), 835 aa.	0.00E+00	19
2307	cg43249083	282	TTGCACCGGGA GCTCCAGATTG C/C/JACCCCGC AGCGCTGCGGA GCCGGCA	C	T			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P20393 V- ERBA RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00 (17q11.2)	17

2308	cg43992723	5608	TGCTCTTCAAAA GACACCTGCCTT Algap/GJTGCAAG GGGAAACCTGTG AAAGCTG	gap	G			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0	4 (4q31.1)
2309	cg43992723	5636	CAAGGGGAAAC CTGTGAAAGCTG CAIG/CJTCAGAG GGAGGAGTTTT CTTACAT	G	C			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2310	cg43992723	5651	GAAAGCTGCAGT CAGAGGGAGGA GTT/CJTTCCTTA CATAATTTGCAA TTTCAG	T	C			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2311	cg43992723	5848	GTTCAGACTTAG TTTTTATAAAATG [G/A]GAAATCTGA CTTACTTAACCA GGTT	G	A			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2312	cg43992723	6085	TGGTACAGTTCA TAATTCACCAA Algap/AJGTTTCATA TAATTTAAAGAAA CACTA	gap	A			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2313	cg43992723	6102	TCACCAAAAGTT CATATAATTTAAA [G/A]AAACACTAA ATTAGTTTAAAT GAA	G	A			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P08235 MINERALOCORTICOID RECEPTOR (MR) - HOMO SAPIENS (HUMAN), 984 aa.	0.00E+00	4 (4q31.1)
2314	cg42507196	172	TTGCTCCTGGGA CTGCACCTTGCTC CIC/gap]GTCGGG TCGCCCGGCTTC ACCGGAC	C	gap			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSNEW-ID:P03372 ESTROGEN RECEPTOR (ER) (ESTRADIOL RECEPTOR) - HOMO SAPIENS (HUMAN), 595 aa.jpcls:SWISSPROT-ID:P03372 ESTROGEN RECEPTOR (ER) (ESTRADIOL RECEPTOR) - HOMO SAPIENS (HUMAN), 595 aa.	0.00E+00	6 (6q25.1)

2315	cg43961967	2265	AAGACCACCTTC CCTTCCTCAGCA G[G]gap]CCAAAG ATGGCCAGACTC CCTTGCT	G	gap			SILENT- NONCODI NG	nucI_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2316	cg43961967	2383	TCCTTTGAGGCC CCAACTCAAGTG T[ap/G]CACCTC CTTCCCAGCTC CCCCAGG	gap	G			SILENT- NONCODI NG	nucI_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2317	cg43961967	2414	CTTCCCCAGCTC CCCCAGGCAGA AA[ap/A]TAGTT GTCTGTGCTTCC TTGGTTCA	gap	A			SILENT- NONCODI NG	nucI_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2318	cg43961967	2464	TGCTTCTACTGT GACACTTATCTC A[ap/G]CTGTGTTT ATAATTAGTCGG GCAIGA	gap	G			SILENT- NONCODI NG	nucI_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2319	cg43961967	455	TGCCACTCCCTG GCCCCCTCCCACC G[G/C]CCGCCCC CCTGGGGCGG AGGGCAT	G	C			SILENT- NONCODI NG	nucI_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2320	cg43961967	469	CCCTCCCACCG GCCGCCCCCTT GG[G/C]GCGGAG GGCATGGTGTGA AAGGCCA	G	C			SILENT- NONCODI NG	nucI_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2321	cg43961967	474	CCACCGGCCGC CCCCCTTGGGG CGG[A]gap]GGGC ATGGTGTGAAAG GCCAAGTGC	A	gap			SILENT- NONCODI NG	nucI_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)

2322	cg43961967	476	ACCGCGCGCCC CCCCTGGGCG GAG[G/C]GCATG GTGTAAAGGCC AAGTGTG	G	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2323	cg43961967	532	GGTATCATGGGT GCTGTGCCCTAG G[G/gap]CCTGGG TGGCAGGGGGT GGGTGGCC	G	gap				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10827 THYROID HORMONE RECEPTOR ALPHA-2 (EAR-7-2) (C-ERBA-ALPHA-2) HOMO SAPIENS (HUMAN), 490 aa.	1.40E-267	17 (17q11.2)
2324	cg43917579	1583	CTGCCTGGCCTG TTTGGACTTTGG G[G/gap]CACAGC CTGTCACCTGCTC TGCCTAA	G	gap				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2325	cg43917579	1745	CGCCTCCCCACCA GGGCTCTCAGG AC[A/G]CCCTGC CACACCCACG GGGCTTGG	A	G				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2326	cg43917579	4479	TCCCCGTGGGG CACCCAGGAGG GCC[C/gap]TGCC GGAATGTGCAGC CTGTGGGTA	C	gap				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2327	cg43917579	4527	GATGTCGGCTG GTGTCCTGTGCG TG[G/C]AGCTGG GGTGGTGATCT GGTGCTC	G	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2328	cg43917579	50	CCCCGCCGCC GCTGCCCTGCC CGC[A/C]GGCCG GGGATGAGTTAG TCGCAGAC	A	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9

2329	cg43917579	4851	GCATCTGGAAAG GTAAGAAAAA A[A/gap]TCTATTT TTGTACAAATGT AATTTT	A	gap			SILENT- NONCODING NG	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2330	cg43917579	58	CCCGCTGCCTG CGCCGCAGGCC GGG[G/C]ATGAG TTAGTCGCAGAC AAGACAC	G	C			SILENT- NONCODING NG	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2331	cg43917579	77	GCCGGGGATGA GTTAGTCGCAGA CA/A/TJGGACACC AAACATTTCTCTG CCGCTC	A	T			SILENT- NONCODING NG	nucl_rec pt	Human Gene SWISSPROT-ID:P19793 RETINOIC ACID RECEPTOR RXR- ALPHA - HOMO SAPIENS (HUMAN), 462 aa.	7.90E-251	9
2332	cg43987181	253	CACACAAAAAAG TGCATCTAAATG A/T/gap]TTTTTTT TTTAAAAACAAT GTCTT	T	gap			SILENT- NONCODING NG	nucl_rec pt	Human Gene SWISSNEW-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa. pcis:SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.	9.40E-248	6

2333	cg43987181	2434	GAGTTCACTGGG ACTCTTCCCTCC TTC/TGGCGTGG CGTCATACGTGG CCCTCA	T			SILENT- NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa. pcis:SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.	9.40E-248	6
2334	cg43987181	264	GTGCATCTAAAT GATTTTITTTTTT ATTAAAAACAAT GTCTTTAATTCCT CAT	T			SILENT- NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa. pcis:SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.	9.40E-248	6

2335	cg43987181	747	TTTCATAAAAAA GACAAAAAGCATA ATT/ATGAGAAAT TAGAGGGATTTT AGTTA	T	A			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa. cds:SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.	9.40E-248	6
2336	cg43315956	1813	GCCAAAGGGGG GACCAGAAATCC CC[C/gap]ATGCG AGCTGTTTGAGG ACTGGGAT	C	gap			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
2337	cg43315956	3757	TACAAACTTTTC CAATTTTAAAAA [gap/ATCAGCCA TTTCATGCAACC AGAAAC	gap	A			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
2338	cg43315956	4535	CATGCCTGATAT TGGGATTTTTTT [T/gap]CCAGCCT TCCTGATGCCAA GGGGCT	T	gap			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
2339	cg43315956	4709	AGTTCTCATTTAA GCACTAGTGGAA [gap/T]TTTTTTT TTTGATATATTAG CAAG	gap	T			SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3

2340	cg43315956	4720	AAGCACTAGTGG AATTTTTTTTTT gap/TGATATATT AGCAAGTCTGTG ATGTA	gap	T				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.30E-244	3
2341	cg43935583	1599	TGTCAGCCAAAT TTGGAGGTC AAG C[G/A]TAATGTCC TTCTGATAAATAA AGCC	G	A				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2342	cg43935583	1605	CCAAATTTGGAG GTCAAGCGTAAT G[T/C]CCTTCTGA TAAATAAAGCCC TTGCT	T	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2343	cg43935583	1646	AGCCCTTGCTGA AGGAAAAGCAAC C[T/A]AGATCACC TTATGGATGTCG CAATA	T	A				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2344	cg43935583	1658	AGGAAAAGCAAC CTAGATCACCTT A[T/C]GGATGTCG CAATAATACAAA CCAGT	T	C				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2345	cg43935583	1666	CAACCTAGATCA CCTTATGGATGT C[G/A]CAATAATA CAAACCAAGTGA CCTCT	G	A				SILENT- NONCODI NG	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
2346	cg43949686	415	AAACAGAAGCAG ATAAAAAA A[gap/A]GATGCA GGACTCCTTCAG TTCTTCA	gap	A				SILENT- NONCODI NG	nucl_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.40E-167	

2347	cg43949686	6483	TCGATGCGTATT CTGTGGCCGCC ATC/TTCGCGCAG GGTGGTGGTATT CTGTCA	C	T				SILENT- NONCODI NG	nuc_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.40E-167	
2348	cg43996179	140	TTTTGGTCACTG GTTTCATTTTTT [C/T]CTTGCTCTA AACCACCTCTTC TCTG	C	T				SILENT- NONCODI NG	nuc_rec pt	Human Gene Homologous to SWISSPROT-ID:Q14739 LAMIN B RECEPTOR (INTEGRAL NUCLEAR ENVELOPE INNER MEMBRANE PROTEIN) (LMN2R) - HOMO SAPIENS (HUMAN), 615 aa.	1.10E-120	
2349	cg43996179	266	GTGCTGGTGGAT GAGTGGGCACAT G[C/gap]CCCCAC CTGGGGTGGTG GAGCCGCT	C	gap				SILENT- NONCODI NG	nuc_rec pt	Human Gene Homologous to SWISSPROT-ID:Q14739 LAMIN B RECEPTOR (INTEGRAL NUCLEAR ENVELOPE INNER MEMBRANE PROTEIN) (LMN2R) - HOMO SAPIENS (HUMAN), 615 aa.	1.10E-120	
2350	cg43933695	3029	ATTTTCGCTTTTA ACAGAGCAGCTT [C/G]CTGCTAGC GGGAGGCAGGC AATTAC	C	G				SILENT- NONCODI NG	nuclease	Human Gene SWISSPROT-ID:P54277 PMS1 PROTEIN HOMOLOG 1 (DNA MISMATCH REPAIR PROTEIN PMS1) - HOMO SAPIENS (HUMAN), 932 aa.	0.00E+00	
2351	cg44128653	616	CCTGGTTCAATC GATCCTCTGGCT TTC/gap]AGTGGC TGGGACTACAGG CATTAT	C	gap				SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa. pcls:SWISSPROT- ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa.	1.40E-203	19

2352	cg43944393	1834	AAGAGAGAGGG AGATAAAAGGGG GA[G/T]ACAAAAG ATGTACAGAAAT GATTTTC	G	T			SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa, pcis:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2353	cg43944393	1869	GTACAGAAATGA TTTCTGGCTGG C[C/gap]AACTGG TGGCCAGTGGG AGGTGATG	C	gap			SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa, pcis:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2354	cg43944393	1971	AGAGAGCCACCA GGAAGGCGCAT CT[T/gap]AGCAG ATGGAGGGAAC GCTGAGAG	T	gap			SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa, pcis:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2355	cg43944393	1977	CCACCAGGAAG GCGCATCTTAGC AG[A/gap]TGGGA GGAACCTGCTGAG AGAAGATG	A	gap			SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa, pcis:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11

2356	cg43944393	1989	CGCATCTTAGCA GATGGGAGGAA CT[G/A]CTGAGA GAAGATGGGCA GAAAGCTG	G	A				SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.lpcis:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2357	cg43944393	297	CGAGCTTAGGAC CGCCTGCCCGG GG[C/gap]AACCC CGAACCAAGCTT TAGCCGCC	C	gap				SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.lpcis:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2358	cg43944393	317	CGGGGCAACCC CGAACCAAGCTT TA[G/gap]CCGCC GAGCCGCGTG TCCCAAAGG	G	gap				SILENT- NONCODI NG	nuclease	Human Gene SWISSNEW-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.lpcis:SWISSPROT-ID:P39748 FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) - HOMO SAPIENS (HUMAN), 380 aa.	2.20E-200	11
2359	cg43942083	400	GTTGAATAGGAG CCCTAACTGTAG TTTAACTTCTTT CACAGCAGGGA AGGAAG	T	A				SILENT- NONCODI NG	nuclease	Human Gene Similar to SWISSPROT- ID:P07998 RIBONUCLEASE PANCREATIC PRECURSOR (EC 3.1.27.5) (RNASE 1) (RNASE A) (RNASE UPI-1) (RIB-1) - HOMO SAPIENS (HUMAN), 156 aa.	9.20E-83	
2360	cg43943773	113	ATTTCATATGTAA CAAAGATAAGGA [C/T]GTGTGCAG GTATAAAACAGA GGCAG	C	T				SILENT- NONCODI NG	nuclease rhilb	Human Gene Similar to SWISSPROT- ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19

2361	cg43943773	197	CTCATTATCCCT GAGGGTAGGG GC[G/C]GGGGAG GAGAGGAGTCA CAGGCAGT	G	C				SILENT- NONCODING	nuclease inhib	Human Gene Similar to SWISSPROT- ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19
2362	cg43943773	228	GGAGAGGAGTC ACAGGCAGTTCA CC[C/A]ACACCTG GAAAATCGATGA CTTCAT	C	A				SILENT- NONCODING	nuclease inhib	Human Gene Similar to SWISSPROT- ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19
2363	cg43943773	312	GAAGTCATGAGA AGAAGGCCCTTC TT[G/C]CCAGGG ATGATGTTTCTC AGTATC	T	G				SILENT- NONCODING	nuclease inhib	Human Gene Similar to SWISSPROT- ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19
2364	cg42685908	176	TACAAATATTTT ACATTTAATAGT C/AJATGAAAAAG AAAAGAACTTGA AAAA	C	A				SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C- MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2365	cg42685908	193	TTAATAGTCATG AAAAAGAAAAAGA A[C/G]TTGAAAAA ACAACCTCAACT CTGTA	C	G				SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C- MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2366	cg42685908	223	AAAAACAACCTC AACTCTGTACAA AT[G/G]TTAATAT CAAGGAGCAGCT GAAGC	T	G				SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C- MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2367	cg42685908	320	TATTAAAAATATC CTTGCTTTTTC C/gapJATGATATA CACATATTTTTC TCTT	C	gap				SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C- MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2

2368	cg42685908	383	TATTATGTATTT TAATGACAGCTT A/CJCTTAACAAC ATTTCATCTGGTG CTTT	A	C			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C-MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2369	cg42685908	92	AGTTATACAAC TTAAACATTGAAT [G/T]AATCATTTCT TATCAAAATACAT CAAG	G	T			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q12866 CELLULAR PROTO-ONCOGENE (C-MER) PRECURSOR - HOMO SAPIENS (HUMAN), 999 aa.	0.00E+00	2
2370	cg43947181	2974	TTCAATTGCATC ATCACTGACCTG TT[gap]AGAATTT AACCCGGAAACA TCGCAA	T	gap			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92738 PROTEIN RELATED N-TERNIMUS OF TRE ONCOGENE - HOMO SAPIENS (HUMAN), 828 aa (fragment).	0.00E+00	10
2371	cg43947181	3937	TCATGCTTTTGA ACATCTTTTTTT [T/gap]TTCATTGA AACAAATTC AAG TCTT	T	gap			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92738 PROTEIN RELATED N-TERNIMUS OF TRE ONCOGENE - HOMO SAPIENS (HUMAN), 828 aa (fragment).	0.00E+00	10
2372	cg43947181	3938	CATGCTTTTGA CATCTTTTTTTTT T[gap]TCATTGAA ACAAATTC AAGT TCTTG	T	gap			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92738 PROTEIN RELATED N-TERNIMUS OF TRE ONCOGENE - HOMO SAPIENS (HUMAN), 828 aa (fragment).	0.00E+00	10
2373	cg43947181	3939	ATGCTTTTGAAC ATCTTTTTTTTTT T[gap]CATTGAAA CAAAATTC AAGTT CTTGG	T	gap			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92738 PROTEIN RELATED N-TERNIMUS OF TRE ONCOGENE - HOMO SAPIENS (HUMAN), 828 aa (fragment).	0.00E+00	10

2374	cg43988571	2942	CCACGGGCACC CCCAGCCTCAG GTG[C/gap]ACTG ACCTGCTGCCTG CCCCCAGCC	C	gap		SILENT- NONCODING	Human Gene SWISSNEW-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT- 10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT] - HOMO SAPIENS (HUMAN), 898 aa. lpcis:SWISSPROT-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT) (H2TF1) (ONCOGENE LYT-10) (LYT10) - HOMO SAPIENS (HUMAN), 898 aa.	0.00E+00	10 (10q24)
2375	cg43939230	341	GTAATAGAGGTC TTTGTAGATGGG TAA/GCTGTATCC CATGGCAGCCCT TGCTG	A	G		SILENT- NONCODING	Human Gene SPTREMBL-ID:Q99907 LATENT TRANSFORMING GROWTH FACTOR-BETA-BINDING PROTEIN-2 - HOMO SAPIENS (HUMAN), 1821 aa.	0.00E+00	14 (14q24)
2376	cg42716300	189	CTGCGGGAAGG TGCGGGGAGCG GAG[G/C]CATGG CCTCCGGTGCGT ATAACCCG	G	C		SILENT- NONCODING	Human Gene SWISSPROT-ID:Q04864 C REL PROTO-ONCOGENE PROTEIN (C- REL PROTEIN) - HOMO SAPIENS (HUMAN), 619 aa.	0.00E+00	2 (2p13)
2377	cg43298442	232	TTTTTTTTTCCA CACAGCAGATGT [A/gap]TCCAAAC ACATAAAATCT CTACAG	A	gap		SILENT- NONCODING	Human Gene SWISSNEW-ID:Q99583 MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT) - HOMO SAPIENS (HUMAN), 582 aa.	0.00E+00	
2378	cg44008321	156	GTTGCTGATATT TATTCAAACGTC ATT[C]CCATACAA TAAAGAACTCTG CTTTT	T	C		SILENT- NONCODING	Human Gene SPTREMBL-ID:Q63406 OST ONCOGENE - RATTUS NORVEGICUS (RAT), 872 aa.	0.00E+00	

2379	cg44008321	279	GGGGAGGGTCA CACAAAGGGCGC GCA[G/gap]CTGT GCGACGAGACG GAGGCACCCGC	G	gap			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q63406 OST ONCOGENE - RATTUS NORVEGICUS (RAT), 872 aa.	0.00E+00	
2380	cg43997159	507	AGCTAGTAAACA GACAAGCCCTGC G[G/A]ACTTTGAA ACCAACTTGACC GGGTC	G	A			SILENT- NONCODING	oncogene	Human Gene TREMBL-NEW- ID:G2736087 ERYTHROBLASTOSIS VIRUS ONCOGENE HOMOLOG 2 PROTEIN - HOMO SAPIENS (HUMAN), 469 aa.	2.30E-260	21 (21q22.3)
2381	cg43997978	111	TCCAGGTTTTT AATTTCCCTGA AT/gap]TTTTTTT TTAAACAACAAA ATTGGC	T	gap			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1
2382	cg43997978	120	TAAATTTCCCTG AATTTTTTTTTTg ap/TAAACAACAA AATTGGCAAGAA GAAA	gap	T			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1
2383	cg43997978	716	ATTTAAAGGGCA GTAGGTGCTGT G[G/gap]CTGCAG CCTCTCCTCCAA GAQGGAT	G	gap			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1
2384	cg43997978	784	GATGTTGCAGGG GAGGGCCGTTA GG[G/gap]CAAGA ACCCAGCAGCTG CGTGGATG	G	gap			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1
2385	cg43997978	822	ATATACCCCACT AGTGTTCAAGGA C[A/gap]AGGCC TCTGATCCCTAT GGCTTGG	A	gap			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q60875 LFC ONCOGENE - MUS MUSCULUS (MOUSE), 573 aa.	2.90E-244	1

2386	cg43917532	511	CCTCCCCACCTT CCCCACCTCCC C[gap/C]ACCCCTC CCCATAGCGCC CCTCCCG	gap	C			SILENT- NONCODING	oncogene	Human Gene SWISSNEW-ID:P01106 MYC PROTO-ONCOGENE PROTEIN (C-MYC) - HOMO SAPIENS (HUMAN), 439 aa. pcls:SWISSPROT-ID:P01106 MYC PROTO-ONCOGENE PROTEIN (C-MYC) - HOMO SAPIENS (HUMAN), 439 aa.	4.20E-236	8 (8q24.12)
2387	cg43988569	383	CTGCTGGAAGAG GAAATCCCGG GG[G/gap]CCGCC GGGCCCTCTTCG ACAGCTAC	G gap	gap			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q13249 ABL BINDING PROTEIN 3 - HOMO SAPIENS (HUMAN), 390 aa.	5.00E-213	2
2388	cg43959113	84	ACCAAGGGGAG AGGGGACGGCC CATT[C]GCCAAT CTGTCCCAGCCC CCCGGGG	T	C			SILENT- NONCODING	oncogene	Human Gene SWISSPROT-ID:P53539 FOSB PROTEIN (G0/G1 SWITCH REGULATORY PROTEIN 3) - HOMO SAPIENS (HUMAN), 338 aa.	6.00E-182	19
2389	cg44008545	1334	TACACITTTAAAA CCAGTTACCCAA A/TATCTGATTAG AAGTATAAGGTG CTC	A	T			SILENT- NONCODING	oncogene	Human Gene SPTREMBL-ID:Q92905 JUN ACTIVATION DOMAIN BINDING PROTEIN - HOMO SAPIENS (HUMAN), 334 aa.	4.30E-179	
2390	cg43298230	1927	AACCCGTCCTCT CCCGAGTTTTTC A/T[G]AACTGAGC CCACTCGCAAGT TGGAG	T	G			SILENT- NONCODING	oncogene	Human Gene SWISSPROT-ID:P54843 TRANSCRIPTION FACTOR MAF2 (PROTO-ONCOGENE C-MAF) - MUS MUSCULUS (MOUSE), 370 aa.	1.60E-158	
2391	cg44010709	1277	AATGCAGAGCCC CTCAGGATGGG GT[gap/G]CCCCG TCAGGGGCTGG ACGGTCGIG	gap	G			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2392	cg44010709	163	CCGGGTCGTCCT CTGCAAGGTTGC C[C/gap]CGGTGG GTCTGACGCCCA GCTGGCG	C gap	gap			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)

2393	cg44010709	164	CGGGTCGTCCTC TGCAAGGTTGCC C[C/gap]CGGTGG TCTGACGCCCCAG CTGGCGT	C	gap			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2394	cg44010709	191	GTGGGTCTGAC GCCCAGCTGGC GTC[C/gap]GGGA GCCGGGGTGA GTCTGGAGG	C	gap			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2395	cg44010709	224	GGGTGGAGTCC TGGAGGGAGGC GAA[gap/G]CGGG ATGTGGAGGGG GCCTGGAGTG	gap	G			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2396	cg44010709	267	CTGGAGTGGGG GGAGGGCGGG TGA[G/C]GCGAG GCCCGGCCCGC CACAGTCCT	G	C			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2397	cg44010709	273	TGGGGGGAGGG GCGGGTGAGGC GAG[G/gap]CCCCG GCCCGCCACAG TCCTGCCTCT	G	gap			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)
2398	cg44010709	68	AACCTTACTTGT TTTTGGGAGGAG [A/G]TTAATGGGT GGGAGGGGTGA GAGGG	A	G			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P17947 31 KD TRANSFORMING PROTEIN (TRANSCRIPTION FACTOR PU.1) - HOMO SAPIENS (HUMAN), 264 aa.	1.30E-147	11 (11p12)

2399	cg43918770	5017	GCGGACCACTG ACCGCTCCCCAG CG[G/gap]CAGAA GGCCTGGTCCC CTGTGGTTC	G	gap			SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa.	1.60E-140	5
2400	cg43918770	8967	TACTTTAAAGGA GTGAGCCAGAA GG[C/gap]CAAGG AGTTCGTGTGCT TCCTCCIG	C	gap			SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa.	1.6E-140	5
2401	cg43966629	1072	ATCCTAGTTTCC CTAACTGCCTCC TTC/A/CACAGGG AGGAGTGTGG GATCCCG	C	A			SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1
2402	cg43966629	1089	TGCCTCCTCCAC AGGAGGAGTG TT[G/gap]GGATC CCCCCTACCCCTG TGCCCCCG	G	gap			SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1
2403	cg43966629	17	TTTTTTTTTTTT GAA/T/GGATATT TAAC/T/TCTTAA AAAAA	T	G			SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1
2404	cg43966629	199	CAGTGTGTATAT TCTATTTCATCAG G/G/AJAGAGTTG GGTGAGGACGT GGTGATG	G	A			SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1
2405	cg43966629	25	TTTTTTTTTTTT GAATGATATTT/A/ GIAC/T/TCTTAA AAAAAAATCTTA A	A	G			SILENT- NONCODI NG	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.30E-123	1

2406	cg439864295	980	AAACATCTGACG TCGTACAAAAA A[A/gap]TTCATC AGTATTCTGGC ACAGAA	A	gap			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2407	cg439864295	1351	AACAACAAAAAT ACAATTAATAA A[A/gap]TAAATAA TAAAGTCATTG TGATCG	A	gap			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2408	cg439864295	1614	GCTGCAAGGGG ACACACAACCCAG GG[G/gap]TACTG TTGACTAGCTTT TTGCATAG	G	gap			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2409	cg439864295	1960	GCTTCTCTTCTC TGCTACCAGCG T[G/A]TACGCCG GCTGCTTGGCAA ACCGG	G	A			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2410	cg439864295	2071	TAGACATTTTGG AGTCTTGTTCT C[G/A]TAATCCTT GATGGGACCG TGTTGG	G	A			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2411	cg439864295	623	GAATACTCCCTA AATGCAGTAGAT T[A/gap]AAAAAA AAATCAAATCTA CAAGTG	A	gap			SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20

2412	cg43964295	633	TAAATGCAGTAG ATTAAAAA [A/gap]TCAAATCT ACAAAGTGGTTCA GTATT	A	gap				SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2413	cg43964295	633	AAATGCAGTAGA TTAAAAA [gap/A]TCAAATCT ACAAAGTGGTTCA GTATT	gap	A				SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2414	cg43964295	73	ATTCACACTTGC TGTTGAATAACA A[G/C]GGAATCAA GGCTCCCTCTAGA TGGGG	G	C				SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2415	cg43964295	697	GAAAGAAATCA GAATTTACAAAG T[A/C]AGATTGGT GTGCTTCCAAAGT TCACA	A	C				SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
2416	cg43317357	87	TGGGTCGACAG CTGGGAGGGCA GGAT[C]TGGGG GGAAGCTGCTG GGCGCAGCC	T	C				SILENT- NONCODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P98083 SHC TRANSFORMING PROTEIN - MUS MUSCULUS (MOUSE), 578 aa.	1.30E-106	
2417	cg43297056	228	CGCTTGTCTTTT TTTTTTTTTTCT /A/AAGAGAGAGG CAATTTTATCTT CC	T	A				SILENT- NONCODING	oncogene	Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.90E-103 (20q13.1)	20
2418	cg43297056	268	TTTATCTTCCAA AAAAATGCACCA A/gap]GAGAGGG TGAGCACAGGA GCACGCC	A	gap				SILENT- NONCODING	oncogene	Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.90E-103 (20q13.1)	20

2419	cg43297058	482	AACAGGGCAGC ACATGGCCCTGT TG[C/gap]CTCCA CCTGAGAGTCTG GGGAGGGG	C	gap			SILENT- NONCODING	oncogene	Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.90E-103	20 (20q13.1)
2420	cg44129020	155	CTGCATAGGTCC AGGCCCCGGGT GG[C/gap]CCCCC AAAGGCTCCCT CCTTCCCA	C	gap			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSNEW- ID:Q15853 UPSTREAM STIMULATORY FACTOR 2 (UPSTREAM TRANSCRIPTION FACTOR 2) (FOS- INTERACTING PROTEIN) (FIP) (MAJOR LATE TRANSCRIPTION FACTOR 2) - HOMO SAPIENS (HUMAN), 346 aa. pcis:SWISSPROT-ID:Q15853 UPSTREAM STIMULATORY FACTOR 2 (UPSTREAM TRANSCRIPTION FACTOR 2) (FOS-INTERACTING PROTEIN) (FIP) (MAJOR LATE TRANSCRIPTION FACTOR 2) - HOMO SAPIENS (HUMAN), 346 aa.	1.60E-99	
2421	cg44129020	519	GCGGGCGTGGG CGCGGGCGGCT GCGT[C]GGTGG TGGCGGGCGTC ACTGCCGGG	T	C			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSNEW- ID:Q15853 UPSTREAM STIMULATORY FACTOR 2 (UPSTREAM TRANSCRIPTION FACTOR 2) (FOS- INTERACTING PROTEIN) (FIP) (MAJOR LATE TRANSCRIPTION FACTOR 2) - HOMO SAPIENS (HUMAN), 346 aa. pcis:SWISSPROT-ID:Q15853 UPSTREAM STIMULATORY FACTOR 2 (UPSTREAM TRANSCRIPTION FACTOR 2) (FOS-INTERACTING PROTEIN) (FIP) (MAJOR LATE TRANSCRIPTION FACTOR 2) - HOMO SAPIENS (HUMAN), 346 aa.	1.60E-99	

2422	cg43922882	91	TGCTACCAAGGC AGTAATATTTTC C T ATATGAACC AGACCAAAATACC CTTT	C	T				SILENT- NONCODING	oncogen	Human Gene Similar to SWISSPROT- ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	6.40E-91	
2423	cg43922882	94	TACCAAGGCAGT AATATTTTTCAT A T TGAACCAGA CCAAATACCCCTT TAAT	A	T				SILENT- NONCODING	oncogen	Human Gene Similar to SWISSPROT- ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	6.40E-91	
2424	cg43922762	1409	CAGGCGTCACCA TCCACCTTCCCT T gap T CTACAA GGACTCCATTGG ATCTGCA	gap	T				SILENT- NONCODING	oncogen	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2425	cg43922762	1442	GACTCCATTGGA TCTGCAAGAACA CT gap TGGACC TTTGGGTTCTTT CTGGGGG	T	gap				SILENT- NONCODING	oncogen	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2426	cg43922762	1443	ACTCCATTGGAT CTGCAAGAACAC TT gap GGACCT TTGGGTTCTTTC TGGGGGG	T	gap				SILENT- NONCODING	oncogen	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2427	cg43922762	1490	GGGATATTTC TAAGGCATGTGG C C gap TTTATCT CAACGGAAGCC CCCTCTT	C	gap				SILENT- NONCODING	oncogen	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2428	cg43922762	1811	GAAATCCATAC TTCTCTCAGATG G G gap AACAGT AAAGAAAGCAGA ATCAACT	G	gap				SILENT- NONCODING	oncogen	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)

2428	cg43282762	1884	TTGAAAAGACCA AGACTTTTGTCT G[A/T]TCAAGTGG TTTACAGCTAC CACCC	A	T				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2430	cg43282762	1885	TGAAAAGACCAA GACTTTTGTCTG A[T/A]CAAGTGGT TTTACAGCTACC ACCC	T	A				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2431	cg43282762	1916	GGTTTACAGCT ACCACCCCTTAGG G[G/gap]TAAATTG GTAATTACCTGG AGAAGAA	G	gap				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3.00E-84	7 (7q31)
2432	cg43967603	212	TCGACITTTTTT TTTTTTTTTCTG TCCACGCTGGC ACATTATTGGC ATT	G	T				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:Q98471 C-MYC BINDING PROTEIN MM-1 - HOMO SAPIENS (HUMAN), 167 aa.	4.80E-77	12
2433	cg43967603	282	ATCACCAGGAAG CCACGCCCAAAG G[G/gap]TGTCCT TCTGCCCATTT CTGCAAA	G	gap				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:Q98471 C-MYC BINDING PROTEIN MM-1 - HOMO SAPIENS (HUMAN), 167 aa.	4.80E-77	12
2434	cg43101925	378	TCCTGGGGAATT CACTTCTCTTCC TTCCTCTCATGG AAGATGCAAGTA AAAG	C	T				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSNEW- ID:P28574 MAX PROTEIN (MYN PROTEIN) (MYC-BINDING NOVEL HLH/LZ PROTEIN) - MUS MUSCULUS (MOUSE), 160 aa. Icds:SWISSPROT- ID:P28574 MAX PROTEIN (MYN PROTEIN) (MYC-BINDING NOVEL HLH/LZ PROTEIN) - MUS MUSCULUS (MOUSE), 160 aa.	2.00E-72 (14q23)	14

2435	cg44029157	1010	CCACCCTTACTT CCTGGCCTCTTC TG[<i>gap</i>]GGCTAC TGCCACTGTGTG CCTTCTG	G	gap			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17082 RAS-RELATED PROTEIN R- RAS2 (RAS-LIKE PROTEIN TC21) (TERATOCARCINOMA ONCOGENE) - HOMO SAPIENS (HUMAN), 204 aa.	5.10E-66	
2436	cg44029157	1012	ACCTTACTTCC TGGCCTCTTCTG G[<i>gap</i>]CTACTG CCACTGTGTGCC TTCTGCC	G	gap			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P17082 RAS-RELATED PROTEIN R- RAS2 (RAS-LIKE PROTEIN TC21) (TERATOCARCINOMA ONCOGENE) - HOMO SAPIENS (HUMAN), 204 aa.	5.10E-66	
2437	cg43975131	2054	GAAGGGAAGTGA AAAGCAGTAGAA G[<i>gap</i>]AACAGTCA GAGATGCCCTCAC TGATA	A	G			SILENT- NONCODING	oncogene	Human Gene Similar to SPTREMBL- ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64 (17p13.3)	
2438	cg43975131	2081	ACAGTCAGAGAT GCCTCACTGATA G[<i>gap</i>]CAGGAGG CCGAACAGGTAA ACCCCA	G	A			SILENT- NONCODING	oncogene	Human Gene Similar to SPTREMBL- ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64 (17p13.3)	
2439	cg43975131	578	AGCCTGACTCCT GCTGGGCACAG CC[<i>gap</i>]ACCCCT GCTGGGCACAG TGACTGGGAG	C	gap			SILENT- NONCODING	oncogene	Human Gene Similar to SPTREMBL- ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64 (17p13.3)	
2440	cg43975131	589	TGCTGGGCACA GCCCACCCCTGCT GG[<i>gap</i>]CACAG TGACTGGAGGTT CCAGGCTG	G	gap			SILENT- NONCODING	oncogene	Human Gene Similar to SPTREMBL- ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64 (17p13.3)	
2441	cg43975131	880	CTCCCTGAGGCT GAGACGTGAAG GT[<i>gap</i>]CCCAG TCTGGGCCGTGA CTCACTCT	G	gap			SILENT- NONCODING	oncogene	Human Gene Similar to SPTREMBL- ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.80E-64 (17p13.3)	

2442	cg43280482	2797	TGGCATATCACC CCGCACTGTGG GGC[<i>gap</i>]CAGGC ACCACTAGCCTG GCTCAAAAT	C	<i>gap</i>			SILENT- NONCODING	oncogene	Human Gene Similar to TREMBLNEW- ID:G2952331 ARG/ABL-INTERACTING PROTEIN ARBP2A - HOMO SAPIENS (HUMAN), 666 aa.	3.90E-62	8
2443	cg43941861	604	ACCATTTCTGAC CTGCAGTTGCAG A[<i>AC</i>]TAGGTGTG ACTTGCATTAA AATAA	A	C			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P01100 P55-C-FOS PROTO- ONCOGENE PROTEIN (GOS7 PROTEIN) - HOMO SAPIENS (HUMAN), 380 aa.	2.60E-61	14
2444	cg17903042	1163	GCCGCGCAGAG CGGCCGCGGG GGG[G[<i>gap</i>]CGCT GCGCACAAACCC GGGAGAAA	G	<i>gap</i>			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P04828 WNT-1 PROTO-ONCOGENE PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 370 aa.	7.90E-61	
2445	cg43943100	1164	TGCAAACTCTAG GACTATTATATAA [<i>gap</i>]TGTAATAAAT CTCTCTTGTGAT ACTGG	gap	T			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03987 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2446	cg43943100	1164	TGCAAACTCTAG GACTATTATATAA [<i>gap</i>]TGTAATAAAT CTCTCTTGTGAT ACTGG	gap	T			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03987 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2447	cg43943100	1180	TATTATATAAGTA AAATCTCTCTT GCTGTACTCTGG AAAGTGATTAGA ATGT	G	C			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03987 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2448	cg43943100	1182	TATATAAGTAAA AATCTCTCTTGT GCTACTCTGGAA AGTGATTAGAAT GTGC	G	C			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03987 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6

2449	cg43943100	1219	GATTAGAATGTG CAAACCTGATATA G(gap/C)TAGCTT TCATCCGCCCTCT TAAAGGG	gap	C			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2450	cg43943100	1278	CAGGAAAGTCCA TTTAAGATGTTG GT/AJAGGTTTAA CAAAGTTGGAAT GCTGG	T	A			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2451	cg43943100	1279	AGGAAAGTCCAT TTAAGATGTTGG TTATGGTTTAAAC AAAGTTGGAATG CTGGC	A	T			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2452	cg43943100	1364	CTCAGAGCTACA ATGCATTTAGTA TTA(gap)TTAAAGC AGCTGACATGAT GACTTT	A	gap			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P03967 RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 187 aa.	3.30E-55	6
2453	cg43979706	1456	CCCCATGTCAGG CGGAGGCGGAA GGC(gap)CCACC GTGCCAGAGGC TGGGCACCA	C	gap			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	2.30E-54	
2454	cg43979706	1814	ATTAAGTCCCT GGGCTGCCCCC TTT(gap)GGGTG CCCCCGCTCC CAGGTTCCC	G	gap			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	2.30E-54	
2455	cg43979706	893	CCCCCGTTCTG TCAGGGTCCCTA A(GA)GGAGGAC ACTCAGGGCCTG TGGCCA	G	A			SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P55258 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - MUS MUSCULUS (MOUSE), 206 aa.	2.30E-54	

2456	cg43268513	633	CCTCTGCCTGTG ACCCGCCGCC GGC[<i>gap</i>]CGCTA GACTGACTTCGC GCAGCGGT	C	<i>gap</i>		SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P04628 WNT-1 PROTO-ONCOGENE PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 370 aa.	7.70E-51	2
2457	cg43307658	2271	GGCCCCAGCCC CCAACCCACAGG CA[G/C]GGAGGG GCATCCCTCCCT GCCGGCC	G	C		SILENT- NONCODING	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0.00E+00	15
2458	cg43307658	2337	GGATGAAACCA CAGGGATTCCG GAT[<i>G</i>]GCCAGA CCCCATTTTATA CTTCACT	T	C		SILENT- NONCODING	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0.00E+00	15
2459	cg43307658	2472	GCTGAATAAAAC AAGGTTTTCTA C[<i>A/T</i>]AAGTGGCT CTGCATGCGGC CTGCTG	A	T		SILENT- NONCODING	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0.00E+00	15
2460	cg43307658	2474	TGAATAAAACAA GGTTTTCTACA A[<i>A/T</i>]GTGGCTCT GCATGCGGCCT GCTGGC	A	T		SILENT- NONCODING	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0.00E+00	15
2461	cg4308761	208	AATAGGCATACA TAAGCAATTATG TIG[<i>A/T</i>]TTATAT CTACTCCTTTCT GAAAC	G	A		SILENT- NONCODING	oxidase	Human Gene SWISSPROT-ID:Q16853 COPPER AMINE OXIDASE PRECURSOR (EC 1.4.3.6) (SERUM AMINE OXIDASE) (SAO) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	17

2462	cg43096761	24	TTTTTTTTTTT TTTTTTTTTT[G/T] TTTGGGCCCAT TATTGTTTATTT	G	T			SILENT- NONCODI NG	oxidase	Human Gene SWISSPROT-ID:Q16853 COPPER AMINE OXIDASE PRECURSOR (EC 1.4.3.6) (SERUM AMINE OXIDASE) (SAO) - HOMO SAPIENS (HUMAN), 763 aa.	0.00E+00	17
2463	cg44028217	36	TTTTTTTTTTT TGAGGCTCTGAG [G/A]GTTTATTGT CTGCCCCAGTGA GGCT	G	A			SILENT- NONCODI NG	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)
2464	cg44024803	166	AACATAGTTCTG ATTTTGAAGTGT T[gap]/GJAGTGGA ACTCAAAACAGAA ATGATTA	gap	G			SILENT- NONCODI NG	oxidase	Human Gene SWISSPROT-ID:P31513 DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 3 (EC 1.14.13.8) (HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 3) (FMO 3) (DIMETHYLANILINE OXIDASE 3) (FMO 3) - HOMO SAPIENS (HUMAN), 531 aa.	4.60E-294	1 (1q23)
2465	cg43271573	1938	TAATGCTAGAGA ATGATAACTAAG A[C/T]TTCTGTGC ATTGAAGGTTG TTGGA	C	T			SILENT- NONCODI NG	oxidase	Human Gene SWISSPROT-ID:Q01740 DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (EC 1.14.13.8) (FETAL HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 1) (FMO 1) (DIMETHYLANILINE OXIDASE 1) - HOMO SAPIENS (HUMAN), 531 aa.	5.30E-293	1 (1q23)
2466	cg42849556	2051	CCACAATAAAAA AAACCTATCAT C[gap]/AJTTACAAA AACAAAGACACCC AAGTCC	gap	A			SILENT- NONCODI NG	oxidase	Human Gene SWISSPROT-ID:P19878 NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) (NEUTROPHIL NADPH OXIDASE FACTOR 2) (P67-PHOX) - HOMO SAPIENS (HUMAN), 526 aa.	2.80E-287	1 (1q25)

2467	cg4394982	294	TTTTAATGACAAT GGAAATTTGATA T/CACAAAAATG GAAGGGTAAATA GAAA	T	C			SILENT- NONCODI NG	oxidase	Human Gene SWISSPROT-ID:Q15800 C 4 METHYL STEROL OXIDASE (EC 1.---) - HOMO SAPIENS (HUMAN), 293 aa.	1.90E-169	4
2468	cg43269428	511	CGCATCAGGTAG ACATGATCATCT G/C/AJATTCITTT TCCACGCTGCAA ATCAC	C	A			SILENT- NONCODI NG	oxidase	Human Gene Homologous to SWISSPROT-ID:Q63448 PRISTANOYL- COA OXIDASE (EC 1.3.3.-) - RATTUS NORVEGICUS (RAT), 700 aa.	1.20E-105	
2469	cg43972840	1584	AGCCCCAGCTTA TCTCCTCCTCCG C/G/gap/CTGTGT AAATGCTCCAGC ACTCAAT	G	gap			SILENT- NONCODI NG	oxygehas e	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.60E-168 (16p13.3)	16
2470	cg44010395	387	TGAGGATGCTGA AGGCAGGGCT GAT/CJCCCTTCG CCCCCTCTGAAG TTTAGG	T	C			SILENT- NONCODI NG	oxygehas e	Human Gene SWISSNEW-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa. lpcis: SWISSPROT-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa.	5.20E-151 (22q12)	22
2471	cg43916857	5785	AAAAGAAGATTT TCCTTAGCAAGA A/A/TJAAAGAGGT CATGTCATTTGT TAATA	A	T			SILENT- NONCODI NG	peptidas e	Human Gene Similar to SPTREMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	3.40E-96	17
2472	cg43916857	5788	AGAAGATTTTCT TTAGCAAGAAAA A/A/TJGAGGTCTAT GTCATTTGTTAAT AAGT	A	T			SILENT- NONCODI NG	peptidas e	Human Gene Similar to SPTREMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	3.40E-96	17
2473	cg43916857	6366	GGAAACAAGAC TTTCCAGCTTG T/G/AJTTACCTAG AAGCGTGAATGT ATAGG	G	A			SILENT- NONCODI NG	peptidas e	Human Gene Similar to SPTREMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	3.40E-96	17

2474	cg43948682	359	CAATTAAAAAT CATAAAGACTG AIG/ATGTTTGA ATAAAATATCAA GAGG	G	A			SILENT- NONCODI NG	peptidas e	Human Gene Similar to TREMBLNEW- ID:G2687937 PEPTIDASE, PUTATIVE - BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE), 592 aa.	5.00E-75	10
2475	cg43254736	278	GAGCCAGGAGC CCGGGATGCGG AGAT/CJGGGCC TCGGTCTCCACA TCCTGGCG	T	C			SILENT- NONCODI NG	peptidas e	Human Gene Similar to SPTRMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	1.10E-67	
2476	cg42923012	237	AATTTGTGTGC CTTAGGCAAAGC CIC/gap/ACCCCC TGCTGAAAGCTC AGTTTC	C	gap			SILENT- NONCODI NG	peptidas e	Human Gene Similar to TREMBLNEW- ID:G2687937 PEPTIDASE, PUTATIVE - BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE), 592 aa.	1.00E-65	X
2477	cg41626506	291	GGAAAACAGTCG TCCTGCTGATTT CIG/CJGATTGCCC TGTGTTTGAAA AGAGT	G	C			SILENT- NONCODI NG	peroxida se	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00	3 (3q26.3)
2478	cg41626506	3179	AGCACAGCGAG CGCTCTCATTCT GA[C/gap]CTTTT TCCTCTTCTCAG CCAACTG	C	gap			SILENT- NONCODI NG	peroxida se	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00	3 (3q26.3)
2479	cg41626506	3180	GCACAGCGAGC GCTCTCATTCTG AC[C/gap]TTTTT CCTCTTCTCAGC CAACTGC	C	gap			SILENT- NONCODI NG	peroxida se	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00	3 (3q26.3)
2480	cg44913844	216	CGAGCCGAGGC CTCCTGCAGTGT TC[C/T]GCACAGC AAACCGCACGCT ATGGCT	C	T			SILENT- NONCODI NG	peroxida se	Human Gene SWISSPROT-ID:P04040 CATALASE (EC 1.11.1.6) - HOMO SAPIENS (HUMAN), 527 aa.	2.70E-296	11 (11p13)

2481	cg42691889	331	CTAAGGCTCCTC AGGACTGGATG GA[G/T]TAGGAG ATCTGTGTGTTG AGCAGTT	G	T			SILENT- NONCODING	peroxidase	Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE- RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa.	8.90E-101	14 (14q24.1)
2482	cg42691889	332	TAAGGCTCCTCA GGACTGGATGG AGT/GJAGGAGA TCTGTGTGTTGA GCAGTTC	T	G			SILENT- NONCODING	peroxidase	Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE- RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa.	8.90E-101	14 (14q24.1)
2483	cg43951241	365	CTCAGGGGAGG CCCCCCCACAA GGG[C/gap]TTCG GGCCCCCTCCTC ATAGAGACA	C	gap			SILENT- NONCODING	peroxidase	Human Gene Similar to SWISSPROT- ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	
2484	cg43951241	372	GAGGCCCGCCCC ACAAGGGCTTCG GG[C/gap]CCCTC CTTCATAGAGAC ACCACCCC	C	gap			SILENT- NONCODING	peroxidase	Human Gene Similar to SWISSPROT- ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	
2485	cg43951241	375	GCCCGCCACACA AGGGCTTCGGG CCC[C/gap]TCCT TCATAGAGACAC CACCCTGA	C	gap			SILENT- NONCODING	peroxidase	Human Gene Similar to SWISSPROT- ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	
2486	cg43951241	519	AGGAAGAAGGA GGCTGGTGGTG TGTA/TGTGTGG GCATGTGGGAG ATGCTGGC	A	T			SILENT- NONCODING	peroxidase	Human Gene Similar to SWISSPROT- ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	

2487	cg43951241	886	GGCCCTTGCAATG ATGGGCAGGG GT[<i>gap</i>]/AJGGGT AGGGTGGGTG GGCATCAGT	<i>gap</i>	A				SILENT- NONCODING	peroxidase	Human Gene Similar to SWISSPROT- ID:P46412 PLASMA GLUTATHIONE PEROXIDASE PRECURSOR (EC 1.11.1.9) (GSHPX-P) - MUS MUSCULUS (MOUSE), 226 aa.	1.30E-62	
2488	cg43917453	13	TTTTTTTTTTTGG /TTTGAATCAGA AGTTTAATATGA CAC	G	T				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2489	cg43917453	1467	ATGAACCGATTG CCCTCCACCCGT A/A/TCTGGATT TTCCACAAATCT CTCTT	A	T				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2490	cg43917453	164	ATTTCGATTAATT AAATTCAGATA G/AJAGAGAAAGTA ATTTTGAAAG AAAT	G	A				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2491	cg43917453	1642	TCCTGACAAACAT CCGTGGGGTGG GG[G <i>gap</i>]/CTCCC CTGAGGCCCT GAGGCTGCC	G	<i>gap</i>				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2492	cg43917453	1662	TGGGGGCTCCC CTGAGGCCCT GAG[G <i>gap</i>]/CTGC CGCTCACTGGG GAAGGGCCTT	G	<i>gap</i>				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2493	cg43917453	270	ATTTTGGCATCA TTCTGTCCGCTC A/GTTAGGCCGT GTTCCCTCTGGT AGGC	G	T				SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7

2494	cg43917453	656	CGCAGTGCGTG CAGGTGCGCCT GATC/TTCCTCT CCCGGAGGGA AATGCTCG	C	T			SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2495	cg43917453	661	TGCGTGCGAGGTC GCCCTGATCTCC TTC/gap/TCCCGG GAGGGAATGCT CGCAGCC	C	gap			SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2496	cg43917453	90	CCGAGGTTTCT CTTCAACATAA GIGTAGTTAGAA ATTACAAGTAGG CAAT	G	T			SILENT- NONCODING	phosphatase	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
2497	cg43920534	1087	CTTGGTTTTCG CTTTTTTTCCT [gap/A]AAAAAAA AAGGCCACTGAA ATGTA	gap	A			SILENT- NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
2498	cg43920534	1097	CGCTTTTTTTCG TTAAAAAAA [gap/A]GGCCACT GAAATGTATAA ATGGTC	gap	A			SILENT- NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
2499	cg43958187	3119	CTATCAAAATAC ATGTATGTTTCA GIG/gap/JATATTT GACCTGTCATTA AAAAA	G	gap			SILENT- NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q15171 PROTEIN-TYROSINE PHOSPHATASE G1 (EC 3.1.3.48) (PTPG1) - HOMO SAPIENS (HUMAN), 780 aa.	0.00E+00 (7q11.23)	7
2500	cg43930478	41	GGCCATTGAGG GGAGCCCATGG GG[G/C]CAGGAA GGCGGCTGTGA GGCGCCCC	G	C			SILENT- NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q15171 PROTEIN PHOSPHATASE 2A 74 KDA REGULATORY SUBUNIT (DELTA OR B HOMO SAPIENS (HUMAN), 570 aa.	1.10E-306	6

2501	cg43928335	1725	GCTTAATAATG ATTAACAAGGA A[G/T]ACGAGTAA AAAAACAATCCCA TTTCA	G	T				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P54613 PROTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, BETA ISOFORM (PROTEIN PHOSPHATASE PP2A SUBUNIT A, BETA ISOFORM) (P65-BETA) - SUS SCROFA (PIG), 602 aa (fragment).	3.20E-302	11 (11q22)
2502	cg43088901	2091	CCCTCCATCCCC CTTTACCCCTCTTT [G/C]CTGCAGAG AAACTTAAGCAA AGGGG	G	C				SILENT- NONCODING	phosphatase	Human Gene SWISSNEW-ID:P30304 M- PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.lpcis:SWISSPROT- ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.	4.00E-288	3 (3p21)
2503	cg43088901	2345	AGCCGGGGCCT TATCGGGGCTCCA GC[C/gap]ATCTC ATGAGGGGAGA GGAGACGGA	C	gap				SILENT- NONCODING	phosphatase	Human Gene SWISSNEW-ID:P30304 M- PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.lpcis:SWISSPROT- ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.	4.00E-288	3 (3p21)
2504	cg43088901	2387	GGAGACGGAGG GGAGTAGAGAA GTTT[gap]ACAC AGAAATGCTGCT GGCCAAATA	T	gap				SILENT- NONCODING	phosphatase	Human Gene SWISSNEW-ID:P30304 M- PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.lpcis:SWISSPROT- ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.	4.00E-288	3 (3p21)
2505	cg43302847	2299	ATGCTCATGTCC CTGTCCCCAGGC C[C/gap]AGCCCT CCCTCAGGGGA GTTGAGGT	C	gap				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P05186 ALKALINE PHOSPHATASE, TISSUE- NONSPECIFIC ISOZYME PRECURSOR (EC 3.1.3.1) (AP-TNAP) (LIVER/BONE/KIDNEY ISOZYME) (TNSALP) - HOMO SAPIENS (HUMAN), 524 aa.	3.20E-286	1 (1p36.1)

2506	cg43302847	2419	CTGGGTGGCCAT CCTACCCAGCGT G[ap]/G[CCCAGG CCGGAAGAGC CACCTGGC	gap	G			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P05186 ALKALINE PHOSPHATASE, TISSUE- NONSPECIFIC ISOZYME PRECURSOR (EC 3.1.3.1) (AP-TNAP) (LIVER/BONE/KIDNEY ISOZYME) (TNSALP) - HOMO SAPIENS (HUMAN), 524 aa.	3.20E-286	1 (1p36.1)
2507	cg43302847	2516	AAGCGACTCTCC TGTTTGGACGG C[ap]/AJAAAAA AAATTTTTTTTC TCCTTT	gap	A			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P05186 ALKALINE PHOSPHATASE, TISSUE- NONSPECIFIC ISOZYME PRECURSOR (EC 3.1.3.1) (AP-TNAP) (LIVER/BONE/KIDNEY ISOZYME) (TNSALP) - HOMO SAPIENS (HUMAN), 524 aa.	3.20E-286	1 (1p36.1)
2508	cg44012067	105	TTTTAATTTTT TTTTTTTTTTTC TTTCAACTTGCT CAGTGCCTTATT GAA	C	T			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P30305 M PHASE INDUCER PHOSPHATASE 2 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 566 aa.	1.00E-285	20
2509	cg43984117	145	TATAGGAGGGGAC GGCGCAGCGG GG[C/gap]CCCCC TGCTGACCCCTCT CTCTGGGG	C	gap			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2510	cg43984117	188	CTCTGGGGGTCTC TCCTATGGCGGG G[C/gap]CCTATT GCTTGAGTGGG GGAGGAGC	C	gap			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2511	cg43984117	190	CTGGGGGTCTTC CTATGGCGGGG CC[C/gap]TATTG CTTGAGTGGGG GAGGAGCCA	C	gap			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	

2512	cg43984117	295	CTCCCCACAGAA TGCCAGGCTGT G[C/gap]CCCCAG CCCCAGCTGCTC CACCTCC	C	gap			SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2513	cg43984117	299	CCACAGAAATGCC CAGGCTGTGCC CC[C/gap]AGCCC CAGCTGCTCCAG CTCCTTCC	C	gap			SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2514	cg43984117	324	CAGCCCCAGCT GCTCCACCTCCT TC[C/T]TCTCTGT CCAGGGAGCAG ACCTCT	C	T			SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2515	cg43984117	95	TAAATAGCTGG GGAGGGGGTG AG[C/gap]CCCAG CCTAGCCCCACC ATGGGGCT	C	gap			SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2516	cg43984117	98	AATAGCTGGGGA GGGGGGTGAGC CC[C/gap]AGCCT AGCCCCACCATG GGGCTATA	C	gap			SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.10E-273	
2517	cg43139469	1922	CTCAAGCCTGGA GTCAGGCTTG C[C/gap]TACAAG AGGAGAGAAAGT AGATAGG	C	gap			SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P30307 M PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 473 aa.	7.00E-259	5 (5q31)

2518	cg43138489	402	GCTCAGGGTTTC TGCAGTGTCTTT T(gap)TJGGTGAC TTGTTAGCAGCC AGTGGCT	gap	T				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P30307 M PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 473 aa.	7.00E-259	5 (5q31)
2519	cg43980696	528	CCCCCAGTGAA AGCTGGGCTGG GC(A)TJGGGAGT CCTCAGAAGCCA CTCTGGC	A	T				SILENT- NONCODING NG	phosphatase	Human Gene SPTREMBL-ID:Q28647 PROTEIN PHOSPHATASE 2A0 B' REGULATORY SUBUNIT ALPHA ISOFORM - ORYCTOLAGUS CUNICULUS (RABBIT), 500 aa.	9.10E-250	11
2520	cg43918944	2303	TGAATGAATTTTA TCATCTATGATA T(A)GAGTGAGAT AATTATGGGAGT GGTA	T	A				SILENT- NONCODING NG	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
2521	cg43918944	2374	TCCTTGATTGTG TTGCACATAGAT ATTGCGGTAGTCT GCTCTGTATATT TTTCC	T	C				SILENT- NONCODING NG	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56- ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
2522	cg43336281	99	CTTCTGGCATC TTGGGACTTGTC C(C)gapJTAAGAA TAGGGAAGACAG TCATQCT	C	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2523	cg43336281	131	TAGGGAAGACAG TCATCCTGTCCT G(G)gapJAGCAA GCTCCCCCTTGC ACAGGAA	G	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2524	cg43336281	141	AGTCATCCTGTC CTGGAGCAAAGC TTC(gap)CCCCCTT GCACAGGAACAC AACTCCC	C	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22

2525	cg43336281	1631	AGCGACTATGTT TAAGGTTTTTTT [T/gap]GTAAATAA GAGACCTTAAGC AATGC	T	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2526	cg43336281	2528	AGAGCCCCGCT GTCGGGCCAG GCA[C/A]CACTAG GTGGCAGTCGC AGCTCCTG	C	A				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2527	cg43336281	299	AGAATGCACAGG ACTCTGGGGCT G[C/gap]CCCCCT TGAGCTACAGAG GCAGAAT	C	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2528	cg43336281	328	CCCCCTGAGCTA CAGAGGCAGAAT C[G/A]AACCAAAA ACACTGCTTCCT TTAAC	G	A				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2529	cg43336281	394	CATTAGCTTGG GACGAGGCTAG GC[C/gap]TAAGA AGGGCCAGAGC TGTCCTCCC	C	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2530	cg43336281	830	ATCTCCCCAGGA CACGCCGGCTC AC[C/T]TGCACCC ACAGCGTTCTAG GAGGTC	C	T				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22
2531	cg43336281	97	GCCCTTCTGGCA TCCTGGGACTTG TC[gap]CCTAAG AATAGGGAAGAC AGTCATC	C	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P49593 PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015) - HOMO SAPIENS (HUMAN), 454 aa.	1.90E-242	22

2532	cg43988504	2416	CAGTTTTCAGG AATAGGCATTG C[C/gap]TAATTC CTGGCATGACAC TCTAGTG	gap			SILENT- NONCODING NG	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.lpcis:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
2533	cg43988504	3028	CCAGGCTGTAAG CATTCTGAGCTG G[G/gap]CTTGTT GTTTTAAGTCC TGTATAT	gap			SILENT- NONCODING NG	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.lpcis:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
2534	cg43988504	60	GGCCTCGGGC TAAGAGCGCGAC GC[G/gap]GCCTA GAGCGGCAGAC GGCGCAGTG	gap			SILENT- NONCODING NG	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.lpcis:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
2535	cg43988504	61	GCCTCGGGCT AAGAGCGCGAC GCG[G/gap]CCTA GAGCGGCAGAC GGCGCAGTGG	gap			SILENT- NONCODING NG	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.lpcis:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
2536	cg43983327	1820	CAGCCAGCCACA TTTCCCTGTGTC T[G/gap]GCTAGA GCCACCATTAGA CTCAGAC	gap			SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P1117 LYSOSOMAL ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) (LAP) - HOMO SAPIENS (HUMAN), 423 aa.	1.90E-233	11 (11p12)

2537	cg43983327	1821	AGCCAGCCACAT TCCCTGTGTCT G[G/gap]CTAGAG CCACCATTAGAC TCAGACA	G	gap			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P11117 LYSOSOMAL ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) (LAP) - HOMO SAPIENS (HUMAN), 423 aa.	1.90E-233	11 (11p12)
2538	cg44004203	103	AATATAGAATCC CACTAGCAGCTT T[G/gap]CTTAGT GATCAAGACGTT TTTGGGA	G	gap			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2539	cg44004203	1659	TACTAAATGTGA TCTAAGAGAATA T[G/C]GTTCCACC CAGTGTGGAGC CATGAA	G	C			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2540	cg44004203	1660	ACTAAATGTGAT CTAAGAGAATAT G[G/C]TTCACC CAGTGTGGAGC CATGAAA	G	C			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2541	cg44004203	1728	ACATAAAGATGC CATTGTAGTAGA A[A/gap]TGCACA AATGCATGTAAT AACTGCA	A	gap			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2542	cg44004203	1827	ACTCAGACTTCG TTCAAAGTGACA G[gap]/G/AACGAG GGGAGTGGAGT GCAAAGGA	gap	G			SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	

2543	cg44004203	2018	GGGTAGGAGGG CAACAAACACAT CC[C]/TTAGGTGA AGGAGTGTAAT ACAGAT	C	T			SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2544	cg44004203	659	CCTCTTTTGTG ATCACTTCTGG C[C]/gap]TTGCGG AGATGACAAACC TGTTCTG	C	gap			SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	
2545	cg43984194	249	TAGCCCCAAGAT TGAGATTCTTAT G[gap]/GJAATACA CTGTATTATTAC CTGCAAT	gap	G			SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P35813 PROTEIN PHOSPHATASE 2C ALPHA ISOFORM (EC 3.1.3.16) (PP2C-ALPHA) (IA) - HOMO SAPIENS (HUMAN), 382 aa.	1.9E-208	14
2546	cg43984194	252	GCCCCAAGATTG AGATTCTTATGA A[T]/JACACTGTA TTATTACCTGCA ATACT	T	C			SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P35813 PROTEIN PHOSPHATASE 2C ALPHA ISOFORM (EC 3.1.3.16) (PP2C-ALPHA) (IA) - HOMO SAPIENS (HUMAN), 382 aa.	1.9E-208	14
2547	cg43307343	460	AAAATTTATAGCT GCAGAATATTCT C/TJAAGTCATGA ATATTAGGTGTC TGTC	C	T			SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P17706 CELL PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.48) (TCPTP) - HOMO SAPIENS (HUMAN), 415 aa.	3.6E-207 (18p11.3)	18
2548	cg43989460	167	CCTGGACTCGGAG GGAAGGCCGAG AG[G]/gap]ACACG GACGGTGGCCA CACCACGCT	G	gap			SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:P36876 PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55) - RATTUS NORVEGICUS (RAT), 447 aa.	1.9E-202	

2549	cg43969460	187	GAGAGGACACG GACGGTGGCCA CAC(C/gap)ACGC TGCAGTGAAGGC CCAAGTGTG	C	gap		SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P36876 PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55) - RATTUS NORVEGICUS (RAT), 447 aa.	1.9E-202	
2550	cg43969460	215	GCTGCAGTGAAGG GCCCAAGTGTGA T(G/C)GCAGAGA AAGAGGGAAAGT TGGAGA	G	C		SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P36876 PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55) - RATTUS NORVEGICUS (RAT), 447 aa.	1.9E-202	
2551	cg43933809	1541	CATTAGTCTTTA AAAAAAAAAAAAA[gap/A]GGATTCTT ATTAACCAACAT ACTTA	gap	A		SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), 327 aa.	1.6E-181	2 (2p23)
2552	cg43933809	2090	GCAGTAAGTAAT ACAATGTGCCAA T(C/T)CATATAAT GTAAGTTAACAG GTTTC	C	T		SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), 327 aa.	1.6E-181	2 (2p23)
2553	cg43933809	2378	TGTTAATACTAA CCCTTAAAAAA[A/gap]GAAATAGG AAAGAAAGGCT GCAAT	A	gap		SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), 327 aa.	1.6E-181	2 (2p23)

2554	cg43933809	3189	AATAGTTGGTGA ATGCTCTGTAAAG CT/CJCTTCCCAT ATTCACATTTTAA AAAT	T	C				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), 327 aa.	1.6E-181	2 (2p23)
2555	cg43933808	3180	ATAGTTGGTGAA TGCTGTGTAAGC TTC/TTTCCCAT TTTCACATTTTAA AATG	C	T				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), 327 aa.	1.6E-181	2 (2p23)
2556	cg43917813	1566	TGAAATTAGTA CACTATGTTCTA Ggap/GJGTCAGT CTAACAGTTTGC CTGCTGT	gap	G				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P11082 SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-BETA, CATALYTIC SUBUNIT (EC 3.1.3.16) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS, 309 aa.	5.3E-174	8
2557	cg43917813	1892	TAAATTACTGTTT TATGTTGATCTG CT/TATATTCTGT ATATTGTCATG ACA	C	T				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:P11082 SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-BETA, CATALYTIC SUBUNIT (EC 3.1.3.16) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS, 309 aa.	5.3E-174	8
2558	cg43269274	15	TTTTTTTTTTT TTC/TTCCCTTTA CTATTTTATTTT ACAC	C	T				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10

2559	cg43269274	164	AACTAACAGACA AAAAGAAAAAA A[A/gap]GTAGTA CCACGTTGC AAA ATCTGCA	A	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2560	cg43269274	208	ATCTGCAAAATCC CAGAAAGTCCACA G[C/gap]TTGAAG ACAACCTCCAGG GGCAGGG	C	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2561	cg43269274	22	TTTTTTTTTTTT TCTCCTTTT[C/A] CTATTTTATTTT ACACTATAAAA	T	C				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2562	cg43269274	40	CTCCTTTTACTAT TTTTATTTTACA[C/gap]TATAAAA ACAAGAACAACA ACAAC	C	gap				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2563	cg43269274	53	TTTTATTTTACAC TATAAAAAACAA[G/C]AACACAAC AACACCAGTAA CATA	G	C				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2564	cg43269274	635	CATGTCCCTACA AACCCGTGAGGG T[G/T]ACTTTCCC AACTAGACGGTG ATCAG	G	T				SILENT- NONCODING NG	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10

2565	cg43269274	816	CCACGTTGCTG C CAGGTATTATT G/C/GCTTATGCT TGAATGAAAAG GCGAA	G				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
2566	cg43972150	119	AACAGCCAGCCA G TGGCCTGCTGGA A/G/gap/CCAGGG GACAAATCTTCA TACACAG	gap				SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17
2567	cg43972150	289	CATGGCGGAGG G CAAGTGCTGGAT GT[G/gap]GGGAC AGGCCATGTCCC CAAAGCCC	gap				SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17
2568	cg43972150	302	GCGGAGGCAAG gap TGCTGGATGTGG GG[gap/G]ACAGG CCATGTCCCCAA AGCCCCCTA	gap				SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17
2569	cg43972150	47	TTTTTTTTTTTT TTTTTTTTTTTTTT// GJTAAAAGCCAC GCTAATAATTAC CCC	T				SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17
2570	cg43972150	809	GAAATCCAGAC C CCTCTGCTCACT G/C/gap/JTCACGG GGACAAAGCTATG AGATGCC	gap				SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q15733 PHOSPHATIDYLINOSITOL (4,5)BISPHOSPHATE 5-PHOSPHATASE HOMOLOG - HOMO SAPIENS (HUMAN), 329 aa (fragment).	5.8E-145	17

2571	cg43967897	119	GGCGGGGAGGC GGTGGCGGCGG CTG[C/gap]CCGG GGCCAACATGAC CAGGCTCTG	C	gap				SILENT- NONCODING	phosphatase	Human Gene Similar to SWISSPROT- ID:P23468 PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP- DELTA) - HOMO SAPIENS (HUMAN), 1912 aa.	2.2E-92	9 (9q)
2572	cg43967897	121	GCGGGAGGCGG TGGCGGCGGCT GCC[C/gap]GGGG CCAACATGACCA GGCTCTGAA	C	gap				SILENT- NONCODING	phosphatase	Human Gene Similar to SWISSPROT- ID:P23468 PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP- DELTA) - HOMO SAPIENS (HUMAN), 1912 aa.	2.2E-92	9 (9q)
2573	cg43967897	197	GGACAGACTCG CTGCGGCTCCG GAG[G/gap]CAGT GATTCCAAGCTG CTCGCGCAC	G	gap				SILENT- NONCODING	phosphatase	Human Gene Similar to SWISSPROT- ID:P23468 PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP- DELTA) - HOMO SAPIENS (HUMAN), 1912 aa.	2.2E-92	9 (9q)
2574	cg43967897	234	AGCTGCTCGCG CACGCTGCTGCC AA[G/gap]CTGCA GGATGGTGAC GTAGCCAGG	G	gap				SILENT- NONCODING	phosphatase	Human Gene Similar to SWISSPROT- ID:P23468 PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP- DELTA) - HOMO SAPIENS (HUMAN), 1912 aa.	2.2E-92	9 (9q)
2575	cg43272594	938	CCGGACCCCGC CCAGGCAGGGA GCT[G/A]CTGTGA GTCCAGCTGAG GCCCACCC	G	A				SILENT- NONCODING	phosphatase	Human Gene Similar to SPTREMBL- ID:Q61469 PHOSPHATIDIC ACID PHOSPHATASE - MUS MUSCULUS (MOUSE), 283 aa.	1.4E-79	19

2576	cg43985274	912	CTTGGCTGGACC TGAGGGCCCTG CC[C]gap/AGCCC TGCTCTGCCCCAG CCCAGCAG	C	gap			SILENT- NONCODING	phosphatase	Human Gene Similar to SPTREMBL-ID:000648 PROTEIN TYROSINE PHOSPHATASE PTPCAAX1 - HOMO SAPIENS (HUMAN), 173 aa. pcids:SPTREMBL-ID:Q63739 TYROSINE PHOSPHATASE - RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS (MOUSE), 173 aa. pcids:TREMBLNEW-ID:G2961199 TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 173 aa.	7.8E-70
2577	cg43948077	1216	ACCCCTCCACCC CATTCCCACCCA ATTG]CCCACCCCT TCTCCATGACCA AAAAAT	T	G			SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146
2578	cg43948077	342	TAGTCTGGAGC TCTGAATAACAA G]G]GCTCTCAA TTGAGGGGGGA AAGAGC	A	G			SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146
2579	cg43948077	352	GCTCTGAATAAC AAGAGCTCTCAA TTTGGAGGGGG GAAAGAGCCTCC AACTG	T	G			SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146
2580	cg43948077	359	ATAACAAGAGCT CTCAATTGAGGG G]G]GAAAGAG CCTCCAAACTGA CACTA	G	T			SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146
2581	cg43948077	369	CTCTCAATTGAG GGGGGAAAGAG CC]T]G]CCAACT GACATCTAAAAA TTCTCTC	T	G			SILENT- NONCODING	phosphatase	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146

2582	cg43948077	373	CAATTGAGGGG GGAAGAGCCTC CA/ATJACTGACA TCTAAAAATTCCT CTTAG	A	T				SILENT- NONCODI NG	phosphat aseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2583	cg43948077	376	TGAGGGGGAA AGAGCCTCCAAA CT[gap/T]GACAT CTAAAAAATTCCT CTTAGAGA	gap	T				SILENT- NONCODI NG	phosphat aseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2584	cg43948077	381	GGGGGAAAGAG CCTCCAAAAGTGA CA/T[gap]CTAAAA ATTCTCTTTAGA GACACCA	T	gap				SILENT- NONCODI NG	phosphat aseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2585	cg43948077	390	AGCCTCCAAAAGT GACATCTAAAAA TT/CJCTCTTAG AGACACCAAGTTA CTCC	T	C				SILENT- NONCODI NG	phosphat aseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2586	cg43948077	393	CTCCAAAAGTGA ATCTAAAAATTC CT/CJCTTAGAGA CACCAGTTACTT CCAAA	T	C				SILENT- NONCODI NG	phosphat aseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2587	cg43948077	413	ATTCTCTTAGA GACACCAAGTTAC TT[gap]CCAAAC AAATCTTTTCCTT TTTAAT	T	gap				SILENT- NONCODI NG	phosphat aseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2588	cg43948077	472	CCCAACTGGTCA TATCCTTTGAAA A[gap/A]CTGCCT TCATAATACACTT AAAAAGT	gap	A				SILENT- NONCODI NG	phosphat aseinhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1

2589	cg43948077	488	CCTTTGAAAACT GCCTTCATAATA C/A/CJCTTAAAG TAATGCCCTTAGA GTAGA	A	C				SILENT- NONCODING	phosphatase inhibitor	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1
2590	cg43931444	1926	TTGTAGCTGTT TAAAAA A[A/gap]AAGGTA GCTGTGATACAA ACCCGAG	A	gap				SILENT- NONCODING	phosphatase inhibitor	Human Gene Similar to SWISSPROT- ID:P39687 POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAPI) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) - HOMO SAPIENS (HUMAN), 249 aa.	1.2E-89	9
2591	cg43931444	1927	TTGTAGCTGTT AAAAA A[A/gap]AGGTAG CTGTGATACAA CCCCAGG	A	gap				SILENT- NONCODING	phosphatase inhibitor	Human Gene Similar to SWISSPROT- ID:P39687 POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAPI) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) - HOMO SAPIENS (HUMAN), 249 aa.	1.2E-89	9
2592	cg43931444	1928	TGTAGCTGTTA AAAAA A[A/gap]GGTAGC TGTGATACAAAC CCCAGGA	A	gap				SILENT- NONCODING	phosphatase inhibitor	Human Gene Similar to SWISSPROT- ID:P39687 POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAPI) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) - HOMO SAPIENS (HUMAN), 249 aa.	1.2E-89	9

2593	cg43931444	612	CGCAGTAGACAG AGACAGACCGA GA[gap]GJAGGAA GGGAGAGACAG AGGGGGCGC	gap	G			SILENT- NONCODING	phosphatase inhibitor	Human Gene Similar to SWISSPROT- ID:P39687 POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAP1) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) - HOMO SAPIENS (HUMAN), 249 aa.	1.2E-89	9
2594	cg43950308	662	TTATGTTACATCA AGGCAGCCATG C[C]gapJAATAAA ATGGAAGGCTAT GAAAGCA	gap	gap			SILENT- NONCODING	phosphorylase	Human Gene SWISSPROT-ID:P46019 PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, LIVER ISOFORM (PHOSPHORYLASE KINASE ALPHA L SUBUNIT) - HOMO SAPIENS (HUMAN), 1235 aa.	0	X (Xp22.2)
2595	cg43950308	806	AGTGGCCCTTG TCAAGGCTACTG C[C]gapJGCCAGG AGGATCTTGCA TCITTAG	gap	gap			SILENT- NONCODING	phosphorylase	Human Gene SWISSPROT-ID:P46019 PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, LIVER ISOFORM (PHOSPHORYLASE KINASE ALPHA L SUBUNIT) - HOMO SAPIENS (HUMAN), 1235 aa.	0	X (Xp22.2)
2596	cg43996195	357	GGCAGGGGCTC CAGCTCTTGTT AA[G]AJAAAGAAC AGGAATGAGAAC AGCTTT	G	A			SILENT- NONCODING	phosphorylase	Human Gene SWISSPROT-ID:P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa.	2.4E-155	
2597	cg43947998	1288	AATAGGGGAG AAGAGAATGGTG GG[G]JTITTTTT TCCCCCTTAAAA TGTAAT	G	T			SILENT- NONCODING	phosphorylase	Human Gene SWISSPROT-ID:Q13126.5 METHYLTHIOADENOSINE PHOSPHORYLASE (EC 2.4.2.28) (MTA PHOSPHORYLASE) (MTAPASE) - HOMO SAPIENS (HUMAN), 283 aa.	2.8E-152	9 (9p21)

2598	cg43958858	2869	TTCTGTTTGCTG TTTTTTGTTTTG [gap/T]TTTTTTTT CTCCAGAGCACT TTGGT	gap	T			SILENT- NONCODING	polymera se	Human Gene SWISSNEW-ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa, pcis:SWISSPROT- ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME- ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa	0	6 (6p12)
2599	cg43958858	2877	GCTGTTTTTTTGT TTTTTTTTTTTTTg ap/T]CTCCAGAG CACTTTGGTCTA GACTA	gap	T			SILENT- NONCODING	polymera se	Human Gene SWISSNEW-ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa, pcis:SWISSPROT- ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME- ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa	0	6 (6p12)
2600	cg44016415	248	AGAAATGAGAAA AAAATAGCAAGC GIC/gap]CAGGGC CAATTAAGCATC CCICICG	C gap	gap			SILENT- NONCODING	polymera se	SAPIENS (HUMAN), 808 aa Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa.	0	X
2601	cg44016415	249	GAATGAGAAAA AAATAGCAAGCG CIC/gap]AGGGCC AATTAAGCATCC CICICCC	C gap	gap			SILENT- NONCODING	polymera se	Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa.	0	X

2602	cg44016415	283	TTAAGCATCCCT CTCCCGTTTTT CTT/gap/GAATAC AACACAGTGATC CTCACC	T	gap			SILENT- NONCODING	polymera se	Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa.	0	X
2603	cg44016415	296	TCCCCGTTTTTC TGAATACAACAC A/G/gap/TTGATCC TCACCGTAACCC CTACACA	G	gap			SILENT- NONCODING	polymera se	Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa.	0	X
2604	cg43282997	819	CGAGACAGGAG GCTGAACCCCG GAG/G/gap/CTGC AGCCAGGGAGG AGGCAGTGGG	G	gap			SILENT- NONCODING	polymera se	Human Gene SWISSNEW-ID:P55199 RNA POLYMERASE II ELONGATION FACTOR ELL (ELEVEN-NINETEEN LYSINE-RICH LEUKEMIA PROTEIN) - HOMO SAPIENS (HUMAN), 621 aa.	5.5e-314	
2605	cg43282997	715	GGGAGGGCCGA GGTGGGCTTGC AGC/C/gap/JACCC GCCAGGGCCAG ACGCTCTGCAG	C	gap			SILENT- NONCODING	polymera se	Human Gene SWISSNEW-ID:P55199 RNA POLYMERASE II ELONGATION FACTOR ELL (ELEVEN-NINETEEN LYSINE-RICH LEUKEMIA PROTEIN) - HOMO SAPIENS (HUMAN), 621 aa.	5.5e-314	
2606	cg4393893	318	CAAAGGTTAAGA AATAAATTAAAGA CTT/gap/CCTATT GGGTTGTGTCTG CCAGGGA	T	gap			SILENT- NONCODING	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.pcls:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178 (8p11.2)	8
2607	cg4393893	321	AGGTTAAGAAAT AAATTAAGACTC CTT/gap/JATTGGG TTGTGTCTGCCA GGGAGGA	T	gap			SILENT- NONCODING	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.pcls:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178 (8p11.2)	8

2608	cg43993993	337	AAGACTCCTATT GGGTTGTGCTG C[<i>gap</i>]/G[CAGGGA GGATACAGGCCT CATTCGC	gap	G			SILENT- NONCODING NG	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.[<i>pcds</i> :SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178	8 (8p11.2)
2609	cg43935562	2098	CAGTCAGTTTCAT CCCTACCCCTGGC C[C]/TAGATGATC ACTGATCTTGTC ATTAT	C	T			SILENT- NONCODING NG	polymera se	Human Gene TREMBLNEW-ID:G300898 A1 REPLICATIVE POLYMERASE ACCESSORY PROTEIN 38 KDA SUBUNIT - HOMO SAPIENS, 315 aa.	4.7E-166	13 (13q12.3)
2610	cg43939941	182	GACAATGATGGA GGCTCAGATCAC A[C]/TGCACCTC TTAGTCTTCCA ACTTG	C	T			SILENT- NONCODING NG	polymera se	Human Gene SPTREMBL-ID:Q19969 SIMILAR TO S. CEREVISIAE SERINE- RICH RNA POLYMERASE I SUPPRESSOR PROTEIN - CAENORHABDITIS ELEGANS, 685 aa.	1.9E-160	13
2611	cg43916712	2631	GAGATTATGTTG TGCTCTTTATTG C[C]/ <i>gap</i> /AAAAAT AAACACTTTTAAA AAGACA	C	gap			SILENT- NONCODING NG	polymera se	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.2E-148	
2612	cg43916712	3207	ACTAACCCAGGAG AGAAAGTCTAGTT G[G]/ <i>gap</i> /TTCCT ACAGGTGCACTG GAAACAC	G	gap			SILENT- NONCODING NG	polymera se	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.2E-148	
2613	cg43916712	4335	TTGGCGTACGGC ATCTGCCCCAGG G[G]/ <i>gap</i> /CCACCA GCCTCCGCGTCT GCTCCGC	G	gap			SILENT- NONCODING NG	polymera se	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.2E-148	

2614	cg43988515	577	AGAAACATTAAA CACTATGACACA TGTJACCTTTT AGCTATTTTAAT AGTC	G				SILENT- NONCODING	polymera se	Human Gene Similar to SPTREMBL- ID:Q92811 RNA POLYMERASE II COMPLEX COMPONENT SRB7 - HOMO SAPIENS (HUMAN), 144 aa.	1.80E-70	12
2615	cg43935115	1077	TCCACAATACTT AGCACCTGTCCC C[gap]/CJAAGTGT AAACACTTCCCA TGGCGTG	gap	C			SILENT- NONCODING	polymera se	Human Gene Similar to SWISSPROT- ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2
2616	cg43935115	1192	TAAGAATTTTCAG GCCAGTTGTGGT G[G/gap]CTCATG CCTGTAATCTCA CCAGTTT	G	gap			SILENT- NONCODING	polymera se	Human Gene Similar to SWISSPROT- ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2
2617	cg43935115	1466	TCTCCATTTAAAAA AAAAA A[gap]GGCATTTC AAACTAACAGCG GTTTA	A	gap			SILENT- NONCODING	polymera se	Human Gene Similar to SWISSPROT- ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2
2618	cg43935115	314	GTTTCCCCCAG ACTGAGATCAAG TIG/AJACTTCACT GCAGTGGCTCAA GAGTG	G	A			SILENT- NONCODING	polymera se	Human Gene Similar to SWISSPROT- ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2
2619	cg43935115	810	GTAGCCTTGTC A TTGGGCACACAA C[A/C]ACCCACAGT TCATACAGCAAA TGGGC	A	C			SILENT- NONCODING	polymera se	Human Gene Similar to SWISSPROT- ID:O15514 DNA-DIRECTED RNA POLYMERASE II 16 KD POLYPEPTIDE (EC 2.7.7.6) (RPB4) - HOMO SAPIENS (HUMAN), 142 aa.	2.90E-70	2

2620	cg43948227	94	AACTCTTATGAT CAAAAAAGGCCA C/ATTTTTTAA GATTGTATTACTT GATT	A	T				SILENT- NONCODING	polymera se	Human Gene Similar to SWISSNEW- ID:P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) - HOMO SAPIENS (HUMAN), 126 aa.pcds:SWISSPROT-ID:P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) - HOMO SAPIENS (HUMAN), 126 aa.	5.40E-62	5
2621	cg43969348	422	TAGCTGCTAACA ATGGCTTGGTC TTC/GIAGGGCAA CCAGGTCCCA TGGTGC	C	G				SILENT- NONCODING	polymera se	Human Gene Similar to SPTREMBL- ID:Q15370 RNA POLYMERASE II TRANSCRIPTION FACTOR SIII P18 SUBUNIT - HOMO SAPIENS (HUMAN), 118 aa.	3.90E-59	16
2622	cg43924683	161	TACAAAACCCCC CATCCAGATATA TTT/gap/CACGTTA ACAACTCTGAGA TAACTG	T	gap				SILENT- NONCODING	polymera se	Human Gene Similar to TREMBLNEW- ID:G300899 A1 REPLICATIVE POLYMERASE ACCESSORY PROTEIN 36 KDA SUBUNIT - HOMO SAPIENS, 325 aa.	1.40E-54	3 (3q27)
2623	cg42534568	104	CGAGGGGATGC GCGCCAGCAAC CCG/C/gap/JAGCT CTCCCCAGAGAG GGGCCGGCC	C	gap				SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2624	cg42534568	132	CTCTCCCCAGAG AGGGCCGGCC GAG/C/GCTGGA GCGAGCCTGA CGCCAGGC	G	C				SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2625	cg42534568	2529	GGTAAGTGGCTT TTTGTACTGTAG TTT/gap/CAGATA GAGATATTTGG GTATATT	T	gap				SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)

2626	cg42534568	2546	ACTGTAGTTCAG ATAGAGATATTT [G/gap]GGTATAT TTTCAAGATACA TGTTGT	G	gap			SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2627	cg42534568	2556	AGATAGAGATAT TTTGGGTATATT [T/gap]CAAGATA CATGTTGTATTTA TGGA	T	gap			SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2628	cg42534568	2585	GATACATGTTGT ATTATGGAAGA AATGTGTTGGT CCTGATGGTTT TCTGT	A	T			SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2629	cg42534568	2617	GTCCTGATGGTT TTTCTGTGTTACT [T/gap]ATATTAGA GTCAGAGATCTT GGTAT	T	gap			SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2630	cg42534568	88	TGACGTCAGGG CCAAGCGAGGG GAT[G/gap]CGCG CCAGCAACCCCC AGCTCTCCC	G	gap			SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)
2631	cg44938709	758	AGACCGCGAAC CGGAGGAGCG CGG[G/gap]CCCC ACCTAAAGAGG GCGCAGCCG	G	gap			SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P17658 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (HBK2) - HOMO SAPIENS (HUMAN), 529 aa.	1.00E-287	12 (12p13)
2632	cg42937321	132	GGTGCCACAC GCTGGTGAACCA CG[G/gap]CTACG CGGAGCCCCCG CGCAGGCCG	G	gap			SILENT- NONCODI NG	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)

2633	cg42937321	137	CCACACGCTGGT GAACCACGGCTA C[G/gap]CGGAGC CCGCCGCGCAGG CCGCGGAGC	G	gap			SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
2634	cg42937321	149	GAACCACGGCTA CGCGGAGCCCC GC[G/gap]GCAGG CCGCGAGCTGC CGCCCCGACA	C	gap			SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
2635	cg42937321	151	ACCACGGCTACG CGGAGCCCCGC CG[C/gap]AGGCC GCGAGCTGCCG CCCCGACATG	C	gap			SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
2636	cg42937321	1820	CTTGGTCTGCCT ATGCCCTTGTT T[gap/T]ATACATT TCCAGACCATTC ATCAAG	gap	T			SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
2637	cg42937321	3084	ACCTTACTACAA GGGACCTTCAG GC[C/gap]TTTCT CTTTAAAAAAA AATACA	C	gap			SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)

2638	cg43333426	1740	TCAGGACAGAGC CAACCCTGGCTC C/A/GTGGACCTT CTGGAGGAAGG TGGGGG	G				SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSNEW-ID:P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HIR) (HRK1) (HIRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa.pcls:SWISSPROT- ID:P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HIR) (HRK1) (HIRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa.	4.40E-241	
2639	cg40991967	78	CAACAGGGCCTC GGGTACCCTCAC C/C/TIAGCATATC CAAACCTCTTGCA TCAAA	T				SILENT- NONCODING	potassiu m_chann el	Human Gene SWISSPROT-ID:P48048 ATP-SENSITIVE INWARD RECTIFIER POTASSIUM CHANNEL 1 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 1) (ATP- REGULATED POTASSIUM CHANNEL ROM-K) (KIR1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.80E-205 (11q24)	11
2640	cg43008113	161	CTGCGGCGTTG GCCCTGGCTTTG GC/C/TITGGCG GCGGCGGTGGA GAAGATGC	T				SILENT- NONCODING	potassiu m_chann el	Human Gene SPTREMBL-ID:O00180 POTASSIUM CHANNEL KCNO1 - HOMO SAPIENS (HUMAN), 336 aa.pcls:TREMBLNEW-ID:G2811120 TWO P DOMAIN POTASSIUM CHANNEL SUBUNIT - HOMO SAPIENS (HUMAN), 336 aa.	1.80E-180	1
2641	cg43008113	1806	AGTGTAGTTCTG AAACTAAGACTA T/A/gap/GATATTT TGTTTCTTTTGAT TTCTC	gap				SILENT- NONCODING	potassiu m_chann el	Human Gene SPTREMBL-ID:O00180 POTASSIUM CHANNEL KCNO1 - HOMO SAPIENS (HUMAN), 336 aa.pcls:TREMBLNEW-ID:G2811120 TWO P DOMAIN POTASSIUM CHANNEL SUBUNIT - HOMO SAPIENS (HUMAN), 336 aa.	1.80E-180	1

2642	cg43917554	1297	GTCCCCACTCAA CTGACTCATACC TTG/TJTTCCGGC TGCATCACTATG TGCCC	G	T			SILENT- NONCODING	potassiu m_chann el	Human Gene Similar to SPTREMBL- ID:Q16558 MAXIK POTASSIUM CHANNEL BETA SUBUNIT - HOMO SAPIENS (HUMAN), 191 aa.	1.80E+00	5
2643	cg43262191	2044	TCTGACCCCAACC CTGGGCCACTG CC[C/gap]TGCTC CAGAGAGTGGA CCTTGACTC	C	gap			SILENT- NONCODING	prostagla ndin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.lpcis:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3
2644	cg43262191	3156	TTCCCAATTTCTC AGCCTCTTCTCA C/gapJTGCCCTCCA GAGAGGTGGGT GCCTGG	C	gap			SILENT- NONCODING	prostagla ndin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.lpcis:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3
2645	cg43262191	3174	CTTCTCACTGCC TCCAGAGAGGTG G[G/A]TGCCCTGG GTTGAGAGACAC AGCTGC	G	A			SILENT- NONCODING	prostagla ndin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.lpcis:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3
2646	cg43262191	3258	AAGGAGGTCATT CATCAACAAATA T[A/G]TTTATTGG AGACCGACTTTG TGCAA	A	G			SILENT- NONCODING	prostagla ndin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.lpcis:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3

2647	cg43262191	3914	ATGGCAATTAA CCACATTTGGAA G[G/gap]CACTGC CTTCAGCTGAGT TTATGAA	G	gap			SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.[pcis:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0.00E+00	3
2648	cg43951366	174	CCCTCAGACAGC AAAGCCTACCCC C[gap/C]GCGCCG CGCCCTGCCCG CCGCTGCG	gap	C			SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.[pcis:SPTREMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa.	0.00E+00	1 (1q25.2)

2649	cg43951366	197	CCCGCGCCGCGC CCCTGCCCGCC GCTG/CJCGATG CTGCCCGCGC CCTGCTGCT	G	C			SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P33354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PGH SYNTHASE H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa, pcis:SPTRMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa	0.00E+00	1 (1q25.2)
2650	cg43951366	198	CCGCGCCGCGC CCTGCCCGCC CTG/CJGATGC TCGCCCGCGCC CTGCTGCTG	C	G			SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P33354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa, pcis:SPTRMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa	0.00E+00	1 (1q25.2)

2651	cg43951366	2441	TTTGAAATTTTAA AGTACTTTTGGT T/CJATTTTCTGT CATCAACAAAA ACA	T	C			SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.lpcds:SPTREMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa	0.00E+00	1 (1q25.2)
2652	cg43951366	2676	CTTGGATTTTAA TCTGTAAATCA G/AJAGAAATTT TACTACAATTGC TTGTT	A	T			SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.lpcds:SPTREMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa	0.00E+00	1 (1q25.2)

2653	cg43951366	2677	TTGGATTTAAAT CTGTAAATCAG AATJGAAATTT ACTACAATTGCT TGTTA	A	T			SILENT- NONCODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE-2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa. pcds:SPREMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa.	0.00E+00	1 (1q25.2)
2654	cg43308254	120	GCGGCTGCGCC CCGCACCATGG GGG[G/gap]CAGC CCAGCCCCCAGC CGCGGTAAAC	G	gap			SILENT- NONCODING	prostaglandin	Human Gene SPTREMBL-ID:Q00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa.	1.40E-211	1 (1p31.2)
2655	cg43308254	171	GCGGACCTCCG CCGCCGCCCGC GCC[G/gap]CGTC TGCCCCCTCCCG CTGCGGCTC	G	gap			SILENT- NONCODING	prostaglandin	Human Gene SPTREMBL-ID:Q00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa.	1.40E-211	1 (1p31.2)
2656	cg43308254	53	TGGCTCCCTCCC GGGCCAGTGAG CC[C/gap]TGGCG CCGCCGCGGCC GCGGTCCCA	C	gap			SILENT- NONCODING	prostaglandin	Human Gene SPTREMBL-ID:Q00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa.	1.40E-211	1 (1p31.2)

2657	cg43306254	73	GAGCCCTGGCG CCGCCGCGGCC GCG[G/gap]TCCC AGCAGCGGAGT AGGGCGGCGG	G	gap			SILENT- NONCODI NG	prostagla ndin	Human Gene SPTREMBL-ID:O00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa.	1.40E-211	1 (1p31.2)
2658	cg42913398	319	TACAAACATAAAA AATAAAATAAGC A[A/G]ACTGTCTG AGGGGTTTATAT AAGGT	A	G			SILENT- NONCODI NG	protease	Human Gene SPTREMBL-ID:O00199 INTEGRAL MEMBRANE SERINE PROTEASE SEPRASE - HOMO SAPIENS (HUMAN), 760 aa.	0.00E+00	2
2659	cg43916732	1438	GCTGCGTCCCA GGACTGAGACG CAG[G/gap]CCAG CCCCGGCCCCCT AGCCCTCAGG	G	gap			SILENT- NONCODI NG	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.20E-247	7 (7q21.3)
2660	cg43916732	1448	AGGACTGAGAC GCAGGCCAGCC CCG[G/gap]CCCC TAGCCCTCAGGC CTTCTTCT	G	gap			SILENT- NONCODI NG	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.20E-247	7 (7q21.3)
2661	cg43916732	1500	ATCCAAATAAAT GTTTCTTAATGA G[A/G]AAAAA AAAAA AAAAA	A	G			SILENT- NONCODI NG	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.20E-247	7 (7q21.3)
2662	cg43967594	641	TTGCTAGGTATA ATTTTATTTTATA T[gap]AAAAAGTG TTTCTGTGATTCT TCAG	T	gap			SILENT- NONCODI NG	protease	Human Gene TREMBLNEW- ID:G2738915 SERINE PROTEASE - HOMO SAPIENS (HUMAN), 529 aa.	6.10E-239	2
2663	cg43922779	2882	TTTTAAACATAA CCAAAAAAGGCC [G/gap]GGTGCTG GGATTACAGGCA TGAGCC	G	gap			SILENT- NONCODI NG	protease	Human Gene SPTREMBL-ID:O00232 PROTEASOME SUBUNIT P55 - HOMO SAPIENS (HUMAN), 456 aa.	4.40E-236	17

2664	cg43986296	540	CATCTGCTCTGC AGTCTGCGGCA G[G/gap]ATTCCC TAGTGAAGCAGC TCAGGCC	G	gap		SILENT- NONCODI NG	protease	Human Gene SPTREMBL-ID:Q62849 SERINE PROTEINASE RPC7 PRECURSOR - RATTUS NORVEGICUS (RAT), 783 aa.	4.60E-223	
2665	cg43986296	833	CTTCTCAACTTAT ATGTGGGAAGG G[G/gap]TCCCCC ATGCTGGGGGA CCTAGGC	G	gap		SILENT- NONCODI NG	protease	Human Gene SPTREMBL-ID:Q62849 SERINE PROTEINASE RPC7 PRECURSOR - RATTUS NORVEGICUS (RAT), 783 aa.	4.60E-223	
2666	cg44932353	143	TTCAGCCACACT GACGGCTCTGA GC[C/gap]AGAGC CACCTCCTGGCC CCACTGGT	C	gap		SILENT- NONCODI NG	protease	Human Gene TREMBLNEW- ID:G2880036 SIMILAR TO FURIN-LIKE PROTEASES - HOMO SAPIENS (HUMAN), 286 aa.	1.10E-155	3
2667	cg43306871	108	GTGTTAAGCCTT ACATGACAATCA C[C/gap]ATGAAG ATTACATACAC ATGTTAT	C	gap		SILENT- NONCODI NG	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa. Jcds:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19
2668	cg43306871	230	AGGTTACAGAG GGCACTTGGCTT G[C/gap]CCAAAG TCACACAGCAGG GAGTGGC	C	gap		SILENT- NONCODI NG	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa. Jcds:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19

2669	cg43306871	232	GTTTCAGAGAGG GCACTTGGCTTG CC[C/gap]AAAGT CACACAGCAGG GAGTGGCAG	C	gap			SILENT- NONCODI NG	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.lpcis:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19
2670	cg43306871	246	CTTGGCTTGCCC AAAGTCACACAG C[A/G]GGGAGTG GCAGAGGAAGT CAGGTTG	A	G			SILENT- NONCODI NG	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.lpcis:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19
2671	cg43306871	313	GCTCTCAGAGGC TGGGTGATGACC G[G/A]CTTCCTG GCTTCTCTGGAA TAAACC	G	A			SILENT- NONCODI NG	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.lpcis:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19

2672	cg43923853	133	ACACITTTAAGAT ACCATTACATGC T(A/G)TGTGTATT TACAAAAAGTTAC AGGTC	A	G			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA- 1) - HOMO SAPIENS (HUMAN), 277 aa. pcis:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4
2673	cg43923853	190	GAAAAAGAAAC TGTCATTGACAA A(T/C)GCGAGCT CATTITTTGAGC AACAAAG	T	C			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA- 1) - HOMO SAPIENS (HUMAN), 277 aa. pcis:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4

2674	cg43923853	295	CTCCGGACCTGC TGAGGCCTGGA GC[C/gap]TGCCT CCCGGGCTGAG GGCTCAGCT	C	gap			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA- 1) - HOMO SAPIENS (HUMAN), 277 aa.lpcis:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4
2675	cg43923853	312	CCTGGAGCCTG CCTCCCGGGCT GAG[G/T]GCTCA GCTCTGGCCTCC GGCTGGAT	G	T			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA- 1) - HOMO SAPIENS (HUMAN), 277 aa.lpcis:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4

2676	cg42918089	1136	TTTGAATGCTTT TCACTCCTTTTAT ATTGGATAAACT CCTTTATGGTGT GACT	A	T			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. pcds:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)
2677	cg42918089	1139	TGAATGCTTTT ACTCCTTTTAAG GATTAACTCC TTTATGGTGTGA CTGTG	A	T			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. pcds:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)

2678	cg42918089	1172	TTATGGGTGTGA CTGTGTCCTATT C[gap/C]ATCTATA CTTGCAGTGGGT AGATGT	gap	C				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[pcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)
2679	cg42918089	1178	GTGTGACTGTGT CTTATTCATCTAT [gap/G]ACTTGCA GTGGGTAGATGT CAATAA	gap	G				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[pcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)

2680	cg42918089	1179	TGTGACTGTGTC TTATTTCATCTATA [gap/G]CTTGCAG TGGGTAGATGTC AATAAA	gap	G			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.lpcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN). 267 aa	2.40E-146	11 (11q21)
2681	cg42918089	1182	GACTGTGTCCTTA TTCATCTATACCTT [gap/T]GCAGTGG GTAGATGTCAAT AAATGT	gap	T			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.lpcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN). 267 aa	2.40E-146	11 (11q21)

2682	cg42918089	1183	ACTGTGTCCTTAT TCATCTATACTT G[<u>gap</u>]TTCAGTGG GTAGATGTCAAT AAATGTT	gap	T			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[<u>pcis</u> :SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267.aa	2.40E-146	11 (11q21)
2683	cg42918089	1188	GTCCTTATTCATCT ATACTTGCAGTG[gap/C]GGTAGAT GTCAATAAATGT TACATA	gap	C			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.[<u>pcis</u> :SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267.aa	2.40E-146	11 (11q21)

2684	cg42918089	1189	TCTTATTCATCTA TACTTGCAGTGG [gap/C]GTAGATG TCAATAAATGTTA CATAC	C			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.lcds:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN). 267 aa	2.40E-146	11 (11q21)
2685	cg42918089	1230	TGTTACATACAC AAATAAATAAAAT [G/A]TTTATTTCCA TGGTAAATTTAA AAAA	A			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.lcds:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN). 267 aa	2.40E-146	11 (11q21)

2686	cg42918089	1235	CATACAGAAATA AATAAAATGTTTA [T/G]TCCATGGTA AATTTAAAAAAA CCG	T	G			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa, pcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)
2687	cg42918089	1236	ATACACAAATAA ATAAAATGTTTAT [T/G]CCATGGTAA ATTTAAAAAAG CCG	T	G			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa, pcis:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa	2.40E-146	11 (11q21)

2688	cg42918089	1251	AAATGTTTATTCCAA ATGGTAAATTTAA A/CJAAAAAACCG CCGATACTGACG GGC	C				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. pcds:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.40E-146	11 (11q21)
2689	cg42918089	1252	AATGTTTATTCCAA TGGTAAATTTAA A/CJAAAAAACCG CGATACTGACGG GC	C				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. pcds:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.40E-146	11 (11q21)
2690	cg43074055	1055	CTCTTCCCGGAA CACTGTGGCGTC C[G/gap]GGACGG CCCCACCCGTCC CCCCACA	gap				SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSPROT-ID:P24158 MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3) (P3) (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN) - HOMO SAPIENS (HUMAN), 256 aa.	5.70E-138 (19p13.3)	19 (19p13.3)

2691	cg43990989	110	ATTCCATGTATG TCATAGGTGTGA A[A/gap]CCTTAAA TCCTTCCCAACAG CCACTG	A	gap			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:Q92876 PROTEASE M PRECURSOR (EC 3.4.21.-) (NEUROSIN) (ZYME) (SP59) - HOMO SAPIENS (HUMAN), 244 aa.lpcis:SPTREMBL-ID:Q92876 PROTEASE M PRECURSOR - HOMO SAPIENS (HUMAN), 244 aa.	7.50E-136	19
2692	cg43990989	235	GGGGACACCGA CAGTAAGCAGCG GA[G/gap]CTGGG ATTCCAGACACG TGGCTGGG	G	gap			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:Q92876 PROTEASE M PRECURSOR (EC 3.4.21.-) (NEUROSIN) (ZYME) (SP59) - HOMO SAPIENS (HUMAN), 244 aa.lpcis:SPTREMBL-ID:Q92876 PROTEASE M PRECURSOR - HOMO SAPIENS (HUMAN), 244 aa.	7.50E-136	19
2693	cg43967243	1072	GCTGGAACCCAC GGGACATGTTGG TA[G/C]AAGCACT ACTTTAAACACA ATCCCT	G	C			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) (P27K) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.lpcis:SWISSPROT-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.	6.40E-130	

2694	cg43987243	209	ATATAGAGTCCT AACCACTTCGGT G[G/gap]TAGGAG GAGTGGGAGAG GCTCCTTT	G	gap			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) (P27K) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.[pcis:SWISSPROT-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa	6.40E-130	
2695	cg43974374	486	GGTCACTGTGTC CGTATTACCAAT G[A/G]CAGTCAC CCCAAGAAACAC AAGCAG	A	G			SILENT- NONCODI NG	protease	Human Gene Homologous to SPTREMBL-ID:Q16242 PROTEASOME SUBUNIT MB1 - HOMO SAPIENS (HUMAN), 215 aa (fragment).	7.40E-113 (14q11.2)	14
2696	cg2510140	22	CAAGCAGATAGG ACACTGGAA[A/G] AAGGAATGCCCA TTAAAACCCAGAA G	A	G			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P03358 POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)] - AKV MURINE LEUKEMIA VIRUS, 1196 aa.[pcis:SWISSPROT-ID:P03356 POL POLYPROTEIN (PROTEASE (EC 3.4.23.); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)] - AKV MURINE LEUKEMIA VIRUS, 1196 aa.	1.90E-105	

2697	cg43917011	186	AACTCTCAATGC TTAACCAATTTCA [G/A]TTGCCAGG AAAGAGGTAGAA ATATC	G	A			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P49662 CASPASE-4 PRECURSOR (EC 3.4.22.-) (CASP-4) (ICH-2 PROTEASE) (TX PROTEASE) (ICE(REL)-II) - HOMO SAPIENS (HUMAN), 377 aa. pcis:SWISSPROT- ID:P49662 CASPASE-4 PRECURSOR (EC 3.4.22.-) (CASP-4) (ICH-2 PROTEASE) (TX PROTEASE) (ICEREL- II) - HOMO SAPIENS (HUMAN), 377 aa.	1.50E-103	11
2698	cg43930253	1288	ATATTGGATGGC GAGGACAGCGT GGT/CJACTGGC TGCGAGTGTCC TGAGAGT	T	C			SILENT- NONCODI NG	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20
2699	cg43930253	1349	ATGACTTATGAC ACTTGCACAGCA T[G/gap]GCTCTG CCTCACAAATGAT GCAGTCA	G	gap			SILENT- NONCODI NG	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20
2700	cg43930253	1350	TGACTTATGACA CTTGCACAGCAT G[G/gap]CTCTGC CTCACAAATGAT CAGTCAG	G	gap			SILENT- NONCODI NG	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20
2701	cg43930253	1400	GCCACCTGGTGA AGAAAGTGACCTG C[G/A]ACACAGG AAACGATGGGAC CTCAGT	G	A			SILENT- NONCODI NG	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20

2702	cg43947922	934	TAGATTGAGAC AACTAGCCTGTT A/C/TTCAGCCCA ATATCCCCCAT GGTTT	C		T			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSNEW- ID:P28070 PROTEASOME BETA CHAIN PRECURSOR (EC 3.4.99.46) (MACROPAIN BETA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX BETA CHAIN) (PROTEASOME CHAIN 3) (HSN3) (HSBPROS26) - HOMO SAPIENS (HUMAN), 284 aa.	1.10E-97	
2703	cg43104740	2154	ACATGGATGAGC ACACACACACCA A/gap/GJTGCGCA CACACACCGATG TACACAC	gap	G				SILENT- NONCODI NG	protease	Human Gene Similar to SWISSPROT- ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	5.00E-94	13
2704	cg43297588	23	GGCACAGCATG CGGGCGGTGTG C/G/GCCCCCCC GGTGCCGCCCT GCTGT	C	G				SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	4.80E-93	1 (1p36.1)
2705	cg43297588	24	GGCACAGCATG CGGGCGGTGTG C/G/CJCCCCCCC GGTGCCGCCCT GCTGTC	G	C				SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	4.80E-93	1 (1p36.1)
2706	cg43297588	26	GGCACAGCATG CGGGCGGTGTG CGC/GJCCCCC GGTGCCGCCCT GCTGTCGG	C	G				SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	4.80E-93	1 (1p36.1)
2707	cg43297610	153	CAGCTGAGCAG GGTGGCTGTCC TC/G/JGCTGGAT TAGGGCTGAATC TGTGGG	G	T				SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	3.20E-92	1 (1p36.1)

2708	cg43297610	2707	GCCGGACATCC CAGGCACACGT GTG[<i>gap</i>]GCCA CCTTCAGCAGGC ATTCGGGTG	C				SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	3.20E-92	1 (1p36.1)
2709	cg43297610	2760	GGGCTGGTGGC TCATCAGGCCTG GG[<i>gap</i>]CCCAC ACTGACAAGCGC CAGATACG	C	gap			SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	3.20E-92	1 (1p36.1)
2710	cg43917924	315	ATTTGTCTCACT CGATTACAGACAC [T/G]TAAATGGGA GTTTTCAGTTTAT CCT	T	G			SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	1.80E-81	3 (3q21)
2711	cg43921680	347	GCCAAGTCATT AAAAAGGATTTA G[<i>gap</i>]CCACTG CCTTTTCTGAG GGAGGAG	G	gap			SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	4.60E-77	15
2712	cg43921680	612	CATGTTGTTAA CAGTAGAGGAG CC[A/G]GGGACT CTGTCTCCATT TCTCATC	A	G			SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	4.60E-77	15
2713	cg43921680	689	AAAAAAAAAACAA AAAAACACAACA A[C/ <i>gap</i>]AAAAAA ACTGTCCTCTGA GGAGGCA	C	gap			SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	4.60E-77	15
2714	cg42033569	513	GCTGTCCATTAG TAGAAGAGCAAG A[G/A]AGCCTTG GATGTCAACGCC TCGCTC	G	A			SILENT- NONCODI NG	protease	Human Gene Similar to SPTREMBL- ID:Q19831 SIMILAR TO NEPRILYSIN AND OTHER ZINC PROTEASES - CAENORHABDITIS ELEGANS, 754 aa.	3.20E-72	

2715	cg44031287	300	TTCACAGGTGCC AGAGCTTAGAGG TGGTTACACAGGC ACCGGGGTGGC TCCTGC	G	T		SILENT- NONCODING	protease	Human Gene Similar to TREMBLNEW- ID:G2738064 UBIQUITIN SPECIFIC PROTEASE 41 - GALLUS GALLUS (CHICKEN), 357 aa.	8.10E-67	1
2716	cg43276961	1111	GATGACAAATAC TGGTTAATTAGC AAGJTTTAAGAC CAGAGCCAAATT ATCCC	A	G		SILENT- NONCODING	protease	Human Gene Similar to SWISSNEW- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE-7) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. pcis:SWISSPROT- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE-7) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	1.90E-59 (11q22.2)	11
2717	cg43276961	1343	GGCCTAAAATTG ATGCAGTCTTCT A/C/TTCATAAAA CAAATACTACTA TTTCT	C	T		SILENT- NONCODING	protease	Human Gene Similar to SWISSNEW- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE-7) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. pcis:SWISSPROT- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE-7) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	1.90E-59 (11q22.2)	11

2718	cg43276961	1686	AGTTTGAAAATA GTTACCTTCAAA G[G/gap]CCAAGA GAATTCTATTG AAGCATG	G	gap			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSNEW- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.jpcl:SWISSPROT- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	1.90E-59	11 (11q22.2)
2719	cg43276961	1693	AAATAGTTACCT TCAAAGGCCAAG A[G/T]AATTCTAT TTGAAGCATGCT CTGTA	G	T			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSNEW- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.jpcl:SWISSPROT- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	1.90E-59	11 (11q22.2)
2720	cg43069905	417	TCAGCGCCCTCC ACAGTGGCAGTG C[C/gap]AGCTTG GAATCCCGCTTC CGGTTGT	C	gap			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSPROT- ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	1.30E-57	13
2721	cg43316919	1645	AAGGAAAGGAGT ATTGGAAATTCA A[A/gap]CAACCA GATACTCAAGGT AGAACCT	A	gap			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSPROT- ID:P22757 HATCHING ENZYME PRECURSOR (EC 3.4.24.12) (HE) (HEZ) (ENVELYSIN) (SEA-URCHIN- HATCHING PROTEINASE) - PARACENTROTUS LIVIDUS (COMMON SEA URCHIN), 587 aa.	8.10E-56	

2722	cg44028327	3348	TGGATGCATTG AACCTCTGAGTT TTCGCTCTTTCAT TTTAAATATTGTC TGTT	G	C				SILENT- NONCODING	protease nhib	Human Gene SWISSPROT-ID:P01042 KININOGEN, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR) (CONTAINS: BRADYKININ) HOMO SAPIENS (HUMAN), 644 aa.	0.00E+00	3 (3q27)
2723	cg44028327	3540	CAAGGTCGAC CCCCAAAGGCA GGG[gap]GJCAGA GCCAGCATCTGA GAGGGAGGT	gap	G				SILENT- NONCODING	protease nhib	Human Gene SWISSPROT-ID:P01042 KININOGEN, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR) (CONTAINS: BRADYKININ) HOMO SAPIENS (HUMAN), 644 aa.	0.00E+00	3 (3q27)
2724	cg43979831	1589	GTTGGGACAA GGATGACACCGA AG[gap]TCCAG GAGTCCAGGACA GCAGGTGC	G	gap				SILENT- NONCODING	protease nhib	Human Gene SWISSPROT-ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa.	1.10E-228	14
2725	cg43979831	1628	GACAGCAGGTG CTGGCCGGTGG GGA[G]JCGGG AGGGGCACCTGA GATGGGCGAG	G	A				SILENT- NONCODING	protease nhib	Human Gene SWISSPROT-ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa.	1.10E-228	14
2726	cg43920929	320	GGAAAAGAAATTT AAAAGGCAAATA A[gap]TJTTTTTT TTCATAAAAAGT AAAAGC	gap	T				SILENT- NONCODING	protease nhib	Human Gene SWISSPROT-ID:P07093 GLIA DERIVED NEXIN PRECURSOR (GDN) (PROTEASE NEXIN I) (PN-1) (PROTEASE INHIBITOR 7) - HOMO SAPIENS (HUMAN), 398 aa.	1.20E-208	2
2727	cg43268468	1394	TGCTGTCGGGT CTGGGAGACCC TC[G]gapJTCCGG GGGGCTGGCAG GGTCTGGC	C	gap				SILENT- NONCODING	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.60E-188 (17p13.3)	17
2728	cg43268468	1560	CTGAGGGGGCT CCAGCCAGCACA GAGTCTTTTTT TGCTGCCCTTCTA ATCCAG	G	T				SILENT- NONCODING	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.60E-188 (17p13.3)	17

2728	cg43932980	93	GAGTTATAGCTA CCCCGGCCGCG GA[G/gap]CCGGC TCACTGCACTAC CCCCGCCC	G	gap			SILENT- NONCODI NG	proteaseI nhIb	Human Gene SPTREMBL-ID:Q92530 PROTEASOME INHIBITOR HPI31 SUBUNIT - HOMO SAPIENS (HUMAN), 271 aa.	1.70E-152	20
2730	cg43932980	3021	GAGAAACACAGT CATTGTCTTAGG T[G/A]TTCTATGG GAGGAAGTGAAT AGAGC	G	A			SILENT- NONCODI NG	proteaseI nhIb	Human Gene SPTREMBL-ID:Q92530 PROTEASOME INHIBITOR HPI31 SUBUNIT - HOMO SAPIENS (HUMAN), 271 aa.	1.70E-152	20
2731	cg43932980	67	GCAAGAACCAGC GCAAGAGGGAA GC[G/A]GAGTTAT AGCTACCCCGG CCGCGGA	G	A			SILENT- NONCODI NG	proteaseI nhIb	Human Gene SPTREMBL-ID:Q92530 PROTEASOME INHIBITOR HPI31 SUBUNIT - HOMO SAPIENS (HUMAN), 271 aa.	1.70E-152	20

2732	cg43980892	159	AAAATAATTCTAATG CAAAAATTTCAA[G/A]CATCACTGC TGTAGATATTCC TCCA	A				SILENT- NONCODING	reductase	Human Gene SWISSNEW-ID:P54886 DELTA 1-PYRROLINE-5- CARBOXYLATE SYNTHETASE (P5CS) [CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5- SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)] - HOMO SAPIENS (HUMAN), 795 aa.[pcis:SWISSPROT- ID:P54886 DELTA 1-PYRROLINE-5- CARBOXYLATE SYNTHETASE (P5CS) (CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) / GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5- SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE))] - HOMO SAPIENS (HUMAN), 795 aa.	0.00E+00	10 (10q24.3)
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2733	cg43990892	446	AAATCTTTCCTTT TTGAAGATGACTT A/GCATGTGAAA GAAATAAAATGT GAAA	A	G			SILENT- NONCODING	reductase	Human Gene SWISSPROT-ID:P54886 DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)] - HOMO SAPIENS (HUMAN), 795 aa. pcids:SWISSPROT-ID:P54886 DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) (CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) / GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)) - HOMO SAPIENS (HUMAN), 795 aa.	0.00E+00	10 (10q24.3)
2734	cg44002608	282	ATTCAAATTA TTATTTTTTTT g ap/TJACAAAGAAA TAAACCTGTAAA GGAT	TA	T			SILENT- NONCODING	reductase	Human Gene SPTREMBL-ID:Q94511 75KDA SUBUNIT NADH:BIQUINONE REDUCTASE PRECURSOR - DROSOPHILA MELANOGASTER (FRUIT FLY), 653 aa (fragment).	4.60E-223	2
2735	cg43969711	722	CAATAAATCAA GCTATTATCGCC TT/CJGTGAGTAC AAACAATGTTTAT TTGT	T	C			SILENT- NONCODING	reductase	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208	2 (2p25)

2736	cg43941472	733	GCTATTATCGCC TTGTGAGTACAA A[gap/A]CAATGTT TATTTGTTTGTA AGTGC	gap	A			SILENT- NONCODI NG	reductas e	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208	2 (2p25)
2737	cg43941472	1139	GGGACAAAGC AGCGTCTGGCTC GA[G]gapJTGGA GCGTCCAAACCT GCTTTTCC	G	gap			SILENT- NONCODI NG	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2738	cg43941472	1208	TTCCGTCAGAGC TTCTGGCTGCTC C[T/A]GAATGGTG GAATGCTGTGTC CCTCTC	T	A			SILENT- NONCODI NG	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2739	cg43941472	1222	TGGCTGCTCCTG AATGGTGGAATG C[gap/C]JTGTC CTCTCTTCTGTC TCCIGCT	gap	C			SILENT- NONCODI NG	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2740	cg43941472	1247	CTGTGTCCTCTC TTCTGTCTCCTG C[T/C]GCCTGGA GGCTTCGGGGC TCTCCCG	T	C			SILENT- NONCODI NG	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2741	cg43941472	1281	GCTTCGGGGCT CTCCCGCCTGCC TT[G/C]TCGGGG CCGACGCGCA GGCACCGA	G	C			SILENT- NONCODI NG	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2742	cg43941472	1440	CTTTTTTAAAG AAGATGGTTTCA gap/GCTTTAATA TAATGCTATTATC TTAA	gap	G			SILENT- NONCODI NG	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)

2743	cg43941472	1474	TAATGCTATTATCA TTAAGACITTAAG A/GAAGTTGCTG GAGTTTGATTT CCAG	A	G			SILENT- NONCODING	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.8.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2744	cg43941472	1475	AATGCTATTATCTA TAAGACITTAAG A/GAGTTGCTGG AGTTTGATTTTC CAGG	A	G			SILENT- NONCODING	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.8.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)
2745	cg43987538	115	ACTTTATTACACA TTATTATGTTAC G/AAGACAAATG CAGATAATTCTT AATT	G	A			SILENT- NONCODING	reductase	Human Gene SWISSPROT-ID:Q08257 QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN) - HOMO SAPIENS (HUMAN), 329 aa.	1.10E-171	1 (1p31)
2746	cg43987538	86	TTTTTTTTTTTT TTTAAATTTTCTA /GJTAGACTTTATT ACACATTATTAT GT	A	G			SILENT- NONCODING	reductase	Human Gene SWISSPROT-ID:Q08257 QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN) - HOMO SAPIENS (HUMAN), 329 aa.	1.10E-171	1 (1p31)
2747	cg40312187	2424	AGGATGATGTAG ATTACTGAAAA T/A/GCAAAATTGC AATCATATAAATA AGTG	A	G			SILENT- NONCODING	reductase	Human Gene Homologous to SWISSPROT-ID:P31213 3-OXO-5- ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA- REDUCTASE 2) (SR TYPE 2) - HOMO SAPIENS (HUMAN), 254 aa.	5.70E-138	2 (2p23)
2748	cg43918176	50	TTTTTTTTTTTT TTTTTTTTTTTTTT CTGTGAGAAAAA GAGACTTTATTA GG	T	C			SILENT- NONCODING	reductase	Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa.	2.00E-133	X

2749	cg43927549	1010	TGGGCATCACGT AAGCAGCACACT A/GC/GAGGCCC AGGCGCAGGCA AAGAGAA	G	C			SILENT- NONCODING	reductase	Human Gene Homologous to SWISSPROT-ID:P16083 NAD(P) ⁺ H DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT- DIAPHORASE) (AZOREDUCTASE) (PHYLLLOQUINONE REDUCTASE) (MENADIOLONE REDUCTASE) - HOMO SAPIENS (HUMAN), 231 aa.	1.60E-124	6 (6pter)
2750	cg43985873	386	GGGGCGGGGCC TCGCCTGCACAA ATTA/G/GGGACG AGGGGGCGCGG GCGGCCAC	A	G			SILENT- NONCODING	reductase	Human Gene Similar to SWISSPROT- ID:P00374 DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) - HOMO SAPIENS (HUMAN), 186 aa.pcds:SWISSPROT-ID:P00374 DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) - HOMO SAPIENS (HUMAN), 186 aa.	1.90E-98	5 (5q11.2)
2751	cg43836109	389	TCCAATAAGCAA ATGGACATTGGT C/C/gap/ATTTGG CATGTGTAATTC TCCTTT	C	gap			SILENT- NONCODING	ribosomal prot	Human Gene SWISSPROT-ID:P49406 PUTATIVE 60S RIBOSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 280 aa.	2.50E-151	2
2752	cg43982087	1708	TTAGTGGCTTCA AAGGCCAGCT GA/C/A/ACCCTCC ACAGCCTAAGGG GTGTCC	C	A			SILENT- NONCODING	ribosomal prot	Human Gene Similar to SWISSPROT- ID:P17103 HYPOTHETICAL 40 KD GTP- BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5'REGION - HALOBACTERIUM CUTIRUBRUM, 370 aa.	2.70E-67	17
2753	cg43982087	1759	TAAAGTGCCTCC CCCTGTATTCCC C/C/TTCCCAGG GCAGCCCTGTC CCAGCAC	C	T			SILENT- NONCODING	ribosomal prot	Human Gene Similar to SWISSPROT- ID:P17103 HYPOTHETICAL 40 KD GTP- BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5'REGION - HALOBACTERIUM CUTIRUBRUM, 370 aa.	2.70E-67	17

2754	cg44923577	838	TCCCAAGAAGAA GGTCAATAAGG TTTGJTTCTTC CTTGAAGGGCAG CCTCC	T	G				SILENT- NONCODI NG	ribosomal prot	Human Gene Similar to SPTREMBL- ID:Q95260 UBIQUITIN/RIBOSOMAL FUSION PROTEIN - SUS SCROFA (PIG), 128 aa.	1.10E-65	19 (19p13.1)
2755	cg42845774	568	TAAATGAAGAC ATTGGGTGTTT CJA/GJGTCAAGT AATTATCTTTCT CTTG	A	G				SILENT- NONCODI NG	ribosomal prot	Human Gene Similar to TREMBLNEW- ID:E1284377 DJ262D12.2 (MITOCHONDRIAL/CHLOROPLAST 30S RIBOSOMAL PROTEIN S14)-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 128 aa.	1.70E-65	1
2756	cg43255045	5967	ATACTTGACAC CTGCCAAAGCTT CIG/CJAGCACGG GAAATGAGAA CACTGG	G	C				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0.00E+00	1
2757	cg43255051	624	AGGAAGTTTTA TGCAGAGGTCAC TTC/AJCCCCCTGCA CTATTCAAGGGT TATAA	C	A				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0.00E+00	1
2758	cg43966202	19	TTTTTCGTCGTTT TTTTTGTTAATA AAGACACTGCTT TTATTAG	G	T				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q14118 DYSTROGLYCAN PRECURSOR (DYSTROPHIN-ASSOCIATED GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 895 aa.	0.00E+00	3
2759	cg43973080	1686	GGCAAAGGCTC CCAGCTGTAAGG CTG/AJGTGTGCA ACATCTACTTTAA CAGAC	G	A				SILENT- NONCODI NG	struct	Human Gene TREMBLNEW- ID:G2304981 MYOSIN VI - HOMO SAPIENS (HUMAN), 1262 aa.	0.00E+00	6
2760	cg43957846	1766	AGAAAAGTGAAA CAAAACCATAAA CJA/GJAGCAGC GGGTTTCACGA CGCTAAA	A	G				SILENT- NONCODI NG	struct	Human Gene SPTREMBL-ID:O00185 BETA CATENIN - HOMO SAPIENS (HUMAN), 596 aa.	0.00E+00	10

2761	cg43957640	2076	AAAGGAATGAAG AGGGTGTGAGG CC[C/gap]AATGG GGCTGGGTGGG AGCGGGTGC	C	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P13796 L- PLASTIN (LYMPHOCYTE CYTOSOLIC PROTEIN 1) (LCP-1) (LC64P) - HOMO SAPIENS (HUMAN), 627 aa.	0.00E+00	13 (13q14.1)
2762	cg44033566	6709	TGACGTTATTAG TTTTGTTTTACCT [gap/G]AATGTAA TAAATTTTATTGT ATAAA	gap	G				SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.[pcls:SWISSPROT- ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.	0.00E+00	14 (14q22)
2763	cg43957486	3192	AAACAAAGGTTG AGATGTAAAGG T[A/G]TTAAATTG ATGTTGCTGGAC TGICA	A	G				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa.	0.00E+00	20 (20p11.2)
2764	cg43957486	3400	ATGTTTCAGAAAGG TTGCTCTAGATT G[A/C]GAGAAAG GACAAACACCTC CCAGGA	A	C				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa.	0.00E+00	20 (20p11.2)
2765	cg43249606	20	TTTTTTTTTTTT TTTTTG[T/A]GAG AAGCTGAGCTGT TTAATCACCT	T	A				SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:Q01082 SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1) - HOMO SAPIENS (HUMAN), 2364 aa.[pcls:SWISSPROT-ID:Q01082 SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1) - HOMO SAPIENS (HUMAN), 2364 aa.	0.00E+00	
2766	cg44818439	2202	TTTTTTTCTTTT TCCTTTTTTTTTTg ap/TCTGTGTAAG ATTAAACACTAATT ATC	gap	T				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P35241 RADIXIN - HOMO SAPIENS (HUMAN), 583 aa.	9.3e-312	11 (11q23)

2767	cg44918439	2375	TCACATTTTCTCA GTGTGCCCTTCT C/GJTATCTGCC ATGTCCATAGCC ATAA	C	G				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P35241 RADIXIN - HOMO SAPIENS (HUMAN), 583 aa.	9.3e-312	11 (11q23)
2768	cg43967978	1187	AGTTCAGAAATTC TAGGCCCAAAAG G[G/gap]TGCAAC ACCCCTTCAACCA GTTTCAG	G	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2769	cg43967978	1522	TAGAGAAAGTAA AGCAACTCAGGC G[gap/G]ATATGA ATTCAAACCTCA GTGTAGA	gap	G				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2770	cg43967978	1582	AAGTCGGTACAG TGTCAGGCACG C[C/gap]GTCCCG GAGACGGAGGA AGTGACTA	C	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2771	cg43967978	1688	GGGAGGCGGG TCTAAAGGCAG GG[G/gap]CAGTC GCCAGGCCTAG GGCACTGGA	G	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2772	cg43967978	1716	GTCGCCAGGCC TAGGGCACTGGA AG[G/A]GTAGGA GGAGCACAGAG AACCTTCC	G	A				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2773	cg43967978	693	AGACCCAGCAC ACTCGGCTTCTG C[C/gap]AGGAGG CCAGTGGAGTG GTTTGGAC	C	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	

2774	cg43967978	814	CTTGGTAAAGAG CTCTGGGGGGTT T[C/gap]CCCAGA GGAGCCTGTCC CTCTGCCC	C	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P49023 PAXILLIN - HOMO SAPIENS (HUMAN), 557 aa.	2.90E-301	
2775	cg44034221	1889	TGCTGTACCTCG ATCTGAATCTGC C[G/gap]GGCCCC CAGCCCACTCCA CCCTGCC	G	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	
2776	cg44034221	1981	CTGTACCTCGAT CTGAATCTGCCG G[G/gap]GCCCCA GCCCACTCCACC CTGCCAG	G	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	
2777	cg44034221	1992	TGTACCTCGATC TGAATCTGCCGG G[G/gap]CCCCAG CCCACTCCACCC TGCCAGC	G	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	
2778	cg44034221	2020	CCAGCCCACTCC ACCCTGCCAGCA G[C/gap]TTCCAG CCAGTCCCCACA GCCTCAT	C	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	
2779	cg44034221	2098	CTATCTTCCCC ACCCCACTAC C[C/gap]ATAGGG GCTGCAGAGTTA TAAGCCC	C	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P26039 TALIN - MUS MUSCULUS (MOUSE), 2541 aa.	8.10E-281	

2780	cg43980812	238	TAAACTCGAGGG ATTATTATTCTT G/AATTGGAGAA AGAGAAGACAGC ATTT	G	A				SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:Q15654 THYROID RECEPTOR INTERACTING PROTEIN 6 (TRIP6) (OPA- INTERACTING PROTEIN 1) (ZYXIN RELATED PROTEIN 1) (ZRP-1) - HOMO SAPIENS (HUMAN), 476 aa.	2.90E-272	7
2781	cg43981165	218	CGGCTCCCGAG TCITGGAGAAGA GC/A/GJCGAGAA CCTAGACCGCCC CCGAAGT	A	G				SILENT- NONCODI NG	struct	Human Gene SPTREMBL-ID:Q14704 MRNA (KIAA0092) FOR ORF (SMOOTH MUSCLE MYOSIN-RELATED) - HOMO SAPIENS (HUMAN), 474 aa.	3.00E-242	11
2782	cg43987609	996	GCACTCCATAAT AACTGGAATCCC A/C/TJGAGTGT ATGCCAAGTCTC ATGAG	C	T				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P32391 ACTIN-LIKE PROTEIN 3 (ACTIN-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 418 aa.	1.10E-226	2
2783	cg42491601	1485	TGGAAGAAATA TCTAAATAGCTA C/C/gapJAGAAGG AGATGCTGCTGA GGTTTIG	C	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa.	1.40E-215	17
2784	cg42491601	1694	AAATTGCCTGCA AAAATGAAATCC A/G/AJTGAGCACT AGAATATTTAAA CATC	G	A				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa.	1.40E-215	17
2785	cg43947066	119	TTTAGCTTTCCA CTGATATCTCAA G/A/CJTACTTTCC AGATATTACAG TACTC	A	C				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2786	cg43947066	1685	CTTAAGCTCTTTT AAATCTGTAATT T/CJGAATTACCC AAAGGATTTTAA AATG	T	C				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2

2787	cg43947066	2228	ATACCACCTAGT GTGCTAAAGACT A/C/T/GACTAGCA GCATTAGAGCAG TAAAG	C	T			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2788	cg43947066	378	TTTTAAACAGAT ATTTTTTTTTTT /gap/CCTGAGGG ACTCATACTTGA CAACT	T	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2789	cg43947066	74	TTATTTCTCAAT CAAATGAAGTA T/CJTTCATGTTAA TTTAGACTGTTTA GC	T	C			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2790	cg43947066	843	CCCAAGATCTAG TACGGGCTATTC A/T/GGGTTCTGA GGCATGTCCAGC ATGCA	T	G			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
2791	cg43963568	140	CAGATGCTTTCT GAAGAGCCCTG GG/G/gap/CAGGG GGCAGCCTTGC CCCTCACAT	G	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207 (1q32.1)	1
2792	cg43963568	230	GGATCCAGGTC TGGAGCCCAAGAA C/G/C/TAGTCCAA AGATCCCCCTCT CCCTT	G	C			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207 (1q32.1)	1
2793	cg43963568	2870	CAGGAGGGAGG TCCACTGCATTT TGT/gap/CTCTC AAGTTGAACCTT TCAGAGAA	T	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207 (1q32.1)	1

2784	cg43963568	2872	GGAGGGAGGTC CACTGCATTTTG TC/T/gap/CTCAA GTTGAACCTTTG AGAGAAGT	T	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207	1 (1q32.1)
2785	cg43963568	317	GGATGTGATGGC ATCTGGGCAGAG C/C/gap/JTATACTT GGGCTAACTCTC CTCCAA	C	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q06828 FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN) - HOMO SAPIENS (HUMAN), 376 aa.	5.90E-207	1 (1q32.1)
2786	cg43983086	139	AGCCTAGGATGG TCAGCAGCAAGG T/C/GJTCCCGGG GGATGGCTTACC TCCCTC	C	G			SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND CANIS FAMILIARIS, 376 aa. pcds:SWISSPROT- ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME- ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 376 aa. pcds:TREMBLNEW- ID:D1025337 ACTIN-RELATED PROTEIN 1 ALPHA-ISOFORM - MUS MUSCULUS (MOUSE), 376 aa.	3.10E-201	10

2797	cg43983086	304	TAGTGGTCAACC CCAGGCCTCAG GC[gap/A]CATCA CCACTGCAGGTA GTTTCATCG	gap	A			SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND CANIS FAMILIARIS, 376 aa. pcds:SWISSPROT- ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME- ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 376 aa. pcds:TREMBLNEW- ID:D1025337 ACTIN-RELATED PROTEIN 1 ALPHA-ISOFORM - MUS MUSCULUS (MOUSE), 376 aa.	3.10E-201	10
2798	cg43983086	432	ACACAGGCAGTT CCTCGCAACAC T[C/A]CGACTCAA GAAAGCGAGTTT TAAAG	C	A			SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND CANIS FAMILIARIS, 376 aa. pcds:SWISSPROT- ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME- ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 376 aa. pcds:TREMBLNEW- ID:D1025337 ACTIN-RELATED PROTEIN 1 ALPHA-ISOFORM - MUS MUSCULUS (MOUSE), 376 aa.	3.10E-201	10

2799	cg43983086	433	CACAGGCAGTTC CTCGCAAAACACT C[C/A]GACTCAAG AAAGCGAGTTTT AAAGT	C	A				SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND CANIS FAMILIARIS, 376 aa.pcls:SWISSPROT- ID:P42024 ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME- ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 376 aa.pcls:TREMBLNEW- ID:D1025337 ACTIN-RELATED PROTEIN 1 ALPHA-ISOFORM - MUS MUSCULUS (MOUSE), 376 aa.	3.10E-201	10
2800	cg43923264	1291	CTGTTCAGTGCC GACCTGCGCCAA TTC/GJCCGCCAT GCTCAGGAGCC ACCAGCA	C	G				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3
2801	cg43923264	1364	GGCCGGGAAGGC TAGATGGGGCAC CC[T/A]GGACAAA GAAATTCCCCAA GCACCT	T	A				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3
2802	cg43923264	1381	GGCACCCCTGG ACAAAGAAATTC CC[C/T]AAGCACC TTCCCTCCATT CCCCAC	C	T				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3
2803	cg43923264	1693	TCAGGGAGGGA AGGGGAGCAGG CTGgap/GJCCCC CAAGCCCTCCCA CGCAGAGGA	gap	G				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3

2804	cg43923264	304	AGCGGGGGCTA CTACGGGGGGG TGC[C/gap]TGCT GTGGAATGCCT GCCCGCGCG	C	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:Q14012 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3
2805	cg43916919	104	CTTTATTGAACAT CTGCAGGGGGC A[C/gap]CTCTGC ACTGACCAGGCA GCCAGAG	C	gap			SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa. pcis:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa.	4.30E-188	2 (2cen)
2806	cg43949677	1733	CCTTTGTGCTGGA TATGCAGAAATG A[T/C]AGGAAAAA AACCAATGGTGA AATT	T	C			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P28289 TROPOMODULIN - HOMO SAPIENS (HUMAN), 359 aa.	2.40E-185 (9q22.2)	9
2807	cg42894986	1438	ATTCAGCTCCT GGCCCTCCTGG AA[C/G]CCAGGC TCTAAACAAGCA GGGAGAG	C	G			SILENT- NONCODI NG	struct	Human Gene SPTREMBL-ID:Q28686 50- KDA DYSTROPHIN-ASSOCIATED GLYCOPROTEIN PRECURSOR - ORYCTOLAGUS CUNICULUS (RABBIT), 387 aa.	1.40E-180	17
2808	cg43971282	606	ATGCTGGGGACA CTACAGGGCACAC A[G/C]AGGAATA GCAGGGCCACC CTCAGAG	G	C			SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P97490 ADENYLATE CYCLASE, TYPE VIII (EC 4.6.1.1) (ATP PYRÖPHOSPHATE- LYASE) (CA(2+)/CALMODULIN ACTIVATED ADENYLYL CYCLASE) - MUS MUSCULUS (MOUSE), 1249 aa.	8.90E-180	2

2809	cg43962437	1425	AGGAGGACCTG GGGGGGGCAAG AGC[gap/C]TCAG GAGAAGGCGTG CCGCCCTTCC	gap	C				SILENT- NONCODI NG	struct	Human Gene SWISSNEW-ID:P08247 SYNAPTOPHYSIN (MAJOR SYNAPTIC VESICLE PROTEIN P38) - HOMO SAPIENS (HUMAN), 313 aa.lpcds:SWISSPROT-ID:P08247 SYNAPTOPHYSIN (MAJOR SYNAPTIC VESICLE PROTEIN P38) - HOMO SAPIENS (HUMAN), 313 aa.lpcds:TREMBLNEW-ID:G2707601 SYNAPTOPHYSIN - HOMO SAPIENS (HUMAN), 313 aa.	4.80E-173	X (Xp11.2 3)
2810	cg43956325	17	TCGTCCTTTTTT TTT[AT]CTTTTAA CAAAAGCAACAA TTTTTA	A	T				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
2811	cg43956325	239	TTATAGAACAAT GAAATTCCTGT T[AC]GGAACACA AGTTGCTGTTTA TATT	A	C				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
2812	cg43956325	312	AGAAGAAGTAAG GTGGAGCTGTTG G[G/A]AAAGCCC ATCGTGGACCTT TGGAGA	G	A				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)

2813	cg43956325	67	ATTATCTTGCTTT ATATTTAATGGA TGTAGAACTAT AAAGATTCTTAA CTTT	T	G				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
2814	cg43985529	126	ATGCAGGGGCG TGCAATTGGCTGC TG[C/gap]CGCTT TTGTAATTGAATT GTTTTAA	C	gap				SILENT- NONCODI NG	struct	Human Gene SPTREMBL-ID:Q95264 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA- E - SUS SCROFA (PIG), 334 aa (fragment)	1.00E-163	
2815	cg43985529	127	TGCAGGGGCGT GCATTGGCTGCT GC[C/gap]GCTTT TGTAATTGAATT GTTTTAA	C	gap				SILENT- NONCODI NG	struct	Human Gene SPTREMBL-ID:Q95264 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA- E - SUS SCROFA (PIG), 334 aa (fragment)	1.00E-163	
2816	cg43305278	336	GGGGGAGCTTC TGGTCCTGGGG GTA[C/gap]CCAC TTGTGAGGGAGT GGGGGGACA	C	gap				SILENT- NONCODI NG	struct	Human Gene SWISSPROT-ID:P51911 CALPONIN H1, SMOOTH MUSCLE (BASIC CALPONIN) - HOMO SAPIENS (HUMAN), 297 aa. pcis: SPTREMBL- ID:Q15416 BASIC CALPONIN - HOMO SAPIENS (HUMAN), 287 aa.	3.10E-162	19
2817	cg44017869	323	AAATGGGAACAA ATATAGATAATC GTT/GJTTCTGG GTCAAAGGCATT TAGAAA	T	G				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:Q83537 SYNAPSIN 2A - RATTUS NORVEGICUS (RAT), 586 aa.	5.20E-148	
2818	cg42814441	116	CCAGACCGTTCC CGGGCCGGCCA GC[G/C]GCCACC ATGGTGGCCCTG AGGCCCTG	G	C				SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P28044 RADIXIN (MOESIN B) - SUS SCROFA (PIG), 583 aa.	5.40E-133 (22q12.2)	22

2819	cg43929931	1325	GCACCGCGTTTC CATAGCAGCATG TTC/gap]CTACGG AAACCCAGCACG TGTGTAG	C	gap			SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:Q64572 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE KINASE (EC 2.7.1.37) (PHOSPHORYLASE B KINASE KINASE) (GLYCOCEN SYNTHASE A KINASE) (HYDROXYALKYL-PROTEIN KINASE) (SERINE(THREONINE) PROTEIN KINASE) - RATTUS NORVEGICUS (RAT), 505 aa.	7.60E-132	12
2820	cg43929931	1326	CACCGCGTTTCC ATAGCAGCATGT CIC/gap]TACGGA AACCCAGCACGT GTGTAGA	C	gap			SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:Q64572 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE KINASE (EC 2.7.1.37) (PHOSPHORYLASE B KINASE KINASE) (GLYCOCEN SYNTHASE A KINASE) (HYDROXYALKYL-PROTEIN KINASE) (SERINE(THREONINE) PROTEIN KINASE) - RATTUS NORVEGICUS (RAT), 505 aa.	7.60E-132	12
2821	cg43918346	913	TTCTGAGTGCAT GAAGTTATAAAG GIA/TJCCTACATG TAATGCATATGT GATGC	A	T			SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.40E-130	
2822	cg43918346	797	CAGCTTCTTTGT TAATACACCCAT GIG/CJTAATTTTC AACAGTGCCACA TCTGC	G	C			SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.40E-130	

2823	cg43918346	848	ATTCTCTGTTCT CAAGGCACCTG GAATJGGTGAC CCGGGGCCGTC CTCTCCTC	A	T				SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.40E-130	
2824	cg43918346	857	TCTCAAGGCACC TGGAAAGGTGACC CIGTJGGGCCGT CCTCTCCTCCTC TTCATG	G	T				SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.40E-130	
2825	cg43942332	1232	GTGTTCCGGTGG GAAGGTGGGATT TTTJGJGGTTCTC TGGAAATTGAATG TTTAGT	T	G				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.10E-124	11
2826	cg43942332	1542	AATAAGAAATTTT AATGCACGAGTA JAGJAGGGGGTG GTGGGTTGTGCA CTTJ	A	G				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.10E-124	11
2827	cg43942332	398	GCTATATAATTTT AATCTAAAGATTJ TJGGGGCATACA GAAAGCATTTCA CATA	T	G				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.10E-124	11
2828	cg43942340	44	TTTTTTTTTTTT TTTTTTTTTTTTTC TJAAAAGGAAAT CCCAATCTTTTAA TT	C	T				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	1.20E-123	11

2829	cg43942338	1072	GTGTTCCGGTGG GAAGGTGGGATT TTT/GJGGTTCCTC TGGAATTGAATG TTTAGT	T	G				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	5.40E-123	11
2830	cg43942338	1194	ACCCACCCGAGAG AAAAAGAGCACC A/GA/GAAAAAGA GCAGAAGAGGA CAAGAGA	G	A				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	5.40E-123	11
2831	cg43942338	1382	AATAAGAAATTT AATGCACGAGTA [A/G]AGGGGGTG GTGGGTTGTGCA CTTTT	A	G				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	5.40E-123	11
2832	cg43961212	882	TACCACGGGTCA TTTAGAAAAACA G/Agap/JAAAAA ATATACACCTAG TCITTC	A	gap				SILENT- NONCODI NG	struct	Human Gene Homologous to TREMBLNEW-ID:G1703715 PANTOPHYSIN=SYNAPTOPHYSIN HOMOLOG - MUS SP, 261 aa.	2.40E-114	7
2833	cg43961212	889	GGTCATTTAGAA AAACAGAAAAA A/Agap/JTATACAC CTAGTCTTTGCA ATTAAA	A	gap				SILENT- NONCODI NG	struct	Human Gene Homologous to TREMBLNEW-ID:G1703715 PANTOPHYSIN=SYNAPTOPHYSIN HOMOLOG - MUS SP, 261 aa.	2.40E-114	7
2834	cg43981852	150	CAGAGGTCGAG GAGCTCGCCTG GGC[G/gap]TAGA CATCCTCCACAG GAACAGTGA	G	gap				SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN- LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.80E-113	
2835	cg43981852	344	AGATGAAGGTGG CGTGTGGCTGTG G/C[gap]CCTACG CATCCCCGTTCT CCATGCG	C	gap				SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN- LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.80E-113	

2838	cg43981852	346	ATGAAGGTGGC GTGTGGCTGTG GCC[C/gap]TACG CATCCCCGTTCT CCATGCCGGC	C	gap			SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN- LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.80E-113	
2837	cg43051163	852	GGGATCTTGGC AGAGGAGTGATC TTA/GJAGAAGAAA CCGAGAGACGT GGCGTC	A	G			SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 196 aa.	5.30E-103	17
2838	cg43051163	292	TTAACTCACCCCT GGTATGGCTAAA G[C/gap]CAAGGG CCAGGCACCTG GAAGACTC	C	gap			SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 196 aa.	5.30E-103	17
2839	cg43051163	293	TAACTCACCCCTG GTATGGCTAAAG C[C/gap]AAGGGC CAGGCACCTGG AAGACTCT	C	gap			SILENT- NONCODI NG	struct	Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 196 aa.	5.30E-103	17
2840	cg42887734	977	GCTTCTATCCAC CCATGAGGCACC TTG/gap]GGGCTT CTCAGCCACCCCG GIGGIGI	G	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.60E-94 (1q31.3)	1
2841	cg42887734	980	TCTATCCACCCA TGAGGCACCTG GG[C/gap]CTTCT CAGCCACCCCGT GGTGTAAC	G	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.60E-94 (1q31.3)	1
2842	cg42887734	866	CCCCACTTCTTC CCTCCAGCCTGC A[gap/AT]GCCCT CCTCTGGAACCTG GGATTAA	gap	A			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.60E-94 (1q31.3)	1

2843	cg42893961	565	GAGAAAGAGGAA TGAGGGGCAGG GC[C/gap]AGGCC ACGGGGGGGCA CCTCAATAA	C					SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:Q01449 MYOSIN REGULATORY LIGHT CHAIN, CARDIAC MUSCLE ISOFORM - HOMO SAPIENS (HUMAN), 175 aa.	2.50E-89	
2844	cg42896604	269	CTTCATTTTTT TTTTTTTTTTT TTAGAAACAAAG ATCAGTTAAATTT TA	A	T				SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:Q14843 MYOSIN LIGHT CHAIN 2 - HOMO SAPIENS (HUMAN), 170 aa.	8.60E-87 (12q23)	12
2845	cg43282400	2067	TAATGAAATAAT TTGTAATAATGTC C/gap]TTTAAAG TTTAATGATACCT CTGA	C	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P45591 COFILIN, MUSCLE ISOFORM - MUS MUSCULUS (MOUSE), 166 aa.	8.00E-84	14
2846	cg43336710	150	CTTCTGTGCTGC ATGCAGAGGGG TG[C/T]AAGGCCA GGGCAGCTGAC CTGGTCA	C	T				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P13928 ANNEXIN VIII (VASCULAR ANTICOAGULANT-BETA) (VAC-BETA) - HOMO SAPIENS (HUMAN), 327 aa.	1.70E-83 (10q11.2)	10
2847	cg43336710	336	TCTCGGTTGGGA TGGATTCTGTGTT C[G/A]TTTCTCAG CTGCTGAAGGAT GTGTG	G	A				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P13928 ANNEXIN VIII (VASCULAR ANTICOAGULANT-BETA) (VAC-BETA) - HOMO SAPIENS (HUMAN), 327 aa.	1.70E-83 (10q11.2)	10
2848	cg43135652	598	TCCTGGGGTTGG GGAGGGGGTCG GG[G/gap]TCCCA GGACCTGAGCCT GGCCATGT	G	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P02591 TROPONIN C, SLOW SKELETAL AND CARDIAC MUSCLES (TN-C) - ORYCTOLAGUS CUNICULUS (RABBIT), 161 aa.	1.20E-82 (3p21.3)	3
2849	cg43976895	433	AGGACGAGAG CCGTGGGTCCC AAC[G/gap]GGGG CCCTGGACACC ACTGGCAAT	G	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P40145 ADENYLATE CYCLASE, TYPE VIII (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-CALMODULIN ACTIVATED ADENYLYL CYCLASE) - HOMO SAPIENS (HUMAN), 1251 aa.	9.40E-82	5

2850	cg43918621	564	AGCATTCTGCT CCCTCCGTGG GA[<i>gap</i>]CAGCG TCTCCTTTCAAT TCATGIG	G		gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P35749 MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) - HOMO SAPIENS (HUMAN), 1086 aa (fragment).	2.80E-81	16 (16p13.1 3)
2851	cg42888003	312	CTTCCAGACAAA GACCCACAAGG GGT[C]CGCGCC TCCCTGGTGGG GACCCGGC	T	C				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P02585 TROPONIN C, SKELETAL MUSCLE - HOMO SAPIENS (HUMAN), 159 aa.	1.50E-80	20 (20q12)
2852	cg42888003	318	GACAAAGACCCA CAAGGGGTGCG GC[C <i>gap</i>]TCCCT GGTGGGACCC GGCAGGGCG	C	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P02585 TROPONIN C, SKELETAL MUSCLE - HOMO SAPIENS (HUMAN), 159 aa.	1.50E-80	20 (20q12)
2853	cg43919386	1505	ATACATATGGAT GTTACTCTCTTG C[A/C]CCAAATTA TCTTGATACATT CAAAAT	A	C				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	9.80E-79	12 (12q21.3)
2854	cg43919386	1554	ATTGTCTGGTT AAAAAATAGGTG G[T/A]AGATATTG AGGCCAAGAATA TTGCA	T	A				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	9.80E-79	12 (12q21.3)
2855	cg42731508	1868	ACACCGGGTGA CCCTTAGGGCA CC[C <i>gap</i>]AGGCA AGATCCCTAAGA GGCACCCA	C	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P27482 CALMODULIN-RELATED PROTEIN NB-1 (CALMODULIN-LIKE PROTEIN) (CLP) - HOMO SAPIENS (HUMAN), 148 aa.	8.10E-75	2
2856	cg42731508	1886	CTCCCTCCGCG GTCGGATTCTGG AG[G/T]GTGGGA GGCATCTTGGCC TGCAGTA	G	T				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P27482 CALMODULIN-RELATED PROTEIN NB-1 (CALMODULIN-LIKE PROTEIN) (CLP) - HOMO SAPIENS (HUMAN), 148 aa.	8.10E-75	2

2857	cg44014373	205	GTGAGACTGTTA CAGAAAAA A/T[<i>gap</i>]AAAAGTT TCTGAGTCTGAT AAJTCC	T	gap		SILENT- NONCODING	struct	Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa.	6.10E-70	17
2858	cg43977049	133	CTGGGGCCCGA GGAGCTCAGGA AA[C/T]GGAAGC GGAGTCTTTGCA TAGTTCT	C	T		SILENT- NONCODING	struct	Human Gene Similar to SWISSPROT- ID:Q01995 SMOOTH MUSCLE PROTEIN 22-ALPHA (SM22-ALPHA) (TRANSGELIN) (WS3-10) (22 KD ACTIN- BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 200 aa.	1.80E-69	
2859	cg42379998	254	ATCAAAACAAAG TAAAGATGTTT A/T[C/J]AAAAGCCA TTTCCTTTTCTTT CCCC	T	C		SILENT- NONCODING	struct	Human Gene Similar to SPTREMBL- ID:Q63811 CALMODULIN-DEPENDENT PROTEIN PHOSPHATASE REGULATORY SUBUNIT BETA 2 ISOFORM - MUS MUSCULUS (MOUSE), 179 aa (fragment).	2.70E-67	
2860	cg43929049	1046	AGAAAGTAAACCT CTAAAACTGAAG A[C/A]GACCTCT AAAGGAGAAAAC TATAG	C	A		SILENT- NONCODING	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa. pcls:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	

2861	cg43929049	253	GGTTTCTATATA CCTTCTGGATTT T[agap]AAAAAAC CCAAAAATTAAT GGCTCA	A	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.lpcis:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189aa	3.40E-67	
2862	cg43929049	259	ATATACCTTCTG GATTTTAAAAAAA [gap/A]CCCAAAA ATTAATGGCTCA AGATAC	gap	A			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.lpcis:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189aa	3.40E-67	
2863	cg43929049	29	TTTTTTTTTTTT TTTTTTTTTTTTT GTTTAAATTCAA TAAACATGTAGA TT	T	G			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.lpcis:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189aa	3.40E-67	

2864	cg43929049	34	TTTTTTTTTTTT TTTTTTTTTTTTA /TATTCAATAAAC ATGTAGATTTATT T	A	T			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.lpcis:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2865	cg43929049	35	TTTTTTTTTTTT TTTTTTTTTTTA /TJTCAATAAACA TGAGATTTATT T	A	T			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.lpcis:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2866	cg43929049	428	AAAATTACAGAA GCTTCAAAATTGT TTA/GJTGTTTTCA CAAAATTTGCTA CATAT	A	G			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa.lpcis:SWISSPROT-ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	

2867	cg43929049	737	AGGCACTTGAAA ACATTAAGTATAT [G/C]TACAAATGT GCAAGTAAACA AACA	G	C			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa. pcis: SWISSPROT-ID: Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2868	cg43929049	853	ATGCAGAGTTTG TTTATGAAATGA A[C/A]CAAAAGCAG TTTGTCATTTCTT ACTA	C	A			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) (CD164 ANTIGEN) - HOMO SAPIENS (HUMAN), 189 aa. pcis: SWISSPROT-ID: Q04900 PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24 (MULTI- GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24) - HOMO SAPIENS (HUMAN), 189 aa.	3.40E-67	
2869	cg43936426	358	GGGAGGAGAG AGAAGGGGACA CCAT/AJTTCCTT AGACACATCTGT GTTTCIG	T	A			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67 1 (1q32)	
2870	cg43936426	430	GGCCAGGAGTTT GGGTGTGCACT GG[G/T]TGCTTT CAACTGGGTGGA ACCAAA	G	T			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67 1 (1q32)	
2871	cg43936426	450	ACTGGGTGCTT TCAACTGGGTGG A[A/gap]CCAAAC TGAGTECTTGAA GTCTCGC	A	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67 1 (1q32)	

2872	cg43936426	480	ACTGAGTCCTTG AAGTCTCGCTCC TGTAGGCTGCA GAAGAATAGATG GCTTT	G	T			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2873	cg43936426	493	AGTCTCGCTCCT GAGGCTGCAGA AGATATATAGATG GCTTTCCCTGC CTCGAG	A	T			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2874	cg43936426	520	TAGATGGCTTTT CCCTGCCCTCGAG GIG/gapJTGCGAT AAGGGAGGCAA AGCTGGGA	G	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2875	cg43936426	524	TGGCTTTTCCT GCCTCGAGGGT GGG/CJATAAGG GAGGCAAGCT GGGAGAAA	G	C			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2876	cg43936426	531	TCCTGCCTCGA GGGTGGGATAA GGG/gapJAGGCA AAGCTGGGAGAA AGAAAGGG	G	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2877	cg43936426	553	AGGGAGGCAAA GCTGGGAGAAA GAAJAGJGGGAG AGAGAGAAAAACG AATGGCCG	A	G			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
2878	cg43936426	587	GAGAAAAACGAAT GGCCGGCACAG GTG/gapJCCTGG GCCCCAGCCTTC AAGTGCGG	G	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)

2879	cg43933305	418	ACAGTTAAGATA CATTAAAAAAA A[A/gap]GGAAAG ATACCCACAATT CCATTCT	A	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P46680 ACTIN INTERACTING PROTEIN 1 - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 615 aa.	3.50E-66	4
2880	cg43933305	686	CACCTGTACAAC CTCCCCTGACAG A[T/C]AGTGAGAG CCGCGGCGGGG CCAGGG	T	C			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P46680 ACTIN INTERACTING PROTEIN 1 - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 615 aa.	3.50E-66	4
2881	cg43933305	740	GCCAGGGGCTC TGTGTGCTTTGG AG[G/gap]CTACT GCCTCTGGAATG TTTCGCAI	G	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P46680 ACTIN INTERACTING PROTEIN 1 - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 615 aa.	3.50E-66	4
2882	cg43986028	43	GGAGGCGCGAG TGAAGGAAGACG AA[G/gap]TGGT GACCCGACCGG CTGTGGTGT	G	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:P91637 RIC (RAS WHICH INTERACTS WITH CALMODULIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 264 aa.	5.00E-59	1
2883	cg43986623	2984	CCATCGGTCCGT CCATCCATGTCC C[C/gap]AGTTGA CCGCCCGGCAC CACTAGCT	C	gap			SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P15941 MUCIN 1 PRECURSOR (POLYMORPHIC EPITHELIAL MUCIN) (PEM) (PEMT) (EPISIALIN) (TUMOR- ASSOCIATED MUCIN) (CARCINOMA- ASSOCIATED MUCIN) (TUMOR- ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN) (EMA) (H23AG) (PEANUT- REACTIVE URINARY MUCIN) (PUM) - HOMO SAPIENS (HUMAN), 1255 aa.	6.60E-57 (7q11.23)	7
2884	cg43919048	1279	GAGGTGAGAGA ATTCCAAGTTT GA[G/A]GGGAGT GGTCCAAAGAGT AACAACT	G	A			SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:Q07569 MYOSIN HEAVY CHAIN - ENTAMOEBA HISTOLYTICA, 2139 aa.	1.70E-56	3

2885	cg43919048	186	GAGAGGCTAGG CAGTGAACACAT CACTGTATGCA ATGAGAAATAA CCAACT	C	T				SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:Q07569 MYOSIN HEAVY CHAIN - ENTAMOEBA HISTOLYTICA, 2139 aa.	1.70E-56	3
2886	cg43927885	2154	ATGCTGGAGGTG GGGGTGCCTGTG TTCTTTAGACCC CCCATATTATCC CAGTGT	C	T				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P19065 SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 115 aa.	1.20E-55	17
2887	cg43927885	641	CTCTCAGCCATA TCTTTCAGCCCC CCTCACTCCCTG GATCCGTGTGTG TGTTGT	C	A				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P19065 SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 115 aa.	1.20E-55	17
2888	cg43927885	782	AGATGATTTTC CGGTTGTCCTTA A/C/AJACCCCTTC CTGAGGTTCCCT TCACC	C	A				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P19065 SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 115 aa.	1.20E-55	17
2889	cg43958532	254	TCCTGACTCCAG GCTAGGTCCTCA A/G/gap]GGGAGG TCAGGCTCAGAC TTGGACC	G	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:Q16943 VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33) - APLYSIA CALIFORNICA (CALIFORNIA SEA HARE), 260 aa.	6.10E-54	20
2890	cg43958532	281	GGAGGTCAGGC TCAGACTTGGAC CTG/AJGGCGCT GGAAGTGTGAGT AATGGTT,	G	A				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:Q16943 VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33) - APLYSIA CALIFORNICA (CALIFORNIA SEA HARE), 260 aa.	6.10E-54	20

2891	cg43958532	69	TTTTCTTTTCAAG C ATGCTACATAGT C/GAAACAGAAC TGGGTTGGTCTT TTAT	G				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:Q18943 VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33) - APLYSIA CALIFORNICA (CALIFORNIA SEA HARE), 260 aa.	6.10E-54	20
2892	cg43977322	25	TTTTTTTTTTTT C TTTTTTTCAGAC/ C TTCAGCCACC AGGTTATTTTCA TG	T				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa.	1.50E-52	16
2893	cg43977322	431	ATGGAAGTTGG G TTTAAGCCAGA A/GATCTGGAGA GATGTCATGCCA GGCAG	A				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa.	1.50E-52	16
2894	cg43977322	62	GGTTATTTTCAT T GCTATAATAAA T/GTTCCTATTA GTCCCATTTTC TTA	G				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa.	1.50E-52	16
2895	cg43961860	215	AGTTAGCAGTC A TGCTTAAATGT T/Agap]AAAAAAA AAATCATAAAAA GCCATT	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:Q84703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment).	3.50E-51	
2896	cg43961860	225	TCTGCTTAAAT A GTTAAAAAAA A/Agap]TCATAAA AAGCCATTGTC IGTTAC	gap				SILENT- NONCODI NG	struct	Human Gene Similar to SPTREMBL- ID:Q84703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment).	3.50E-51	
2897	cg43918310	535	ATGCTGAATCCC T CTATCCCATTTCT G/TGJGATGAGT CCCATTTGCCTT GCAAT	C				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT- ID:P22528 CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) - HOMO SAPIENS (HUMAN), 89 aa.	4.00E-50 1 (1q21)	

2898	cg42673122	249	ACCAGGAGGGG GCTGGGGGCGG CCA[G/gap]CACC AGCGGCGTCCT GCTCAGCCCC	G	gap			SILENT- NONCODING	sulfotransferase	Human Gene SPTREMBL-ID:Q99999 CEREBROSIDE SULFOTRANSFERASE HOMO SAPIENS (HUMAN), 423 aa.	1.50E-209	22
2899	cg43974392	1785	CCAGAGGGTGG TGTGGTGTCCAG GG[G/A]TCCATCT TTCCAGAAATCCA TGCCTG	G	A			SILENT- NONCODING	sulfotransferase	Human Gene TREMBLNEW- ID:G2921306 HNK-1 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 356 aa.	1.40E-159	2
2900	cg43974392	2178	GATTCCTTTCAT CTCAGCAAAATG G[G/gap]CACTGC CAGAGCCATTTC TGATCAC	G	gap			SILENT- NONCODING	sulfotransferase	Human Gene TREMBLNEW- ID:G2921306 HNK-1 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 356 aa.	1.40E-159	2
2901	cg43974392	2311	AGTGGGCTTCC TGGCAACAAGT A[G/gap]GCCCTG GTGCAGGGCAA GCCGCAGC	G	gap			SILENT- NONCODING	sulfotransferase	Human Gene TREMBLNEW- ID:G2921306 HNK-1 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 356 aa.	1.40E-159	2
2902	cg43999676	1452	AAAATTAGCCAG GAGCATTGGCTC A[G/gap]TGTCTG TAATCCCAGCAC TTTGGGA	G	gap			SILENT- NONCODING	sulfotransferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157 2 (2q12)	
2903	cg43999676	1592	AAATTAGCCGGG CATGGTGGTGCA C[A/G]CCTATAGT CCCAGCTACTCG GGAGG	A	G			SILENT- NONCODING	sulfotransferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157 2 (2q12)	

2904	cg43989876	1615	ACACCTATAGTC CCAGCTACTCGG G/A/GJGGCTGAG GTAGGAGAATCG TTTGAA	A	G			SILENT- NONCODING	sulfotransferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157	2 (2q12)
2905	cg43989876	1738	TCTCAAAAAGAA AGAAAGTGACTAG G/G/gapJTTTCAGA GAACCAGGGTTC AAAGCCCC	G	gap			SILENT- NONCODING	sulfotransferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157	2 (2q12)
2906	cg43317375	751	CAC TAGGTCCTC AGAATGGACGTC C/T/CJCTGCCAG AGACTTCCAGCG GGCGG	T	C			SILENT- NONCODING	sulfotransferase	Human Gene Homologous to TREMBLNEW-ID:E1253895 DJ388M5.3 (SULFOTRANSFERASE (SULFOKINASE, EC 2.8.2.1) LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 284 aa.	8.50E-133	22
2907	cg43972499	141	AATGAAGATGGG GCAGACTGGGC CC/C/gapJAGCAT CTGAGGCCCCA CCCCCATGC	C	gap			SILENT- NONCODING	synthase	Human Gene SWISSPROT-ID:P27708 CAD PROTEIN (CONTAINS: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.5), ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2), DIHYDROOROTASE (EC 3.5.2.3)) - HOMO SAPIENS (HUMAN), 225 aa.	0.00E+00	2

2908	cg43972499	50	TTTTTTTTTT TTTTTTTTTTT ATTCAAGGGACA GCTGGGCTGTT ATT	T	A			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P27708 CAD PROTEIN (CONTAINS: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.5), ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2), DIHYDROOROTASE (EC 3.5.2.3)) - HOMO SAPIENS (HUMAN), 2225 aa.	0.00E+00	2
2909	cg43988130	186	CGCACACAATAA GCTGGGCCTGA GC[C/gap]AGGAG GCAGGCGGGGT GTTGGGGGA	C	gap			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:Q05932 FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 6.3.2.17) (FOLYLPOLY-GAMMA- GLUTAMATE SYNTHETASE) (FPGS) - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	9
2910	cg43988130	279	GGGAGCCCTC TGCTATCTCAGC CA[A/G]GAGGAA GGAGAGACCAA GGCACAGA	A	G			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:Q05932 FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 6.3.2.17) (FOLYLPOLY-GAMMA- GLUTAMATE SYNTHETASE) (FPGS) - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	9
2911	cg43988130	47	AAACAAAGGCT TTAATTCACCTC A[G/A]CCACCCTC TGTCGCCGAGTG TCCCA	G	A			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:Q05932 FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 6.3.2.17) (FOLYLPOLY-GAMMA- GLUTAMATE SYNTHETASE) (FPGS) - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	9
2912	cg43988130	83	TCCCGCAGTGTC CCAGGCAGAGG CC[C/gap]TCTCC CTTCCAGAAAGG CACTGGGA	C	gap			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:Q05932 FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 6.3.2.17) (FOLYLPOLY-GAMMA- GLUTAMATE SYNTHETASE) (FPGS) - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	9

2913	cg43054994	2317	CATGGTGAATAT AAGAACTGAATT CTT/gapJACATGT GCTGCATGAAGA GCTAATT	T	gap			SILENT- NONCODI NG	synthase	Human Gene SWISSNEW-ID:P54840 GLYCOGEN [STARCH] SYNTHASE, LIVER (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 703 aa.lpcis:SWISSPROT- ID:P54840 GLYCOGEN (STARCH) SYNTHASE, LIVER (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 703 aa.lpcis:TREMBLNEW-ID:E1228798 LIVER GLYCOGEN SYNTHASE - HOMO SAPIENS (HUMAN), 703 aa.	0.00E+00	12
2914	cg43054994	2820	AGAACCATGATT TAGATGTAGTTT TTA/GJGAGAGACA AAATCCATGAG TGAAT	A	G			SILENT- NONCODI NG	synthase	Human Gene SWISSNEW-ID:P54840 GLYCOGEN [STARCH] SYNTHASE, LIVER (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 703 aa.lpcis:SWISSPROT- ID:P54840 GLYCOGEN (STARCH) SYNTHASE, LIVER (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 703 aa.lpcis:TREMBLNEW-ID:E1228798 LIVER GLYCOGEN SYNTHASE - HOMO SAPIENS (HUMAN), 703 aa.	0.00E+00	12
2915	cg40388639	5040	GCCGGCTGCAA GTTTGTAAAGCGC GG[G/gap]ACAGA CACTGCTGAACC TTTCCTCT	G	gap			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0.00E+00 (12q24.2)	12
2916	cg43987111	680	TTGAGAAACAAG GTGACCGATGG GGC/gapJACTCT GCAGCCCCCACC CACCATCGG	C	gap			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP-- AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa.	0.00E+00 (1p34.1)	18
2917	cg43981333	18	TTTTTTTGTAGCT ATCC[G/A]ATAAT TATTATTGAAAG AAATGAC	G	A			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P18858 DNA LIGASE I (EC 6.5.1.1) (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) - HOMO SAPIENS (HUMAN), 819 aa.	0.00E+00 (19q13.2)	19

2918	cg43971304	2483	CCCCGATCCAGAT TCTGCACGGGGT G[T/C]GGCCCCG CAGTGCCCCCAC CCAGTC	T	C			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2919	cg43971304	2559	TCCAGTTTCCAA GTTCCCTGCACTC C[A/T]GAATCCAC AAAGCCGTGCCT TTCTC	A	T			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2920	cg43971304	2654	TGGACCGCTTCC CAGAGGCCAGG AA[gap/A]TCTGC CATTACTCTGCG GTGGIGCC	gap	A			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2921	cg43971304	2953	GAGGGATGTTCT AGCCCTCCCTGG C[A/gap]TGTCAG AGCCAGGCTCTG CCTGGAG	A	gap			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2922	cg43971304	68	GAGCGTCTTGCA AGCTTCCCCTCG G[G/gap]CACCAG CTACTCGGCCCC GCACCT	G	gap			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
2923	cg43918681	33	TTTTTTTTTACC ATTTTTTTTTTTT /A]TTTATTTCCAG GACTATGTTTTTA C	T	A			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P13196 5- AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA- AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-H) - HOMO SAPIENS (HUMAN), 640 aa.	0.00E+00	3 (3p21.1)

2924	cg43983214	484	GACCCAAGTGAA GCGCAGGTGGG GTGTTTGAATCC TAGGCAGCTGG CTTCTCA	G	T				SILENT- NONCODI NG	synthase	Human Gene SPTREMBL-ID:Q13735 5-AMINOLEVULINATE SYNTHASE PRECURSOR - HOMO SAPIENS (HUMAN), 587 aa.	0.00E+00	X (Xp11.2 1)
2925	cg43949316	211	TATTTAAACAG GGATCCATCAGA [G/C]GTGGTGAA CTATCAAGGTCA AGGTT	G	C				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P48651 PHOSPHATIDYLSERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.-) (KIAA0024) - HOMO SAPIENS (HUMAN), 473 aa.	9.80E-269	8
2926	cg43949316	348	GAACAAACCCGA TGTAAGGCAC CTTAAGCTGG GAGAACTGTG GTGTCA	T	A				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P48651 PHOSPHATIDYLSERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.-) (KIAA0024) - HOMO SAPIENS (HUMAN), 473 aa.	9.80E-269	8
2927	cg43949316	591	TTCTGCTCTAGA AGGAAGGGAA CC[C/gap]TTCCC CCAGTATCAATT TCAGCAGC	C	gap				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P48651 PHOSPHATIDYLSERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.-) (KIAA0024) - HOMO SAPIENS (HUMAN), 473 aa.	9.80E-269	8
2928	cg43967343	384	CCCCGGGTGCA GAACCCCTGCTG CA[G/gap]CTCAG GTTTCGGGGTGC TTGAGGAG	G	gap				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:Q92903 PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) - HOMO SAPIENS (HUMAN), 461 aa. pcds:SPTREMBL-ID:Q00163 CDP-DIACYLGLYCEROL SYNTHASE - HOMO SAPIENS (HUMAN), 461 aa.	8.50E-254	4

2929	cg43976335	108	AAGGCAGAAATTA GGGAAAGGCTAT G[C/gap]CCCTCC ACTCCCCCTCCT CCTACCA	C	gap			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa.	5.30E-240	20 (20q11.2)
2930	cg43976335	111	GCAGAAATTAGGG AAAGGCTATGCC C[C/gap]TCCACT CCCCCTCCTCCT ACCACTC	C	gap			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa.	5.30E-240	20 (20q11.2)
2931	cg43976335	182	ACTGGAACCTGCG TGAAAGGCTGA TIG/AJAGGGCT GACAGGAGTGG GGCAGGG	G	A			SILENT- NONCODI NG	synthase	Human Gene SWISSPROT-ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa.	5.30E-240	20 (20q11.2)
2932	cg43959826	522	GCCGATGCCCTG GCTCCATCCAGA GC[C/gap]AGCCC AGCCCAGGGAG GCTGCATGG	C	gap			SILENT- NONCODI NG	synthase	Human Gene Homologous to SWISSPROT-ID:P10746 UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75) (UROS) (UROPORPHYRINOGEN- III COSYNTHETASE) (HYDROXYMETHYLBILANE HYDROLYASE (CYCLIZING)) (UROIIIS) HOMO SAPIENS (HUMAN), 265 aa.	7.00E-140	10 (10q25.2)
2933	cg43953338	2968	TTTGTGTTTTCAT CTCCTAAAAGTG[T/GTTTTTATTTT CTTGATATCTGTA GTC	T	G			SILENT- NONCODI NG	synthase	Human Gene Homologous to SWISSPROT-ID:P44708 GLUCOSAMINE-FRUCTOSE-6- PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE- 6- PHOSPHATE AMIDOTRANSFERASE) (GFAT) (L- GLUTAMINE-D-FRUCTOSE-6- PHOSPHATE AMIDOTRANSFERASE) (GLUCOSAMINE-6-PHOSPHATE SYNTHASE) - HAEMOPHILUS INFLUENZAE, 609 aa.	3.10E-107	2 (2p13)

2934	cg43982623	106	TCTGCTCCTCCTC TCTCAGACAGGG A[G/A]GCGGGAA CCAGACTTACTG ATCCAA	G	A			SILENT- NONCODI NG	synthase	Human Gene Homologous to SWISSPROT-ID:P08037 N- ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N- ACETYLGLUCOSAMINE (BETA 1- >4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT) - BOS.TAURUS.(BOVINE).402.aa.	8.20E-105	1
2935	cg43982623	200	GCAGCGACACA GCATCCCCTCTG GT[C/gap]CCCTC CTGGGGCTGCT CCTCAGCAG	C	gap			SILENT- NONCODI NG	synthase	Human Gene Homologous to SWISSPROT-ID:P08037 N- ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N- ACETYLGLUCOSAMINE (BETA 1- >4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT) - BOS.TAURUS.(BOVINE).402.aa.	8.20E-105	1
2936	cg43982623	211	GCATCCCCTCTG GTCCCCTCCTGG G[G/gap]CTGCTC CTCAGCAGGGG GCGCACCA	G	gap			SILENT- NONCODI NG	synthase	Human Gene Homologous to SWISSPROT-ID:P08037 N- ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N- ACETYLGLUCOSAMINE (BETA 1- >4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT) - BOS.TAURUS.(BOVINE).402.aa.	8.20E-105	1
2937	cg43987048	35	TTTTTTTTTTTT TTTTTTTTTTTAA /G/CATTTAAAAAT CAGTATTTAATTA C	A	G			SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:G2984031 3-OXOACYL-[ACYL- CARRIER-PROTEIN] SYNTHASE II - AQUIFEX AEOLICUS, 415 aa.	1.20E-86	

2938	cg43124627	1928	TTTCATTAAATTAC CATATCTATAAA A/gap]CAAAACATA GTATCTGTCAAT CTCTA	A	gap			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. pcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.70E-79	16
2939	cg43933068	289	AGCCAGGGTCG GTGAAGGATCCC AA[A/G]ATGGCTG GGCGAAAACTTG CTCTAA	A	G			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa.	1.90E-75	12
2940	cg43275028	3001	ACACCTAAGCCA AGACACTGGTTC TTC[gap]CTTCCG GAATGAGGCCCT GGGAGGA	C	gap			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT- ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa. pcis:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)
2941	cg43275028	3213	ATGAAGACACAG CTGTTAACAATT G[gap]CTGATC AGCCCCCAGAAT GCCTCAG	G	gap			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT- ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa. pcis:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)

2942	cg43275028	705	CTTACCTTGACC ACACATTCCTG C[G/A]GAGAAGA TGGACGACGCT GTGGCTC	G	A			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT- ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.lpcis:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)
2943	cg43275028	7134	ATTTTATACAAGA AGATAAAAAAAT A/G]TAACCTCCT GCTACCAGTAAG TAAG	A	G			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT- ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.lpcis:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)
2944	cg43275028	852	AAAATCTGATCG AGGATTTCAACT C[G/T]GGGCTGA TTGGGCCCCCTGC TTATCT	G	T			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT- ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.lpcis:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.2E-65	1 (1q23)
2945	cg42521802	1609	AGTCTCCAGAAC CCATGATGAAC G[T/gap]GATCTG CCGTGGTCCTGC CGTGGTC	T	gap			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT- ID:P15535 N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N- ACETYLGALACTOSAMINE (BETA 1- >4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT) - MUS MUSCULUS (MOUSE), 399 aa.	3.7E-65	

2946	cg43064068	1672	TCCGGAAAAGCCCA CGTGGCAGTG AGJA/GJCATCTAA GAGACATTCATT TGGATT	G			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS. 572.aa	7.4E-65	
2947	cg43064068	1674	CGGAAAAGCCC GTGCGCAGTGA GACJA/GJTCTAAG AGACATTCATTT GGATTCC	G	A		SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS. 572.aa	7.4E-65	
2948	cg43064068	1679	AAGCCCGTGCG CAGTGAGACATC TAJA/GJGAGACAT TCATTTGGATT CCCTCT	G	A		SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS. 572.aa	7.4E-65	

2949	cg43084068	1741	CTTTCCCTTTG GGCCCTTGGCCT TTC/ACTATGATG ATATGAGATTCT TTATG	C	A			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.4E-65	
2950	cg43084068	1767	CTATGATGATAT GAGATTCCTTAT G/G/AAGAACAT GAATATAAGTTTT GTCT	G	A			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.4E-65	
2951	cg43084068	1780	AGATTCCTTTATG GAAGAACATGAA TTA/GTTAAGTTTT GTCTGGCCCTGG TTTTG	A	G			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.4E-65	

2952	cg42875572	162	GCAGTTTTTAC TATTTACAAATG TTCATTTAGAG TGGAGGTGGCC ACCTT	T	C				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2953	cg42875572	168	TTTTACTATTAC AAATGTCATTI A/GGAGTGGAG GTGGCCACCTTC AGTAG	A	G				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2954	cg42875572	174	TATTTACAAATG TCATTTAGAGTG G/AJAGGTGGCCA CCTTCAGTAGCT GAGG	G	A				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2955	cg42875572	213	CAGTAGCTGAGG CAATGCTTTCA C/GATGAGATG GCCACAGAAAGT TGGTTC	G	A				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2956	cg42875572	226	AATGCTTTTAC GTGAGATGGCCA C/A/TJGAAAGTGT GTTCTTGGAAC GGCTC	A	T				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2957	cg42875572	245	GGCCACAGAAAGT GTGGTTCTTGA A/C/TJTGCTCAG AAAGGCCACAG GCTGTC	C	T				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14
2958	cg42875572	253	AAGTGTGGTTCC TGGAAGTGGCTC A/C/GJAAAGGCC ACAGGCTGTCT GGGTGA	C	G				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.8E-53	14

2959	cg42875572	324	GCACCAAAAAGG CTCAGTCTTCTG TTTCJCTTCATA CGTCGTCICGTC AAAGG	T	C				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.80E-53	14
2960	cg42875572	333	AGGCTCAGTCTT CTGTTTCTTCATA [C/G]GTCGTCCTC GTCAAAGGGCCT GTCCA	C	G				SILENT- NONCODI NG	synthase	Human Gene Similar to TREMBLNEW- ID:E1245723 POLYKETIDE SYNTHASE STREPTOMYCES COELICOLOR, 2297 aa.	6.80E-53	14
2961	cg43931248	2107	CATGGGGGCTG TATTTAAGGACA CC[C/gap]GTGCC CCAAGCCCCACCT GGGGCCCC	C	gap				SILENT- NONCODI NG	tgf	Human Gene SWISSPROT-ID:P01137 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) - HOMO SAPIENS (HUMAN), 390 aa.	9.7E-214	19
2962	cg43931248	713	ACCACTGCGCCC TTCTCCCTGAGG Algap/G]CCTCAG CTTCCCTCGAG GCCCTCC	gap	G				SILENT- NONCODI NG	tgf	Human Gene SWISSPROT-ID:P01137 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) - HOMO SAPIENS (HUMAN), 390 aa.	9.7E-214	19
2963	cg43274187	57	TGAGTATCTACA TTCAATTGCTTTA [G/gap]CTAAATTA ACAAAAACATG CAAAAT	G	gap				SILENT- NONCODI NG	tgf	Human Gene SWISSPROT-ID:000292 TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4) (ENDOMETRIAL BLEEDING- ASSOCIATED FACTOR) - HOMO SAPIENS (HUMAN), 370 aa.	1.4E-186	
2964	cg43980446	1401	GTCCATCAATTG AAAGCACATTCC C[A/G]TACGTTTG CTGGAAGGATG GCAIGT	A	G				SILENT- NONCODI NG	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166 (15q21.1)	15
2965	cg43980446	1658	TGATGATTCTGA TTGGGGGAAAT ATTCTAGTTCTAC CTATCTATATTG TTTT	T	C				SILENT- NONCODI NG	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166 (15q21.1)	15

2966	cg43980446	1701	TTTGTTTTCTTT TAATTATTGGT C/TCTGGATGG TGAATTAATGAA GCAA	C	T				SILENT- NONCODI NG	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)
2967	cg43980446	795	ATCCATGCAAGA ACACAAAGCCTA TT/GJTAAACT AAAAAAAGAAG AGATT	T	G				SILENT- NONCODI NG	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)
2968	cg43980446	796	TCCATGCAAGAA CACAAAGCCTAT TT/GJTAAACTA AAAAAAAGAAGA GATTG	T	G				SILENT- NONCODI NG	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)
2969	cg43980446	797	CCATGCAAGAAC ACAAAGCCTATT TT/GJTAAACTAA AAAAAAGAAGAG ATTGT	T	G				SILENT- NONCODI NG	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)
2970	cg4332146	777	TCAAACTCTGT CAAGAACTCCGT CT/GGCTTGGG GTTATTCAGTGT GACCTA	T	G				SILENT- NONCODI NG	tgf	Human Gene Similar to SWISSPROT- ID:P01135 TRANSFORMING GROWTH FACTOR ALPHA PRECURSOR (TGF- ALPHA) (EGF-LIKE TGF) (ETGF) (TGF TYPE 1) - HOMO SAPIENS (HUMAN), 160 aa.	5.2E-84 2 (2p13)	
2971	cg43047272	1700	GGCGGCCTAGG GGAAGATCGGG GAG[gap/GJCTGG TTTTGATGAAAG TAIGTTAAC	gap	G				SILENT- NONCODI NG	tgf	Human Gene Similar to SPTREMBL- ID:Q13118 TGF-BETA INDUCIBLE EARLY PROTEIN - HOMO SAPIENS (HUMAN), 480 aa.	5.2E-74	
2972	cg43047272	1740	GTATGTTAACTTT TCTTTCCACTT gap/GJGGGACCC TGTCAGTATCT TTTGTA	gap	G				SILENT- NONCODI NG	tgf	Human Gene Similar to SPTREMBL- ID:Q13118 TGF-BETA INDUCIBLE EARLY PROTEIN - HOMO SAPIENS (HUMAN), 480 aa.	5.2E-74	

2973	cg43272560	3230	CCAGCCCAAGCTG CAGCTCAGCTAC T[<i>gap</i>]CCAAGG GCAGGACCAATG GCTGAGC	G	gap				SILENT- NONCODI NG	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2974	cg43272560	3459	GCCCTCACAG GCTTGGGGTTT TCATATGTGAA ACACATGCCAGT TCTTAA	A	T				SILENT- NONCODI NG	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2975	cg43272560	3700	AATTGCACCTT TGCTGGATGCA CAATCTCTGAC CTTGCTGCCACA ACCTG	A	T				SILENT- NONCODI NG	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2976	cg43272560	3744	CAACCTGTGGG GTCTGATGTGC CCATATGATGGG TGCTGCCCTCAG GGACTG	T	A				SILENT- NONCODI NG	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2977	cg43272560	3745	AACCTGTGGGT CTGATGTGCCC TTATGATGGGTG CTGCCCTCAGG GACTGC	T	A				SILENT- NONCODI NG	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2978	cg43272560	4243	TAGGCCCTTTCA TAAAACCAAC TTCGTAGCAAGA TGCAATGCATG GCATA	C	G				SILENT- NONCODI NG	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
2979	cg43272560	4338	ACCAAGACAGTG CTGAGATTGGAA ATA[<i>gap</i>]GGGCAC TCATTGGGATTG CCTTACT	A	gap				SILENT- NONCODI NG	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)

2980	cg43261247	3334	CCCTAAACACTA CCAAATAGCTCT TACJTGCGGCA GGCTGGGCATG TCCAAAG	A	C				SILENT- NONCODING	tgfrecept or	Human Gene SWISSPROT-ID:P37173 TGF-BETA RECEPTOR TYPE II PRECURSOR (TGFR-2) - HOMO SAPIENS (HUMAN), 567 aa.	2.0e-316	3 (3p22)
2981	cg43982633	458	CAGATACTATAT TTGGATGTGACA GIGTGTGTTTT CTTTGTACAAG AGTGC	G	T				SILENT- NONCODING	tgfrecept or	Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF- BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.5E-254	
2982	cg43982633	459	AGATACTATATTT GGATGTGACAG GTGTGTGTTTTTC TTTTGTACAAGA GTGCA	T	G				SILENT- NONCODING	tgfrecept or	Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF- BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.5E-254	
2983	cg43982633	742	GAAGTAAACTG TTAAATCATCAT [C/gap]ATGATCA TGATGATCATCA TCATGA	C	gap				SILENT- NONCODING	tgfrecept or	Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF- BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.5E-254	
2984	cg43982633	843	GCTTCTTAAAA GGAAAAA A[A/gap]TGTTC AGTTGAATGGAA CTGTTC	A	gap				SILENT- NONCODING	tgfrecept or	Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF- BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.5E-254	
2985	cg43921327	1385	CCATGGACTCTT GCCTCGGTGCA GTCTTCCACTC TTGACCCCCACC TCCTAC	C	T				SILENT- NONCODING	thioester ase	Human Gene Homologous to TREMBLNEW-ID:G2501961 PALMITOYL-PROTEIN THIOESTERASE 2 - HOMO SAPIENS (HUMAN), 302 aa.	1.1E-141	

2986	cg43918322	1108	CACAGCCCTGCC CATCTCTGGGG C[C/gap]TGGGG GACGACATCTAG TTCAATG	C	gap		SILENT- NONCODING	thioesterase	Human Gene Similar to SPTREMBL- ID:Q19781 SIMILAR TO ACYL-COA THIOESTERASE. NCBI GI: 1213545 - CAENORHABDITIS ELEGANS, 343 aa.	1.1E-53	20
2987	cg36988276	172	TGGAGGTTTTTC TCTGCAAATGCA G[G/A]AAGAAATC AGGTGGATGGAT GCATA	G	A		SILENT- NONCODING	tm7	Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa.	0 2 (2p21)	
2988	cg44030467	1747	TTCTCAAACGGT ACACAGACTATT G[A/G]CATCAGC ATCACCTAGAAA CTGGT	A	G		SILENT- NONCODING	tm7	Human Gene TREMBLNEW- ID:E1248507 C3A ANAPHYLATOXIN RECEPTOR - HOMO SAPIENS (HUMAN), 482 aa.	3.9E-265	12
2989	cg43338230	264	GGGCTCGGCA AGGGAGGGTGA TGC[A/T]ATGTGG TCTGAAGCCCTG GAAGGGC	A	T		SILENT- NONCODING	tm7	Human Gene SWISSPROT-ID:P11229 MUSCARINIC ACETYLCHOLINE RECEPTOR M1 - HOMO SAPIENS (HUMAN), 460 aa.	7.7E-253	
2990	cg43946035	1974	GGGACTCTGATA TAAAGGAAGAAT A[A/gap]GTCACT GTAAACACAGAAC TTTAA	A	gap		SILENT- NONCODING	tm7	Human Gene SWISSPROT-ID:P24530 ENDOTHELIN B RECEPTOR PRECURSOR (ET-B) (ENDOTHELIN RECEPTOR NON-SELECTIVE TYPE) - HOMO SAPIENS (HUMAN), 442 aa.	1.1E-242 (13q22)	13
2991	cg41084924	1896	GGCATGGTACCA GCCCTGGGGCT GG[G/gap]CCCCC CAGCTCAGGGG CAGCTCATA	G	gap		SILENT- NONCODING	tm7	Human Gene SWISSPROT-ID:P14416 D(2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.7E-241	11
2992	cg43985000	1935	AGAAATGCTTTC CAAAACCGCAAG G[G/gap]TAGACT GGTTATCCACC CACAAACA	G	gap		SILENT- NONCODING	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4

2993	cg43985000	2222	TTCTACTTTTTT AAGTGATTTTTT T/gap]GTCCTTCA GCCAAACACAAT ATGGG	T	gap				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2994	cg43985000	2252	TTCAGCCAAACA CAATATGGGCTC A/A/G]GTCACITTT TATTTGAAATGT CATT	A	G				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2995	cg43985000	2787	AAAGATCGAATT TTTCAGATGATT C[G/A]GAAATTTT CATTGAGGTATT TGTA	G	A				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2996	cg43985000	2863	ATCACCTCCTAT TCTCTTAATTTT [G/C]TTAAATGT TAACTGGCAGTA AGTC	G	C				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2997	cg43985000	2988	AATAATTACCCA CAAATGCCACCA G[gap/]TAACTTA CGATTCTTCACT TCTTGGG	gap	T				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.6E-236	4
2998	cg43985000	2994	TACCCACAAATG CCACCAGAACTT A[gap/]JCGATTTC TTCACCTCTTGG GGTTTC	gap	A				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.60E-236	4
2999	cg43985000	3324	GTGTGCCAAAG TGCAATAGTCTGA G[gap/]CTAAAT CTAGGTGATTGT TCATCAT	gap	C				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.60E-236	4

3000	cg43985000	4080	AGCCAGAAAGCCA AGGCCCTGAGTT G[G/gap]CAGTGG CCCATAAAGTGTA AAATAAA	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.60E-236	4
3001	cg39565524	1715	CTAGCCTCAGCC GCTCCTGGTGG GG[gap]GAATGG CTGGGGCTGGG CAGGACCCT	gap	G			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P51575 P2X PURINOCEPTOR 1 (ATP RECEPTOR) (P2X1) (PURINERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 399 aa.	2.00E-220	17
3002	cg39565524	1727	CGCTCCTGGTG GGGAATGGCTG GGG[C/G]TGGGC AGGACCCCTCCCA CACACCCTG	C	G			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P51575 P2X PURINOCEPTOR 1 (ATP RECEPTOR) (P2X1) (PURINERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 399 aa.	2.00E-220	17
3003	cg36847035	217	GTGCTCCTGGCT ACCTCGCACAGC G[G/gap]TGCCCG CCCGGCCGTCA GTACCATG	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P35372 MU-TYPE OPIOID RECEPTOR (MOR-1) HOMO SAPIENS (HUMAN), 400 aa.	1.40E-219	6 (6q24)
3004	cg42704619	120	GGGGCTGGGCC CCGCACCATGG GGG[G/gap]CAGC CCAGCCCCCAGC CCGGGTAAAC	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3005	cg42704619	171	GCCGACCTCCG CCGCCGCCCGC GCC[G/gap]CGTC TGCCCCCTCCCG CTCGGGGCTC	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)

3006	cg42704619	53	TGGCTCCCTCCC GGGCCAGTGAG CC[C]gapTTGGCG CCGCCGCGGCC GCGGTCCCA	C	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3007	cg42704619	73	GAGCCCTGGCG CCGCCGCGGCC GCG[G]gapTTCCC AGCAGCGGAGT AGGGCGGCGG	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3008	cg43306266	120	GCGGCTGCGCC CCGCACCATGG GGG[G]gap]CAGC CCAGCCCCAGC CGCGGTAAC	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3009	cg43306266	171	GCCGACCTCCG CCGCCGCGCCG GCC[G]gap]CGTC TGCCCCCTCCCG CTGCGGCTC	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3010	cg43306266	53	TGGCTCCCTCCC GGGCCAGTGAG CC[C]gapTTGGCG CCGCCGCGGCC GCGGTCCCA	C	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
3011	cg43306266	73	GAGCCCTGGCG CCGCCGCGGCC GCG[G]gapTTCCC AGCAGCGGAGT AGGGCGGCGG	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)

3012	cg44031327	952	CTCCTAAAGCAC GGACCAGCCGTT G[gap]AGCCCC CAAATCCAGTAG GGGGTGG	G	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P35414 PROBABLE G PROTEIN-COUPLED RECEPTOR APJ - HOMO SAPIENS (HUMAN), 380 aa.	5.70E-209	11
3013	cg43263108	1724	CCAAGCCACTCC AAGAGCCAGCC CC[gap]CJTTCCT GCTCCACAAAA CCACAGTT	gap	C			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43119 PROSTACYCLIN RECEPTOR (PROSTANOID IP RECEPTOR) (PGI RECEPTOR) - HOMO SAPIENS (HUMAN), 386 aa.	8.30E-208	19 (19q13.3)
3014	cg43282263	1976	CTGGAGGCTCC CATGGGCTAGGA GC[C/gap]AGTGT GAGGCTGTAAC TATACTAA	C	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P41231 P2U PURINOCEPTOR 1 (ATP RECEPTOR) (P2U1) (PURINERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 377 aa.	9.90E-205	
3015	cg43329467	2631	CCAGGACAATGA AATACTCCAGCA C[G/C]GTGGCT GACGAATTTGTT TCTACA	G	C			SILENT- NONCODI NG	tm7	Human Gene SWISSNEW-ID:Q99527 CHEMOKINE RECEPTOR-LIKE 2 (IL8- RELATED RECEPTOR DRY12) (FLOW- INDUCED ENDOTHELIAL G PROTEIN- COUPLED RECEPTOR) (FEG-1) (G PROTEIN-COUPLED RECEPTOR GPR30) (GPCR-BR) - HOMO SAPIENS (HUMAN), 375 aa.lpcis:SWISSPROT- ID:Q99527 CHEMOKINE RECEPTOR LIKE 2 (IL8-RELATED RECEPTOR DRY12) (FLOW-INDUCED ENDOTHELIAL G PROTEIN-COUPLED RECEPTOR) (FEG-1) (G PROTEIN- COUPLED RECEPTOR GPR30) - HOMO SAPIENS (HUMAN), 375 aa.lpcis:TREMBLNEW-ID:G2656121 G- PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 375 aa.	8.20E-201	7

3016	cg43329467	680	CTTTCGGCAAT CTTGAAAGCTGC AIGCJGGCGCAG AGACATGGATGT GACTTC	G	C			SILENT- NONCODI NG	tm7	Human Gene SWISSNEW-ID:Q99527 CHEMOKINE RECEPTOR- LIKE 2 (IL8- RELATED RECEPTOR DRY12) (FLOW- INDUCED ENDOTHELIAL G PROTEIN- COUPLED RECEPTOR) (FEG-1) (G PROTEIN-COUPLED RECEPTOR GPCR30) (GPCR-BR) - HOMO SAPIENS (HUMAN), 375 aa.jpcl:SWISSPROT- ID:Q99527 CHEMOKINE RECEPTOR- LIKE 2 (IL8-RELATED RECEPTOR DRY12) (FLOW-INDUCED ENDOTHELIAL G PROTEIN-COUPLED RECEPTOR) (FEG-1) (G PROTEIN- COUPLED RECEPTOR GPCR30) - HOMO SAPIENS (HUMAN), 375 aa.jpcl:TREMBLNEW-ID:G2656121 G- PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 375 aa.	8.20E-201	7
3017	cg38277960	1396	AGCTACCTCAAC CAATGCCGAAAA Aigap/AJGACAGG GCTGATAAGCTA ACACCAG	gap	A			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P32248 C- C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CC-CKR-7) (CCR-7) (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1) (EBI1) (BLR2) - HOMO SAPIENS (HUMAN), 378 aa.	4.10E-199 (17q12)	17
3018	cg2751286	1554	TTTGTGCTTAAA CGTGAGAGCAAA Igap/AJTGCAATGT AATCCAACATGG CTACTT	gap	A			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3019	cg2751286	1566	AACGTGAGAGCA AATGCATGTAAT C[C/gap]AACATG GCTACTTGCTTT GAAGGCT	C gap	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X

3020	cg2751286	1587	AATCCAACATGG CTACTTGCTTTG A/A/gapJGGCTCA CCAGAAATTAATTT TAAGTG	A	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3021	cg2751286	1601	ACTTGCTTTGAA GGCTCACCAGAA TTT/gapJATTTTAA AGTGGTTTAAAT AAAAA	T	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3022	cg2751286	1607	TTTGAAGGCTCA CCAGAAATTAATTT T/gapJAAAGTGGT TTTAATAAAATAA CAAAAT	T	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3023	cg2751286	1616	TCACCAGAAATTA TTTTTAAAGTGTT T/ATTAATAAAAT AACAAATTTTGA CCTA	T	A			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3024	cg2751286	414	TAAGAGTTCTAT GTTTTCTCACA G/gap/GJAAGGCA TAAGAACTAGGA GCTGCTG	gap	G			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X
3025	cg43031008	540	CTTCTAGCCAT TTGTTGGCAAGA A/A/gapJTAATAAT TAAATTTTTTATT AAAAAC	A	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P32249 EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2) - HOMO SAPIENS (HUMAN), 361 aa.	7.10E-195 (17q12)	17
3026	cg43031008	551	TTTGTGGCAAG AAATAATAATTA A/gapJTTTTTTAT TAAACAAAACCT TTTTA	A	gap			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P32249 EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2) - HOMO SAPIENS (HUMAN), 361 aa.	7.10E-195 (17q12)	17

3027	cg43031008	635	TATTCGTTTACAA ATAAAAATGAAA gap/AJTATTATTT GCATTTTATTGT GCT	gap	A				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P32249 EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2) - HOMO SAPIENS (HUMAN), 361 aa.	7.10E-195	17 (17q12)
3028	cg43031008	720	TACTTCGAGTT GGAGATGGGAA AGT/CJGCCCAAT GAAAGAAATATA AAAGAA	T	C				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P32249 EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2) - HOMO SAPIENS (HUMAN), 361 aa.	7.10E-195	17 (17q12)
3029	cg42704646	117	GCGGCTGCGCC CCGCACCATGG GGG[ap/G]CAGC CCAGCCCCAGC CGCGGTAAAC	gap	G				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.10E-194	1 (1p31.2)
3030	cg42704646	167	GCGGACCTCCG CCGCCGCCCGC GCC[ap/G]CGTC TGCCCCCTCCCG CTGCGGCTC	gap	G				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.10E-194	1 (1p31.2)
3031	cg42704646	52	TGGCTCCCTCCC GGGCCAGTGAG CC[ap/C]TGGCG CCGCCGCGGCC GCGTCCCAAG	gap	C				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.10E-194	1 (1p31.2)
3032	cg42704646	71	TGAGCCTGGCG CCGCCGCGGCC GCG[ap/G]TCCC AGCAGCGGAGT AGGGCGGCGCG	gap	G				SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.10E-194	1 (1p31.2)

3033	cg43308845	1524	AGTGAGGGGAA ACCAGGGCCTG AGC[C/gap]AAGC TAGAATTCCTC TCTCTGACT	C	gap		SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P49238 PROBABLE G PROTEIN-COUPLED RECEPTOR GPR13 (V28) (BETA CHEMOKINE RECEPTOR-LIKE 1) (CMK BRL-1) (CMKBLR1) - HOMO SAPIENS (HUMAN), 355 aa.	2.00E-190	3 (14q11.2)
3034	cg43308845	2847	CCCCCTAGAAA CGTTTGAACAA TTC[G]TAAAACTT TAAAGCTCGAAA ACAAT	C	G		SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P49238 PROBABLE G PROTEIN-COUPLED RECEPTOR GPR13 (V28) (BETA CHEMOKINE RECEPTOR-LIKE 1) (CMK BRL-1) (CMKBLR1) - HOMO SAPIENS (HUMAN), 355 aa.	2.00E-190	3 (14q11.2)
3035	cg43047341	671	GAAGGCAGGCC CAGGCTGTGACA GC[C/gap]GCCAG TATCCAGCAGCA CGCCCAGG	C	gap		SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P21731 THROMBOXANE A2 RECEPTOR (TXA2- R) (PROSTANOID TP RECEPTOR) - HOMO SAPIENS (HUMAN), 369 aa.	2.80E-190	
3036	cg43328050	1796	GCGGACGTGAC CACTCAGGCCT GC[A/G]GGGACT CAGCACAGCTCT GGATTCT	A	G		SILENT- NONCODI NG	tm7	Human Gene TREMBLNEW-ID:E322207 P2Y-LIKE G-PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 367 aa.	3.30E-188	2
3037	cg42268169	7500	CACTTGAGCCCA GGAGTTTGAGAC T[A/G]CAGTGAAC TATGATTGCACC ACTGC	A	G		SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P56486 THROMBOXANE A2 RECEPTOR (TXA2- R) (PROSTANOID TP RECEPTOR) - CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET), 343 aa.	4.90E-177	
3038	cg42268169	7533	CTATGATTGCAC CACTGCACCTCA G[A/C]CTAGGTG ACAGAGTAAGAC CCTGAC	A	C		SILENT- NONCODI NG	tm7	Human Gene SWISSPROT-ID:P56486 THROMBOXANE A2 RECEPTOR (TXA2- R) (PROSTANOID TP RECEPTOR) - CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET), 343 aa.	4.90E-177	

3039	cg44011188	1412	AGCTGAGCTGAC CCCAAGCCGAA GG[gap/G]TCCCG ACTCCTCTCGGG AGCCTGGA	gap	G			SILENT- NONCODI NG	tm7	Human Gene Homologous to SWISSPROT-ID:P35626 BETA- ADRENERGIC RECEPTOR KINASE 2 (EC 2.7.1.126) (BETA-ARK-2) (G- PROTEIN COUPLED RECEPTOR KINASE 3) - HOMO SAPIENS (HUMAN), 688 aa.	3.10E-119	22
3040	cg43993798	131	ATCCACATAAGA GCTCTGAGGGG AA[G/A]GAATGAT TATTATCCTTATT TTAAA	G	A			SILENT- NONCODI NG	tm7	Human Gene Homologous to SWISSPROT-ID:P31421 METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR - RATTUS NORVEGICUS (RAT), 872 aa.	6.90E-109	3 (3p21)
3041	cg42891000	1295	TGAGTCCAAGCC CTTCTCTGGTAC A[C/gap]TTAGTC CCAGTCTCTGGA ATATTG	C	gap			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)
3042	cg42891000	1606	TGGAGGGAGAT GTGGAGCTGAC CCT[G/C]TCCAG CCTGTCCACGGA GAGGAAGG	G	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)
3043	cg42891000	530	AGCAGGCCCTTAT TATTATTATTAT T/ATTTTTTTTGG CTGACAAAGTCCA AGA	T	A			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)
3044	cg42891000	649	CCTGCTTCCTTT TGCCTGTATTA AT[C]CGCTGCAA TAAAGCCATTAG AATGT	T	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)
3045	cg42891000	973	CCCCAGGATTCC AAGAGCCCAAAAT C[C/gap]TGCAGT GGGAGTGAAGG GGAGGCAG	C	gap			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.50E-92	3 (3p21)

3046	cg43285474	2177	TGGTTGAATGAT TTCCCACTCAGG G[C/gap]CTGGGG CCAAGAGGAAAA ACAGGGA	C	gap				SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P30083 VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR) (PACAP TYPE II RECEPTOR) (PACAP- R-2) - RATTUS NORVEGICUS (RAT), 459 aa.	4.40E-85	3 (3p22)
3047	cg42284367	1202	TTTCCAGCAAG AGGCTCCCGAG CGA/GJGCAAGC TCAGTTTACACC CGATCCA	A	G				SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.80E-83	3 (3q21)
3048	cg42284367	1218	GCTCCGAGCG AGCAAGCTCAGT TTTATCACCCGA TCCACTGGGGA GCAGGAA	A	T				SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	5.80E-83	3 (3q21)
3049	cg11687629	323	TCAGCTTCCAGT CTTATCTGAAGA C/C/TCCGGCAC CAAAGTGACCAG GAGGCA	C	T				SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 99D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	8.90E-83	
3050	cg43970708	258	TCAGCTCACTGC AGCCTCCACCTC C/C/TGGGTTCAA GCGATTCTCCTG CCTCA	C	T				SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P23275 OLFACTORY RECEPTOR 15 (OR3) - MUS MUSCULUS (MOUSE), 312 aa.	2.40E-82	
3051	cg43970708	282	CTCACTGCAGCC TCCACCTCCCGG G/T/CJCAAGCGA TTCTCCTGCCTC AGCCT	T	C				SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P23275 OLFACTORY RECEPTOR 15 (OR3) - MUS MUSCULUS (MOUSE), 312 aa.	2.40E-82	
3052	cg43970708	277	ACCTCCCGGTT CAAGCGATTCTC C/T/CJGCCTCAG CCTCCCAAGTAG CTGGGA	T	C				SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P23275 OLFACTORY RECEPTOR 15 (OR3) - MUS MUSCULUS (MOUSE), 312 aa.	2.40E-82	

3053	cg43970708	324	GGGACTACAGG CGCATGCCACCA TG[C/T]CTGGCTA ATTTTGTATTT TAGTA	C	T			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P23275 OLFACTORY RECEPTOR 15 (OR3) - MUS MUSCULUS (MOUSE), 312 aa.	2.40E-82	
3054	cg43089531	408	TTTAAAGCTTT GATTAGAAGCCA A[C/T]TTGATTTA GGAGTCCCACCT GGCAA	C	T			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	1.20E-78	3
3055	cg43089531	435	TGATTAGGAGT TCCCACTGGCAA A[A/T]TAGGGAAC AATATGAGCATC AAGGA	A	T			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	1.20E-78	3
3056	cg43089531	803	AGCATTTTCACG TTTGACATGATA G[T/C]AACTCAAA CTAACTCTTTAC CACAT	T	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	1.20E-78	3
3057	cg21411454	1822	AATGTGCTCTCC TAGGCCACACAGG G[C/gap]TTTGG CAGGTGCAGCC CCCACCTGCC	C	gap			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3058	cg21411454	466	CAGCTTTCAAAA AGAGTGCTGCC A[G/T]AAAAAGCC TTCCACCCCTCCT GTCTG	G	T			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3059	cg21411454	492	AAAAAGCCTTCC ACCCTCCTGTCT G[G/gap]CTTTAG AAGGACCCCTGAG CCCCAGG	G	gap			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2

3060	cg21411454	523	GAAGGACCCTGA GCCCCAGGCGC CA[G/gap]CCACA GGACTCTGCTGC AGAGGGGG	G	gap			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3061	cg21411454	563	GCAGAGGGGG TTGTGTACAGAT AG[gap/G]TAGGG CTTTACGCCTAG CTTCGAAA	gap	G			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3062	cg21411454	568	AGGGGGTTGT GTACAGATAGTA GG[G/gap]CTTTA CGCCTAGCTTCG AAATGGAT	G	gap			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3063	cg21411454	574	TTGTGTACAGAT AGTAGGGCTTTA C[gap/C]GCCTAG CTTCGAAATGGA TAACGTC	gap	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
3064	cg43040271	2038	CGTTTAAGAAGA TCATTAAAGTGA A[G/C]TTCTGCCG CCAGTGATGACG GAGGA	G	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa. [pcis: SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.80E-74	
3065	cg40359282	1381	TTTAAAGTGCAC AAGTTGACTTGC C[G/A]TTTGCAGT GGGGTCGCCTA AGCGAC	G	A			SILENT- NONCODI NG	tm7	Human Gene Similar to SPTREMBL- ID:Q93127 G PROTEIN-COUPLED RECEPTOR - BALANUS AMPHITRITE, 379 aa.	2.10E-67	

3066	cg43040273	2989	TTTCTACTTTTAA AGACCCCCCCC C[G/C]CCCAACA GAACACTAAACA GACTAT	G	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
3067	cg43040273	3473	GCTTCAGTTGTT TTCCCGAGCAAA G[gap/G]TCTAAA GTTACAGTAAA TAAATTG	gap	G			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
3068	cg41554459	1566	ATGATGAATGAG ATGTAATGTGC C/A/CJAGAATATA TTATATAAAGAAT TTTA	A	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT- ID:P53453 D(2)-LIKE DOPAMINE RECEPTOR - FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES), 463 aa.	9.10E-50	2
3069	cg43028527	2928	AAAATACAGCTG GATTGGGTATG A[G/A]TATTACG TTTTTGTAATTA ATCT	G	A			SILENT- NONCODI NG	tnf	Human Gene SPTREMBL-ID:P78536 TNF-ALPHA CONVERTING ENZYME - HOMO SAPIENS (HUMAN), 824 aa.	0.00E+00	2
3070	cg43028527	3214	AAATATATATCTA AATTTAGAAATC[A/G]TTTGGGTTA ATATGGCTCTTC ATAA	A	G			SILENT- NONCODI NG	tnf	Human Gene SPTREMBL-ID:P78536 TNF-ALPHA CONVERTING ENZYME - HOMO SAPIENS (HUMAN), 824 aa.	0.00E+00	2
3071	cg43336100	1661	GGTATGTACCTT ATTACAAAAAAA ATT[gap]GATGAA AACATATTTATAC TACAAG	T	gap			SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG- 14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	3 (3q25)
3072	cg43336100	35	AATTCGCGCTCA AACTCAGCTCAC TTT[gap]GAGAGT CTCCTCCCGCCA GCTGTGG	T	gap			SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG- 14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	3 (3q25)

3073	cg43336100	45	CAAACCTCAGCTC ACTTGAGAGTCT C[C/gap]TCCCGC CAGCTGTGGAAA GAACCTT	C	gap			SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG- 14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	3 (3q25)
3074	cg44131329	1022	CCTGTGTTCTCT CCAAAGAGCAGA A[A/gap]GTGGT ACTATACGTGGC TACGTTG	A	gap			SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:Q13829 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN) - HOMO SAPIENS (HUMAN), 316 aa.	2.90E-166	17
3075	cg44131329	2372	GACCCAGGCAG CAGCAGCATGG GGT[T/gap]GGCC AATGGGGCGGG TTCCACACGGA	T	gap			SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:Q13829 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN) - HOMO SAPIENS (HUMAN), 316 aa.	2.90E-166	17
3076	cg43303573	272	TACATATATACAT ATACCACAAATA G/CJAAAAATGAC TGAAAGAAAAA ATAT	G	C			SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:P98066 TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-6 PRECURSOR (HYALURONATE- BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 277 aa.	8.90E-156	
3077	cg43303573	515	GTTTGGATCATC CTTTTCTTTTTT T/gap]TATAAGTG GCTAAATCTTCC AGCTA	T	gap			SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:P98066 TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-6 PRECURSOR (HYALURONATE- BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 277 aa.	8.90E-156	
3078	cg43303573	516	TTTGGATCATCCT TTTTTTTTTTTT gap]ATAAGTGGC TAAATCTTCCAG CTAA	T	gap			SILENT- NONCODI NG	tnf	Human Gene SWISSPROT-ID:P98066 TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-6 PRECURSOR (HYALURONATE- BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 277 aa.	8.90E-156	

3079	cg43965652	1131	TTTTTAAAAAAA GAAATTCTGTTCT A/GJAAAGTATTT CAGACCAAAAAGG AGGT	A	G			SILENT- NONCODI NG	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
3080	cg43965652	56	ATTAAACTTGA AAGCTATGGCTT GIC/gapJGCCAT CAATGACGCCTA TTGGGT	C	gap			SILENT- NONCODI NG	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
3081	cg43965652	57	TTAAACTTTGAA AGCTATGGCTTG CIC/gapJGCCATC AATGACGCCTAT JGGGTT	C	gap			SILENT- NONCODI NG	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
3082	cg43965652	677	GTCTCTGAAAC TAAATCAGACT TTT/CJAGATTCT CTGAAACAGTTC TGGT	T	C			SILENT- NONCODI NG	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
3083	cg43962131	136	AGAGCGGCGT GGGACCAGACC CTC/gap/TJCCAC AGCCAGCCTGG CCAAGGTGGC	gap	T			SILENT- NONCODI NG	tnfirecept or	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9
3084	cg43962131	210	AAGCACCAGG GGTCTAGGAATG CTC/gapJCCCCT TCTCTCCAGGGG CCAGAGGG	C	gap			SILENT- NONCODI NG	tnfirecept or	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9
3085	cg43962131	213	CACCCAGGGGT CTAGGAATGCTC CGC/gapJCTTCT CTCCAGGGGCC AGAGGGGAG	C	gap			SILENT- NONCODI NG	tnfirecept or	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9

3086	cg43982131	214	ACCCAGGGGTCT AGGAATGCTCCC C[gap]TCTCT CCAGGGGCCAG AGGGGAGA	C	gap				SILENT- NONCODING NG	Intrecept or	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9
3087	cg43982131	89	CACTTTACCCGC AGCTGTGCTGTG C[gap]CCTCCC ACACAGTGGTCT GAGCAGA	A	gap				SILENT- NONCODING NG	Intrecept or	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.20E-257	9
3088	cg43985041	1779	GGCCAAGAGCA GAGCAGCGAG TTG[G/] TT GAAAG CCTCTGCTGCCA TGGTGTC	G	T				SILENT- NONCODING NG	Intrecept or	Human Gene SWISSPROT-ID:P20333 TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) - HOMO SAPIENS (HUMAN), 461 aa. ID:P20333 TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B) - HOMO SAPIENS (HUMAN), 461 aa.	1.30E-255 (1p36.3)	1
3089	cg43984024	113	TAGGTCCCATTC TTTTATTGTCAT [G/AT]GGTTACAA TATAAATACACTT GCC	G	A				SILENT- NONCODING NG	Intrecept or	Human Gene SWISSPROT-ID:P36941 LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR) - HOMO SAPIENS (HUMAN), 435 aa.	2.40E-242	12
3090	cg43335558	1178	AGACTCTGAGAC AGTGCCTCGACA A[G/C]TTTGCAAA CATGGTGCCCTT TGACT	G	C				SILENT- NONCODING NG	Intrecept or	Human Gene Similar to TREMBLNEW- ID:G2653845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	5.50E-89	8

3091	cg43335558	1183	GAGACAGTGCTT CGACAAGTTTGC ATA/GACATGGTG CCCTTTGACTCC TGGGA	A	G				SILENT- NONCODI NG	tnfrecept or	Human Gene Similar to TREMBLNEW- ID:G2653845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	5.50E-89	8
3092	cg43335558	1186	ACAGTGCTTCGA CAAGTTTGCAAA CIA/TJGGTGCCCC TTTGACTCCTGG GAGCA	A	T				SILENT- NONCODI NG	tnfrecept or	Human Gene Similar to TREMBLNEW- ID:G2653845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	5.50E-89	8
3093	cg43335562	1386	TCTGCCATGTCC TAAGTGTGATTC TTC/TJTTTCAGGAA GTGAGACCTTCC CTGGT	C	T				SILENT- NONCODI NG	tnfrecept or	Human Gene Similar to TREMBLNEW- ID:G2653845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	2.30E-55	8
3094	cg43335562	1397	CTAAGTGTGATT CTCTTCAGGAAG TIG/CJAGACCTTC CCTGGTTTACCT TTTT	G	C				SILENT- NONCODI NG	tnfrecept or	Human Gene Similar to TREMBLNEW- ID:G2653845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	2.30E-55	8
3095	cg43943896	372	AACAGCATGGAA GAGAACCAAGTTT CIG/CJTTGCAGCT ACCTGGGAAGAC GGTIG	G	C				SILENT- NONCODI NG	traffic	Human Gene SPTREMBL-ID:P97412 LYSOSOMAL TRAFFICKING REGULATOR - MUS MUSCULUS (MOUSE), 3788 aa.	0.00E+00 (1q42.1)	1
3096	cg43988937	73	TTTTTTTGAGTT ATTAAAAAAA A/gap]CAAAAAAC ACAACCAAAAGA ACTGA	A	gap				SILENT- NONCODI NG	traffic	Human Gene SPTREMBL-ID:Q99408 PUTATIVE NUCLEOLAR TRAFFICKING PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 1410 aa.	0.00E+00 5 (5q32)	5
3097	cg43994751	532	CAGATTTAGGTC CATAAAAAGAAAG G/gap/AJAAAAA ATTATTCTAGTTA TATAA	gap	A				SILENT- NONCODI NG	traffic	Human Gene Similar to SPTREMBL- ID:008547 VESICLE TRAFFICKING PROTEIN SEC22B - MUS MUSCULUS (MOUSE), 215 aa.	1.70E-88	

3098	cg43934751	1050	GGCTGCCTGATC CAGGTGCACAG GC[<i>gap</i>]TCCGG TCACGGTTAAAG CCAAGCTG	C	<i>gap</i>			SILENT- NONCODI NG	traffic	Human Gene Similar to SWISSPROT- ID:Q02792 RIBONUCLEIC ACID TRAFFICKING PROTEIN 1 (5'-3' EXORIBONUCLEASE) (EC 3.1.11.-) (P116) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1006 aa.	6.50E-55	
3099	cg43934751	709	CTCCCTCCACGA TCATCTCGTCTG G[<i>gap</i>]TGGATA CCCACCAAGGCC CAGCTAGC	G	<i>gap</i>			SILENT- NONCODI NG	traffic	Human Gene Similar to SWISSPROT- ID:Q02792 RIBONUCLEIC ACID TRAFFICKING PROTEIN 1 (5'-3' EXORIBONUCLEASE) (EC 3.1.11.-) (P116) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1006 aa.	6.50E-55	
3100	cg43995002	124	TTCAATGGAACA TCCCCGCTTTAG C[<i>gap</i>]CAGTGT TGAATCTAACAC CGAAAAA	G	<i>gap</i>			SILENT- NONCODI NG	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3101	cg43995002	575	AAAACCCACGC TTTAAACAACAT [AC]TTTGGGGT GGCTATGGCACC TTGA	A	C			SILENT- NONCODI NG	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3102	cg43995002	77	TTTTTTTTTTT TTTTTTTTTTTTT A/GAAACACACA CTGCTCTTTATT CA	T	A			SILENT- NONCODI NG	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3103	cg43995002	79	TTTTTTTTTTT TTTTTTTTTTT TTAAACACACT GCTCTTTATTCA AT	A	T			SILENT- NONCODI NG	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3104	cg43995002	80	TTTTTTTTTTT TTTTTTTTTTT TTAAACACACTG CTCTTTATTCAA TG	A	T			SILENT- NONCODI NG	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11

3105	cg43995002	791	AGATAAAGAAAGT AACAAAGGAAAA A[G/A]AAAAAAT TAATAAAAAATTC ACGA	G	A			SILENT- NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q15913 TRANSCRIPTION FACTOR ZFM1 - HOMO SAPIENS (HUMAN), 571 aa.	0.00E+00	11
3106	cg43948839	329	GGTGCCTGCAG AGCAAGGAGGG GGG[C/gap]CCCC CAAAATGGCTCG GCCCTGCA	C	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa. Jc1:SWISSPROT-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.	0.00E+00	17
3107	cg43949599	376	CACCCACCTTG GATTGGCCGC AG[G/gap]TGTGG AGGCCCTCATCA AACTCTTT	G	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P17480 NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-90) - HOMO SAPIENS (HUMAN), 764 aa.	0.00E+00	17
3108	cg44027791	185	ATACCTCAAGCA GTTACAACATAA A[A/T]TAAAGTTG GATTTTGTTTAA TTTA	A	T			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17
3109	cg44027791	572	ACAGTGTTTCATC ATCTGAAGTAGA G[gap]GTATAA GGCAACGTTCTC CATAGAA	A	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17
3110	cg44027791	60	GTTATTTTGAAG ATTTTGCCTCAG G[gap]CJAACATA ATTATTAGCAA GAAAAA	gap	C			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17

3111	cg43328754	22	GGAATTCCTTT TTTTTTTTT/GJT GGCTCAAAAAC CATCTTTATTGG	T	G			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01201 TRANSCRIPTION FACTOR RELB (- REL) - HOMO SAPIENS (HUMAN), 579 aa.	0.00E+00	19
3112	cg4333098	417	CAGCCTGAGGAT GAGGCACAGGG AG[gap]CAGGG CCCATCACTCAG GAGGCCAT	G	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa. pcis:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22
3113	cg4333098	425	GGATGAGGCAC AGGGAGGCAGG GCC[C/gap]ATCA CTCAGGAGGCC ATGGGAGAAA	C	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa. pcis:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22

3114	cg43933098	458	AGGAGGCCATG GGAGAAACAGTC TC[C/T]GGGAGG TGCTGCACCTGG GGACCCA	C	T			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.lpcis:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22
3115	cg43933098	57	TTTTTTTTTTTT TTTTTTTTTTTTT[//] GTTGGGTGGTA CCAATCTGTGT TAT	T	G			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.lpcis:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22
3116	cg43933098	58	TTTTTTTTTTTT TTTTTTTTTTTTT[//] CTGGGTGGTAC CAATCTGTGTT ATT	T	C			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.lpcis:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22

3117	cg43933098	582	CCCTCTGCCAC TCTGAAAAGAGG G[G/gap]CTTGCC GCTGGGAGGG ATTAGGGG	G	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.lpcis:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22
3118	cg43933098	704	CCTCAACTTACC ATGGGGTTACTT C[C/T]TGATAAAC CCATCATAAATG AAAT	C	T			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.lpcis:SWISSPROT-ID:Q12772 STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 2) HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	22
3119	cg43934374	5008	AGTGAACATATG CCACTGCCTGGC C[T/C]TTTTTCTT CAGAGCTTGTTG TCCT	T	C			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:Q99081 TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX- BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.lpcis:SWISSPROT-ID:Q99081 TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX- BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.	0.00E+00 (15q21)	15

3120	cg43921342	2083	GGTTTGTGTTTAC TGGAATAAAAAA A[A/gap]ATGCTC CTGTACGCCAG GCAACAG	A	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.lpcis:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa	0.00E+00	
3121	cg43921342	2084	GTTTGTGTTTACT GGAAAAATAAAAA A[A/gap]TGCTCC TGTCAGCCCAGG CAACAGG	A	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.lpcis:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa	0.00E+00	
3122	cg43936136	1135	ATGCCAGTGTGA CTCTTAAACCT TTC/TCCATCTGG AGTCCTGTATTT TCTCT	C	T			SILENT- NONCODING	transcript factor	Human Gene SPTREMBL-ID:Q99840 TRANSCRIPTION FACTOR NFATX2 - HOMO SAPIENS (HUMAN), 1068 aa	0.00E+00	
3123	cg44028034	254	CAGAACACAGCC AGTTACGCAACA G[C/gap]GCAAGG CCTGCTCCAGGC CCCACCT	C	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P42230 SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 5A (MAMMARY GLAND FACTOR) - MUS MUSCULUS (MOUSE), 793 aa	0.00E+00	

3124	cg44130900	1668	TTAGTACACAGA AATTCTGCAGAT G[C/G]TATTGTAC ACATGTGACAAC CTATG	C	G				SILENT- NONCODI NG	transcript factor	Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment).	7.5e-310	2
3125	cg44130900	2140	TTGTATCCAGAA ATGTATACTCAT C[G/A]TATTTAA AGCTAAATTTATT TTTT	G	A				SILENT- NONCODI NG	transcript factor	Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment).	7.5e-310	2
3126	cg43968711	277	TTAGGAGAAACA TCTTTTATTCTTT C[G/T]AAAGAGGT GAAAATAAGATT TTTT	C	G				SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3127	cg43968711	286	ACATCTTTTATT CTTCTAAAGAGG T/GIGAAATAAG ATTTTTTAATAT TTC	T	G				SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3128	cg43968711	303	TAAAGAGGTGAA AATAAGATTTTT [T/gap]AATAATTC TCACTCATAAGA TTTT	T	gap				SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3129	cg43968711	351	TTTAAACTCTTAA AAATGCAATATC T/CITCTTTTCAAA GCACATGCCATC TTA	T	C				SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3130	cg43968711	467	AATTCTGCATTA AAAAACCCTATG C[G/A]ACTTTCTG CAATATATTCC GTCTT	G	A				SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11

3131	cg43968711	473	GCATTAAAAAAC CCTATGCGACTT TTC/TGTGCAATA TATCCCTCTTTA TTAT	C	T				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.3E-292	11
3132	cg43968711	486	CTATGCGACTTT CTGCAAAATATAT TTC/GCCTCTTTA TTATTCAGGGAC TCCAA	C	G				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3133	cg43968711	557	TATTTATCGTTTC TTATTTCCGTAGI Ggap/AAACACAG AACCAATGATGT CTTCT	G	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3134	cg43968711	566	TTTCTTATTTCCG TAGGAAACACAG [AVG]ACCAATGAT GTCCTCTGACAA CTGT	A	G				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P32780 BASIC TRANSCRIPTION FACTOR 62 KD SUBUNIT (P62) - HOMO SAPIENS (HUMAN), 548 aa.	2.30E-292	11
3135	cg43947662	2433	GGCCCCCTCCCT CCCAGGTCTCGC TGT/gap]CTCTCTT TCCCCTCCAGGC CTCGCT	G	gap				SILENT- NONCODING	transcript factor	Human Gene TREMBLNEW-ID:G545525 LBP-1C=TRANSCRIPTION FACTOR ALPHA-GLOBIN CP2 HOMOLOG {ALTERNATIVELY SPLICED} - HOMO SAPIENS, 502 aa.	3.70E-276	12
3136	cg43947662	2462	TCITTCCTCCCTCC AGGCCTCGCTTC CTT/gap]GGTCAG TCCACGATCAG TTCCGGT	T	gap				SILENT- NONCODING	transcript factor	Human Gene TREMBLNEW-ID:G545525 LBP-1C=TRANSCRIPTION FACTOR ALPHA-GLOBIN CP2 HOMOLOG {ALTERNATIVELY SPLICED} - HOMO SAPIENS, 502 aa.	3.70E-276	12
3137	cg43011561	1783	AGGCTTGGTCCA ATACATGGCTCT GIC/gap]CCCCCA GAACCTAAGGCT CTCACTG	C	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P35269 TRANSCRIPTION INITIATION FACTOR IIF, ALPHA SUBUNIT (TFIIF-ALPHA) (TRANSCRIPTION INITIATION FACTOR RAP74) - HOMO SAPIENS (HUMAN), 517 aa.	4.30E-275 (19p13.3)	19

3138	cg44024015	1729	CCGGGATGGGC CGACCAACCCCT TA/G/CJACGCC AGCATTTCCCGA AGCCCCGA	G	C				SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:P23769 ENDOTHELIAL TRANSCRIPTION FACTOR GATA-2 - HOMO SAPIENS (HUMAN), 480 aa.	1.60E-250	3
3139	cg44024015	2456	TGTGTCCCTTT ACTGAGCGCACA G/C/gapJACAGC CTGTCTTGTCAG GTGGACC	C	gap				SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:P23769 ENDOTHELIAL TRANSCRIPTION FACTOR GATA-2 - HOMO SAPIENS (HUMAN), 480 aa.	1.60E-250	3
3140	cg44024015	2457	GTGTCCCTTTA CTGAGCGCACA GC/C/gapJACAGC CTGTCTTGTCAG GTGGACCC	C	gap				SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:P23769 ENDOTHELIAL TRANSCRIPTION FACTOR GATA-2 - HOMO SAPIENS (HUMAN), 480 aa.	1.60E-250	3
3141	cg43917801	175	ATACATTATTCA TGCCAGTCTGTT G/A/CATGCAGGC TTTTGGCTTCC TACC	G	A				SILENT- NONCODI NG	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa. Jcds:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249 (6p22.3)	6
3142	cg43917801	2344	AGAAAGAAAG TAAGCAGGGCTG G/C/gapJTCGCC CGCGTTCTCGTC GTCGGAT	C	gap				SILENT- NONCODI NG	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa. Jcds:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249 (6p22.3)	6
3143	cg43917801	3091	GGGAGCTGGCG GCGCGGCTGC TGG/G/gapJCCTC CGCCTTCCTTC TACGTGAAA	G	gap				SILENT- NONCODI NG	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa. Jcds:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249 (6p22.3)	6

3144	cg43917801	377	GGAATCAACTGC TTCAGGGAAAA G[A/gap]AAAAAA AAAAAAAAGA CTTGCCT	A	gap			SILENT- NONCODI NG	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.lpcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3145	cg43917801	393	GGGAAAAAGAAA AAAAAAAAAAAA A[A/gap]GACTTG CCTGGGAGGCC GCGAGAAA	A	gap			SILENT- NONCODI NG	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.lpcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3146	cg43917801	635	GGACTTTTCTCT CTTTACCCACCT C[C/gap]GCCCCCT GCGAGGAGTTG AGGGGCCA	C	gap			SILENT- NONCODI NG	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.lpcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3147	cg43917801	654	CACCTCCGCCCC TGCGAGGAGTTG A[G/gap]GGGCCA GTTGGGCCGCC GCGCGCGT	G	gap			SILENT- NONCODI NG	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.lpcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3148	cg43917801	657	CTCCGCCCTGCG GAGGAGTTGAG GG[G/gap]CCAGT TCGGCCGCCCGC GCGCGTCTT	G	gap			SILENT- NONCODI NG	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.lpcis:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.30E-249	6 (6p22.3)
3149	cg42906458	22	TTTTTTTTTTTT TTTTTTTTT[G]T AGCTATCATAAC TTTATTAAACA	T	G			SILENT- NONCODI NG	transcript factor	Human Gene SPTREMBL-ID:Q92759 TRANSCRIPTION FACTOR TFIH - HOMO SAPIENS (HUMAN), 462 aa.	4.20E-245	

3150	cg43920700	1897	GCCTTCCTCCCC CTGACCCCGCC CC[G/C]GCCTTCT GGGAAGGAAC AAAGTCC	G	C				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q14938 NUCLEAR FACTOR 1X (NFI-X) (NF-1X) (CCAAT-BOX BINDING TRANSCRIPTION FACTOR) (CTF) (TGGCA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 441 aa.	2.10E-243	19 (19p13.3)
3151	cg43918762	1031	AAGATCAGATAA ATAAAAAA A[A/gap]GGCTTA AACAGACTCAC CATATTT	A	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P05549 TRANSCRIPTION FACTOR AP-2 - HOMO SAPIENS (HUMAN), 437 aa.	2.70E-241	6 (6p12)
3152	cg43918762	1452	TTTGTGTTTTGT TTAAAAA gap[A]GGGTTTAC AACTTGGCAGA ACTTT	gap	A				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P05549 TRANSCRIPTION FACTOR AP-2 - HOMO SAPIENS (HUMAN), 437 aa.	2.70E-241	6 (6p12)
3153	cg43918762	699	GTGGAATAAAAT AACTTTTTTTTT T[gap]CTCCCTAC AATACATAGAAG GGTTA	T	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P05549 TRANSCRIPTION FACTOR AP-2 - HOMO SAPIENS (HUMAN), 437 aa.	2.70E-241	6 (6p12)
3154	cg43988635	277	TGCTGAGAAAGA GGAAGGAGTCTC CTTATGAGCTCC AGCATCAGGGG CAGAAA	T	A				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P43694 TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4) - HOMO SAPIENS (HUMAN), 442 aa.	1.60E-236	8 (8p23.1)
3155	cg43128605	1480	CTTGAGGGAC CAGGGTTCCAG AGATAGCTCAC CTGTCTCTGCA GCCCTG	A	T				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20

3156	cg43129605	1481	TTGGAGGGACCA GGGTTCCAGAG AATJGCTCACCT TGCTCTGCAGC CCTGG	A	T			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F-1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3157	cg43129605	1811	TCCACATGTGTG TGCATGAGTCCA TIG/CJTGTGCGC GTGGGGGGCT CTAACTG	G	C			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F-1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3158	cg43129605	1813	CACATGTGTGTG CATGAGTCCATG TIG/CJTGCGCGT GGGGGGGCTCT AACTGCA	G	C			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F-1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3159	cg43129605	1857	AACAGCATTTC GGCCCTTTTGCT CTT/GJGGGGTC CCACAAGGCCCA GGGCAG	T	G			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F-1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20

3160	cg43129805	1858	ACTGCACCTTCG GCCCTTTTGCTC TGTGGGGTCC CACAAAGGCCCA GGGCAGT	G	T				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20
3161	cg43129805	2054	TGGTGAGCCTG GGGAATCAGCAA A[gap/A]GGGGAG GAGGGGTGTGG GGTTGATA	gap	A				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3162	cg43129805	2265	TCTCCAGGGGG CCAGTTCAGGGC CC[C/gap]AGCTG CCCCCAGGAT GGATATGAG	C	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
3163	cg43921348	341	GCCCACCCAGA CCTAGGGGCAG GGC[C/gap]AGGA GCAAAACAAGAG GGAGAGGCA	C	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.[pcls:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa	3.80E-228	

3164	cg43984259	363	CCTGCAGGTTCT AGGGCTAAAGG CC[C/gap]AGCAG AAGTGGGCACGT GAGAGGGC	C	gap			SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:Q16254 TRANSCRIPTION FACTOR E2F4 (E2F-4) - HOMO SAPIENS (HUMAN), 413 aa.	5.50E-211	16 (16q22.1)
3165	cg43984259	457	GCTAGAAAGTGGT GCTGGCATGTGC C[C/gap]AGTTCC ACCCACCCCTTC CCTCCTA	C	gap			SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:Q16254 TRANSCRIPTION FACTOR E2F4 (E2F-4) - HOMO SAPIENS (HUMAN), 413 aa.	5.50E-211	16 (16q22.1)
3166	cg42345420	223	CTTACCTATAA TGCAACTAATCA T[G/C]TACTTAGT TGCTATGTTAAT CTATT	G	C			SILENT- NONCODI NG	transcript factor	Human Gene SPTREMBL-ID:Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR - HOMO SAPIENS (HUMAN), 399 aa.	1.50E-210	
3167	cg42479822	235	GTAATATTTTACC AAAAAAAAAAAAA gap/A]GAAAAAGT GAACAGTCTGCC AGTGT	gap	A			SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:Q06547 GA BINDING PROTEIN BETA-1 CHAIN (GABP-BETA-1 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-53) (GABPB1) (NUCLEAR RESPIRATORY FACTOR-2 SUBUNIT BETA 2) - HOMO SAPIENS (HUMAN), 383 aa.	2.00E-197	15
3168	cg42479822	433	AAAGCAATTTT TCCGTAAGAATC A/GTTTCCTGGG GAGAAATAAGTC CATA	A	G			SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:Q06547 GA BINDING PROTEIN BETA-1 CHAIN (GABP-BETA-1 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-53) (GABPB1) (NUCLEAR RESPIRATORY FACTOR-2 SUBUNIT BETA 2) - HOMO SAPIENS (HUMAN), 383 aa.	2.00E-197	15
3169	cg21846034	93	TGTGTGTAGCGG GGCCGCGTCAG CC[C/gap]GGCCG GGTACGAGGCG CCTCGGGTC	C	gap			SILENT- NONCODI NG	transcript factor	Human Gene SWISSPROT-ID:Q06545 GA BINDING PROTEIN BETA-2 CHAIN (GABP-BETA-2 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-47) (GABPB2) - HOMO SAPIENS (HUMAN), 347 aa.	9.00E-179	15

3170	cg21846034	97	TGTAGCGGGC CGCGTCAGCC GGC[C]gap]GGGT ACGAGGCGCCT CGGGTCCCCG	C	gap			SILENT- NONCODING NG	transcript factor	Human Gene SWISSPROT-ID:Q06545 GA BINDING PROTEIN BETA-2 CHAIN (GABP-BETA-2 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-47) (GAPBP2) - HOMO SAPIENS (HUMAN), 347 aa.	9.00E-179	15
3171	cg43988870	1481	CCACAGACTGAG CTGGCCAGAG GG[G]gap]TGGA CTGCTGATGGA TTCCCTC	G	gap			SILENT- NONCODING NG	transcript factor	Human Gene SPTREMBL-ID:Q07279 TRANSCRIPTION FACTOR NF-E2 - MUS MUSCULUS (MOUSE), 373 aa.	1.70E-177	12
3172	cg43947199	1485	AATATGTTTGAA ACAGGTACCAT C/AJAATTATTATA TGGTCTCCCTAC TGA	C	A			SILENT- NONCODING NG	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa. cds:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8
3173	cg43947199	236	AAACATTATTCA AAAATGTACTTT G/C]TTTTTGAAT AAACAAAATCT TCA	G	C			SILENT- NONCODING NG	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa. cds:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8

3174	cg43947199	299	CAAAATAGAGGT GAGTTGGTACCA GT/CJGGGCCAA TTCTTAACACGG ACATTT	T	C			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.lpcis:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8
3175	cg43947199	423	CAAAGCATGTAC TGAGGTCCTTCT A/C/TJGGGTGCC TGACAGAATGCA GATTCA	C	T			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.lpcis:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8
3176	cg43947199	550	ACAATTTTGTCT TACTCCAAACAG A/gapJAAAAAATG GTACACACTTTA ACAAA	A	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.lpcis:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8

3177	cg43947199	556	TTTGCTTACTC CAACAGAAAA A[<i>gap</i>]TGGTAC ACACTTTAACA AAGCAA	A	gap			SILENT- NONCODING	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa. [<i>pcds</i> :SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8
3178	cg43948504	483	GAGTTTGGTAAT TTGCACCTGTTTT [<i>gap</i>]TGTAACT GAACTGCTCCTC TCCICA	gap	T			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P29084 TRANSCRIPTION INITIATION FACTOR IIE, BETA SUBUNIT (TFIIE-BETA) - HOMO SAPIENS (HUMAN), 291 aa.	9.50E-152	8 (8p21)
3179	cg43948504	515	GAACTGCTCCTC TCCTCAGCCGCA A[<i>gap</i>]A[GAAGCA GATAGGAAGACA GTCTTCA	gap	A			SILENT- NONCODING	transcript factor	Human Gene SWISSPROT-ID:P29084 TRANSCRIPTION INITIATION FACTOR IIE, BETA SUBUNIT (TFIIE-BETA) - HOMO SAPIENS (HUMAN), 291 aa.	9.50E-152	8 (8p21)
3180	cg43992817	137	TGGAAGAATCAG TTCGAAGACATA ATT[<i>A</i>]AGCCTTTA CTTTTCTTTTA TTAT	T	A			SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q14469 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY- LIKE) (HHL) (HAIRY HOMOLOG) - HOMO SAPIENS (HUMAN), 280 aa.	1.50E-144	3
3181	cg43992817	499	GGGTTGGGGAG TTTAGGAGGAGG GGT[C]GGCCTG AGCCCCCTCAGT TCCGCCA	T	C			SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q14469 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY- LIKE) (HHL) (HAIRY HOMOLOG) - HOMO SAPIENS (HUMAN), 280 aa.	1.50E-144	3

3182	cg43992817	508	AGTTAGGAGGA GGGTGGCCTG AG[C/gap]CCCCCT CAGTCCGCCAC GGCCTCCA	C	gap		SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q14469 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY-LIKE) (HHL) (HAIRY HOMOLOG) - HOMO SAPIENS (HUMAN), 280 aa.	1.50E-144	3
3183	cg43935832	3340	AACTGGTGCAT ACTGGCATTGGC C[C/gap]TTGGTG GGGAGCACAGA CACAGGAT	C	gap		SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:P42224 SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA (TRANSCRIPTION FACTOR ISGF-3 COMPONENTS P91/P84) - HOMO SAPIENS (HUMAN), 750 aa. pcis:SWISSPROT-ID:P42224 SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1- ALPHA/BETA (TRANSCRIPTION FACTOR ISGF-3 COMPONENTS P91/P84) - HOMO SAPIENS (HUMAN), 750 aa. pcis:TREMBLNEW-ID:G2281071 TRANSCRIPTION FACTOR ISGF-3 - HOMO SAPIENS (HUMAN), 750 aa.	3.20E-144	
3184	cg43299377	1472	TGGTACAAAGAA TAGATGCAGGCA G[C/T]CATAGGTA CAAGGGATTCCC TTAAT	C	T		SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL- SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138 (5q31.1)	5
3185	cg43299377	1635	TGAGATGACGTT AACAGGACCCCT G[G/gap]CCAGTT TCCATGAGATCT GGGTCTC	G	gap		SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL- SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138 (5q31.1)	5

3186	cg43289377	1666	TTCCATGAGATC TGGGCTCTGTC A/C/T/T/TTCAGGG GGTAGGCTCCTG GAGGC	C	T			SILENT- NONCODING NG	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL- SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138	5 (5q31.1)
3187	cg43289377	1840	GAGAGACCTGG GGATGTAGGTGC CG[G/gap]CTCCG CAGGGCTAGTAA GCAGTTCT	G	gap			SILENT- NONCODING NG	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL- SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138	5 (5q31.1)
3188	cg43289377	524	CAAAGTGCTGGG ATTACAGGCGTG A[G/gap]CCACCG CGCCTGGCCCCG GCAGCCCT	G	gap			SILENT- NONCODING NG	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00417 T-CELL- SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7) - MUS MUSCULUS (MOUSE), 303 aa.	1.70E-138	5 (5q31.1)
3189	cg43283688	1091	GAGTTTATAAAT TAAAGGTCAAAT A/C]CTGAAGCTT TTTATTAGGCTT TTC	A	C			SILENT- NONCODING NG	transcript factor	Human Gene Homologous to SWISSPROT-ID:P18846 CYCLIC-AMP- DEPENDENT TRANSCRIPTION FACTOR ATF-1 (TREB36 PROTEIN) - HOMO SAPIENS (HUMAN), 271 aa.	1.90E-137	12
3180	cg43283688	1092	AGTTTATAAAT AAAAGGTCAAAT C/ATGAAGCTT TTATTAGGCTT TCC	C	A			SILENT- NONCODING NG	transcript factor	Human Gene Homologous to SWISSPROT-ID:P18846 CYCLIC-AMP- DEPENDENT TRANSCRIPTION FACTOR ATF-1 (TREB36 PROTEIN) - HOMO SAPIENS (HUMAN), 271 aa.	1.90E-137	12
3181	cg44012692	2080	CTCTTGACACCTG AGAGTGGGAGTT TTC/TGTAGGAAC ACAGGAAGGAG ACCAAC	C	T			SILENT- NONCODING NG	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13886 TRANSCRIPTION FACTOR BTEB1 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 1) (GC BOX BINDING PROTEIN 1) - HOMO SAPIENS (HUMAN), 244 aa.	6.70E-135	9

3192	cg44012692	4499	ATCACCCCGACG CGGGTGGCGAG GGTTC CCCCGCC GAGCGCCAGGT CTAAGAGA	C			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13886 TRANSCRIPTION FACTOR BTEB1 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 1) (GC BOX BINDING PROTEIN 1) - HOMO SAPIENS (HUMAN), 244 aa.	6.70E-135	9
3193	cg44012692	4581	AACCCCTGCTCC GGCCGGTCCGC AC C gap GTTCC GGCATTCTCTTG CTCAGTAA	gap			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13886 TRANSCRIPTION FACTOR BTEB1 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 1) (GC BOX BINDING PROTEIN 1) - HOMO SAPIENS (HUMAN), 244 aa.	6.70E-135	9
3194	cg43982109	1896	AGTGACCCGACCG CCAATCTCGGAG A G gap CCTCCT GGCAATACACAA CTCCAGC	gap			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00059 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (MTTF1) - HOMO SAPIENS (HUMAN), 246 aa.	5.60E-131	10 (7p)
3195	cg43310921	98	TGTTCCCTTCAAA TTAAAAA [gap A TACAAAA GCTACGTAGAAA ACGTCA	gap	A		SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SPTREMBL-ID:O00112 LIVER- SPECIFIC BHLH-ZIP TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 429 aa (fragment).	7.20E-124	19
3196	cg43263063	174	GCGCAGGCCCC GCAGCCGGGCC AGC G C GCGCG CCCCCGGCCCGC GGCTGCCTC	C			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13887 TRANSCRIPTION FACTOR BTEB2 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 2) (GC BOX BINDING PROTEIN 2) - HOMO SAPIENS (HUMAN), 219 aa.	3.50E-122	
3197	cg43263063	491	CACCAGAGTGAA ACGACTGCCCCCT C C gap TCCGGC CCCGACCCAGG CCCTCCCT	gap			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q13887 TRANSCRIPTION FACTOR BTEB2 (BASIC TRANSCRIPTION ELEMENT BINDING PROTEIN 2) (GC BOX BINDING PROTEIN 2) - HOMO SAPIENS (HUMAN), 219 aa.	3.50E-122	

3198	cg43918209	934	CGATGGCTCCCC GGGACAGAGT CC[C/gap]TCTCC GGGCTCTCAG CAGCCCCGGG	C	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3199	cg43918209	105	TCTAACAAACG CCAGGTAGACG GA[G/gap]TTAA AAGAATCCACCG CACGAAAG	G	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3200	cg43918209	1841	CAGGTGCACTCC GGACAACGGC TC[G/T]CTCACGC CTCTCTACACAA ACCAAC	G	T			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3201	cg43918209	346	CGCTGGAACCTG GGAACCTACTGG G[C/G]ACCTCTAA TGCAGATGAGAA AAACT	C	G			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3202	cg43918209	490	GCCACTCTCCTC CCCCTGCCCCAG G[G/gap]CGGGTG CAGCCCCCAGG ACCTCCTC	G	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3203	cg43918209	511	AGGCGGGTGC ACGCCCCAGGA CCT[gap/T]CCTC CCAGGCCCCAC ACCCACGCAA	gap	T			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3204	cg43918209	517	GGTGCACGCC CCAGGACCTCCT CC[C/gap]AGGCC CCACACCCACGC AAGGCGAC	C	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19

3205	cg43918209	524	CGCCCCAGGAC CTCTCCAGGC CC[C/gap]ACACC CACGCAAGGCG ACAGGAAGC	C	gap			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3206	cg43918209	532	GACCTCCTCCCA GGCCCCACACC CA[C/G]GCAAGG CGACAGGAAGCT CCCCACG	C	G			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3207	cg43918209	533	ACCTCCTCCAG GCCCCACACCCA C[G/C]CAAGGCG ACAGGAAGCTCC CCACGC	G	C			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3208	cg43918209	869	GTCCTCGGGAA GGCGCCCGCGC CC[C/gap]CGGCT CAGACTCCTCGG TGCCGTCC	C	gap			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3209	cg43918209	870	TCTCTGCGGAAG GGCGCCCGCGC CC[C/gap]GGCTC AGACTCCTCGGT GCCGTCCC	C	gap			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
3210	cg43918942	203	CATGGGGAGGA TGAGGCCCCCTG GGG[G/gap]TCAG TGAGGCACGGC TCTGCCTCAA	G	gap			SILENT- NONCODI NG	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14

3211	cg43918942	290	TCGGCCACATCC GGGGCAGCCAT GC[C/gap]AGAGC TGAGACCTCCTA CGAGTGGT	C	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
3212	cg43918942	476	GCCAGGACACTA TGCAGGCTATGC C[C/gap]GCACGT CCTACAGAGCTA TGCTCAG	C	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
3213	cg43918942	544	CTCAGCTGTCGG GCACTCAGTTCA C[C/gap]TGCCGG CAGCCGCAGGC GCTCCTGG	C	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
3214	cg43918942	93	AAGCCCTCGAGA AGCCCTGGCAG GA[C/C]CCAGGC TGGCTACTGAGC TCTGGGC	A	C			SILENT- NONCODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
3215	cg43983354	1336	CCACCCCGCCC CCAGTGCTGGG GCG[G/gap]CCCC GGCTCCGGCCCC CTGGGGGAGC	G	gap			SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa. [pcis:SWISSPROT-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.60E-103 (19q13.2)	19

3216	cg43993354	1377	CTGGGGGAGCG CCAGCGGGTGG TGA[T/C]CAGAGC AGGGCCACAC CCCGGCAG	T	C				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa. pcis:SWISSPROT-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.60E-103	19 (19q13.2)
3217	cg43993354	1508	GGTGATTGGATC TGGCCAGAAAG GC[gap/C]AGCCA TGCCGAGGTCC CAGGGGACG	gap	C				SILENT- NONCODING	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa. pcis:SWISSPROT-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.60E-103	19 (19q13.2)
3218	cg43995484	3358	TGGAAGAAAGAA GCATTGAAACA A[A/C]GACATTCT TCCCACTTCTTG GATTT	A	C				SILENT- NONCODING	transcript factor	Human Gene Similar to SWISSPROT- ID:Q62318 TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN) (KRIP-1) - MUS MUSCULUS (MOUSE), 834 aa.	1.80E-96	
3219	cg42930883	1095	GGAAGGAGACA CATTACAAAAGA AA[C/A]GTTGCGA AAATTGCGAAAT CTGTTG	C	A				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q91151 MYOGENIC REGULATORY FACTOR, TRANSCRIPTION FACTOR - NOTOPHTHALMUS VIRIDESCENS (EASTERN NEWT) (TRITURUS VIRIDESCENS), 219 aa (fragment).	2.30E-95	12 (12q21)
3220	cg42930883	1125	CGAAAATTGCGA AATCTGTTGTGC A[T/C]GCTCAAAT GAAAACGCCTTT CGGCT	T	C				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q91151 MYOGENIC REGULATORY FACTOR, TRANSCRIPTION FACTOR - NOTOPHTHALMUS VIRIDESCENS (EASTERN NEWT) (TRITURUS VIRIDESCENS), 219 aa (fragment).	2.30E-95	12 (12q21)

3221	cg42930883	1348	TTAATGTATTTT GTAAATAGTTTA AGTCACCTTCTTT TTTTACGTAAAC CTG	A	G			SILENT- NONCODI NG	transcript factor	Human Gene Similar to SP TREMBL- ID:Q91151 MYOGENIC REGULATORY FACTOR, TRANSCRIPTION FACTOR - NOTOPHTHALMUS VIRIDESCENS (EASTERN NEWT) (TRITURUS VIRIDESCENS), 219 aa (fragment).	2.30E-95	12 (12q21)
3222	cg43051067	1933	TGTCGTACTTT ACAATCAACTA C/ATTTGTTCTAC CCAGCATTTAAC GGCAA	A	T			SILENT- NONCODI NG	transcript factor	Human Gene Similar to SWISSNEW- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.pclis:SWISSPROT- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.30E-91	
3223	cg43297584	222	ACTTGGGACAAG TTGCCGGAGCC GC[G/gap]GGGC GCGGCGGCGG ACAGATTGAC	G	gap			SILENT- NONCODI NG	transcript factor	Human Gene Similar to TREMBLNEW- ID:E1172965 TRANSCRIPTION FACTOR TFE3 - HOMO SAPIENS (HUMAN), 575 aa.	2.60E-90	
3224	cg43917302	1743	CATTACGGCGA AGCCGCCACGC GG[C/gap]CCCCG ACGCCGCCCTTG CGGCCAG	C	gap			SILENT- NONCODI NG	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.pclis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.90E-68	7
3225	cg43917302	1802	GCTCCCCCGA GGTGGCGCCGC CCC[C/gap]GCTC TTCTTCTGAGCC TAGTTCTCA	C	gap			SILENT- NONCODI NG	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.pclis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.90E-68	7

3226	cg43917302	1949	GCCGCGGGGACA CCTGTTTCCTTC CC[G/gap]CAGTG TCTGCGTCCGCA CAGCATAC	G	gap			SILENT- NONCODI NG	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.pcds:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.90E-68	7
3227	cg43917396	497	GACTTGCCAGAC GAGGCTCTATTG C[G/gap]GGCTGC TGCAGCCCACTT TTCTCCT	G	gap			SILENT- NONCODI NG	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
3228	cg43917396	660	TCCCGGCCCTGG GGAGAGGGCTC GCT[G/gap]GCTC TCCAGCCCACTC ACCACTCTC	G	gap			SILENT- NONCODI NG	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
3229	cg43917396	677	GCTCGCTGGCTC TCCAGCCCACTC A[gap]C[CCAGTC TCTGGATGCTCT GCAGTTC	gap C	C			SILENT- NONCODI NG	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
3230	cg43917396	679	CTCGCTGGCTCT CCAGCCCACTCA C[C/gap]AGTCTC TGGATGCTCTGC AGTTCAT	C	gap			SILENT- NONCODI NG	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
3231	cg43917396	76	CCCTGGGGAC TCAAGGCAGAAG TG[C/gap]CACTC CCTCCGTTGACC ACGGCTGG	C	gap			SILENT- NONCODI NG	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	

3232	cg42702130	675	GAGGGGCACAC AGACTGTGGCAG AGC/gapJTGCGC CCATCCCGCAGA GGCCCCCTG	C	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16520 TRANSCRIPTIONAL FACTOR - HOMO SAPIENS (HUMAN), 125 aa.	1.30E-62	14
3233	cg42702130	706	CCATCCCGCAGA GGCCCCGTGCCA C/C/ATGGAGAC CCGGAGACAGA GGCCTGG	C	A				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16520 TRANSCRIPTIONAL FACTOR - HOMO SAPIENS (HUMAN), 125 aa.	1.30E-62	14
3234	cg42702130	899	AGTCCCATGGCA CAGAGCAAGGC GGG/gapJGAGGG AACGGTTATTTT CTAAATA	G	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16520 TRANSCRIPTIONAL FACTOR - HOMO SAPIENS (HUMAN), 125 aa.	1.30E-62	14
3235	cg43317047	1488	GAAGCTACTGTT TTCTCTTTGTTC [A/G]TTTTACCTC TTTCTTACTCTTA CTA	A	G				SILENT- NONCODING	transcript factor	Human Gene Similar to SWISSPROT- ID:Q07231 ZINC FINGER PROTEIN ZFP 38 (CTFIN51) (TRANSCRIPTION FACTOR RU49) - MUS MUSCULUS (MOUSE), 555 aa.	3.80E-61	8
3236	cg43944978	227	TTGTGGTAAATT TTTTTATCTAAA [A/gap]CAAACTCA CCTGGCCGAAA AATGGG	A	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa.	3.40E-60	17
3237	cg43944978	284	CCCAAGGTCCTCC TACTAGGCCGGA G[gap]AGAAAA GGACCTACCTCC TACAGGG	G	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa.	3.40E-60	17
3238	cg43944978	339	AAACAAGGAGAG CTAGGACTCAAT G[gap]TCGCCC AAGGCCCAAGG GTCTCCAG	G	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa.	3.40E-60	17

3239	cg43944978	591	ACTGAGCCTCTG GATCAGCACCCCT CTTCGATAGGAA GCAAGGAAGCA CACTAC	T	C			SILENT- NONCODI NG	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa.	3.40E-60	17
3240	cg43922509	38	TGCTTTTTTTTT TTTTTTTTTTTTTT GTTGCTTTTCATA GAGTTTATTGA AA	T	G			SILENT- NONCODI NG	transcript factor	Human Gene Similar to SWISSPROT- ID:P14741 TRANSLATION INITIATION FACTOR EIF-2B ALPHA SUBUNIT (EIF- 2B GDP-GTP EXCHANGE FACTOR) (GUANINE NUCLEOTIDE EXCHANGE FACTOR SUBUNIT GCN3) (GCD COMPLEX SUBUNIT GCN3) (TRANSCRIPTIONAL ACTIVATOR GCN3) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 305 aa.	1.20E-55	12
3241	cg42746806	143	GGAATTCGCCCA CGCAGGAGGCA GGGCGCTGCTGC GGAGACCCCGAG GGCTACGA	G	C			SILENT- NONCODI NG	transcript factor	Human Gene Similar to SPTREMBL- ID:O00343 BASIC HELIX-LOOP-HELIX TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 113 aa (fragment). pcds:TREMBLNEW- ID:G1732371 NEUROGENIC BHLH TRANSCRIPTION FACTOR - RATTUS NORVEGICUS (RAT), 113 aa (fragment).	2.00E-55	
3242	cg42746806	145	AATTCGCCACG CAGGAGGCAGG GC[G/T]CTGCGG AGACCCCGAGG CTACGAGA	G	T			SILENT- NONCODI NG	transcript factor	Human Gene Similar to SPTREMBL- ID:O00343 BASIC HELIX-LOOP-HELIX TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 113 aa (fragment). pcds:TREMBLNEW- ID:G1732371 NEUROGENIC BHLH TRANSCRIPTION FACTOR - RATTUS NORVEGICUS (RAT), 113 aa (fragment).	2.00E-55	
3243	cg44928765	237	CTGCAGAGACTT AAGTTCTCTTTG C[C/T]CCAGTGC CCAGACCTGCCT TCTCTT	C	T			SILENT- NONCODI NG	transcript factor	Human Gene Similar to SWISSPROT- ID:Q07231 ZINC FINGER PROTEIN ZFP 38 (CTFIN51) (TRANSCRIPTION FACTOR RU49) - MUS MUSCULUS (MOUSE), 555 aa.	2.10E-53	16

3244	cg44828765	421	GTAAGGGGGAG GAGAAACACAAA CA[C]CTTCGGT GTGAATCTAAAG CATGGA	C	T				SILENT- NONCODING	transcript factor	Human Gene Similar to SWISSPROT- ID:Q07231 ZINC FINGER PROTEIN ZFP 38 (CTFIN51) (TRANSCRIPTION FACTOR RU49) - MUS MUSCULUS (MOUSE), 555 aa.	2.10E-53	16
3245	cg43979598	1031	CACCCCTAAAAGG TTAGGTCAGGCT C[C]ATCCCAAGT GCCCTCAAAAA TAAAT	C	A				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3246	cg43979598	134	AAACAGTGGAGA CGAGTGTAGCAC TTGATCCCCCAA ATCACCAACCCC CAGGT	G	A				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3247	cg43979598	178	CCCAGGTCCCAA GGCCTGGGCTG GG[C]gap]CAGCG CTAACAGGTGAG CCCAGGAG	C	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3248	cg43979598	179	CCAGGTCCCAAG GCCTGGGCTGG GC[C]gap]AGCGC TAACAGGTGAGC CCAGGAGT	C	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3249	cg43979598	563	TGGAGTACTGGC TGGAGGGGGCC CC[gap/C]AGACG GGACACACCCC CCAAAAAA	gap	C				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3250	cg43979598	703	CCCTGGCCAAAA AGTTGGTTGAAA A[gap/A]GGATAA GCTGCTGAGAG AAAGGTT	gap	A				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)

3251	cg43979598	732	AAGCTGCTCTGAG AGAAAGGTTGGG Ggap/GJAGGTGG AAATTTCTATTCC AAGGGT	gap	G				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	8.40E-52	X (Xp11.2)
3252	cg41074975	149	GGAAAAGCCAG CGAGAGGCAGG TGT[G/C]TAAAGG GAGCCTCTCAGC ATGCAGG	G	C				SILENT- NONCODING	transcript factor	Human Gene Similar to SWISSPROT- ID:Q13263 TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1) - HOMO SAPIENS (HUMAN), 835 aa.	5.70E-51	11
3253	cg43946772	1795	ACTACTGATGTG CAAGCAAACCAT A/A/GJAAAGGTACA GTTCTCCAGAAA GCATA	A	G				SILENT- NONCODING	transferase	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0.00E+00	18
3254	cg43946772	895	TCCTTGGCTAAG TCATTTAAAAATT T/CJTITTTTAAAC ATTTTCAGTCAA ATTT	T	C				SILENT- NONCODING	transferase	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0.00E+00	18
3255	cg43946772	896	CTTTGGCTAAGT CATTTAAAAATT T/CJTITTTTAAACA TTTTCAGTCAAAT TTT	T	C				SILENT- NONCODING	transferase	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0.00E+00	18
3256	cg42166807	1619	AGAAGAATCCIT TGACTGAAGCAT GJA/TATGTAGAC TCGAAAGTACAG CATGG	A	T				SILENT- NONCODING	transferase	Human Gene SWISSPROT-ID:Q09328 ALPHA-1,3(6)- MANNOSYLGLYCOPROTEIN BETA-1,6- N-ACETYL- GLUCOSAMINYLTRANSFERASE V (EC 2.4.1.155) (ALPHA-MANNOSIDE BETA- 1,6-N- ACETYLGALACTOSAMINYLTRANSFERAS E) (N-ACETYLGALACTOSAMINYL- TRANSFERASE V) (GNT-V) (GLCNAC-T V) - HOMO SAPIENS (HUMAN), 741 aa.	0.00E+00	2 (2q21)

3257	cg42168807	1672	TAGTCTAGTATA AGGGATCGGATC ATGTTTGCTCAGC CTCTCCCTTGAG TGACA	G	T				SILENT- NONCODING	transferrase	Human Gene SWISSPROT-ID:Q09328 ALPHA-1,3(6)- MANNOSYLGLYCOPROTEIN BETA-1,6- N-ACETYL- GLUCOSAMINYLTRANSFERASE V (EC 2.4.1.155) (ALPHA-MANNOSIDE BETA- 1,6-N- ACETYLGLUCOSAMINYLTRANSFERASE E) (N-ACETYLGLUCOSAMINYL- TRANSFERASE V) (GNT-V) (GLCNAC-T V) - HOMO SAPIENS (HUMAN), 741 aa.	0.00E+00	2 (2q21)
3258	cg43916882	141	CTCAGCTCACTG CAAGCTCTGCCT CTTCTGGATTCA TGCCCTTCTCCT GCCTC	T	C				SILENT- NONCODING	transferrase	Human Gene SWISSPROT-ID:P39656 DOLICHYL- DIPHOSPHOOLIGOSACCHARIDE-- PROTEIN GLYCOSYLTTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0843) - HOMO SAPIENS (HUMAN), 456 aa.	5.30E-245	1
3258	cg43916882	533	TCCCACGGCTTT AAACAAAGCAAA ATCATAAACCAC CAATCCTAATAA CCCCC	C	A				SILENT- NONCODING	transferrase	Human Gene SWISSPROT-ID:P39656 DOLICHYL- DIPHOSPHOOLIGOSACCHARIDE-- PROTEIN GLYCOSYLTTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0843) - HOMO SAPIENS (HUMAN), 456 aa.	5.30E-245	1

3260	cg439416882	563	CCACCAATCCTA ATAACCCCTC C/C/TTGCCCGT CTCCACGCTGTG CGGAG	C	T				SILENT- NONCODING	transferrase	Human Gene SWISSPROT-ID:P39656 DOLICHYL- DIPHOSPHOOLIGOSACCHARIDE-- PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) - HOMO SAPIENS (HUMAN), 456 aa.	5.30E-245	1
3261	cg43948635	1630	TTGGAGCAGCT CATCCATCTCTC A/GA/GTGGGG TCCTCCGGCAG GCAGCTT	G	A				SILENT- NONCODING	transferrase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
3262	cg43948635	816	CAATGCCAAACA CATAGTATGAGA A/T/GTTTACTTT TTAAGAAATTAAT TTAT	T	G				SILENT- NONCODING	transferrase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
3263	cg43948635	818	ATGCCAAACACA TAGTATGAGAA TTT/GTACTTTT AAGAAATTAATTT ATT	T	G				SILENT- NONCODING	transferrase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
3264	cg43948635	985	TGCACITCAGCT ACGTGAAAATAA A/A/GTTTCTTTG GGAAGGTGACAT TTGGC	A	G				SILENT- NONCODING	transferrase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
3265	cg43311354	1596	GAGAACACAGTG GCTGGTTTAA A/A/gap/TTCTTTC CACACCTGTCAA ACCAA	A	gap				SILENT- NONCODING	transferrase	Human Gene TREMBLNEW-ID:G385673 FARNESYL-PROTEIN TRANSFERASE BETA SUBUNIT, FTPASE BETA SUBUNIT=PRENYL-PROTEIN TRANSFERASE DPR1/RAM1 HOMOLOG - BOS TAURUS, 437 aa.	8.50E-238	14 (14q23)

3266	cg4401777	229	ACATCATTCCCTTT TGATCTCCTGTG[G/TATCCCTATA GTTATTTCAAGT AAAG	G	T			SILENT- NONCODING	transfere se	Human Gene SWISSPROT-ID:Q13508 TESTIS ECTO-ADP- RIBOSYLTRANSFERASE PRECURSOR (EC 2.4.2.31) (TESTIS NAD(P)+)- ARGININE ADP- RIBOSYLTRANSFERASE (TESTIS MONO(ADP-RIBOSYL)TRANSFERASE) - HOMO SAPIENS (HUMAN), 367 aa.	9.00E-195	
3267	cg43995237	239	GTATACACAAAG AACTGTAGTCAG A/TJTAACAGGA CTTCAGAATAAA AAGCA	A	T			SILENT- NONCODING	transfere se	Human Gene SWISSPROT-ID:P53811 GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (EC 2.5.1.-) (RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB GERANYL- GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) - HOMO SAPIENS (HUMAN), 331 aa.	1.40E-182	1
3268	cg43258046	495	ATGTGGTGAAC GGATGTGCTACC G[C/gap]AAGACA GAGGACTTCTTC ACCATCT	C	gap			SILENT- NONCODING	transfere se	Human Gene Homologous to TREMBLNEW-ID:G2673964 LECITHIN:CHOLESTEROL ACYL TRANSFERASE - AKODON TORQUES, 294 aa (fragment).	3.20E-146 (16q22.1)	16
3269	cg44000740	274	TGCTCTGGGACT TGGGCAAGTCTT A/A/G/GCAAGCC ATTCTGCTTTC TGGGCC	A	G			SILENT- NONCODING	transfere se	Human Gene Homologous to SWISSPROT-ID:P30711 GLUTATHIONE S-TRANSFERASE THETA 1 (EC 2.5.1.18) (CLASS-THETA) - HOMO SAPIENS (HUMAN), 239 aa.	1.60E-117	16
3270	cg43949162	109	TTACAGCTCAGA GGAGAGTCATTT A/C/TTAGACATT CGGTTGTTATTA AACAC	C	T			SILENT- NONCODING	transfere se	Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa.	1.30E-115	6

3271	cg43949162	18	TTTTTTTTTTTT TTTTT/ATCAAT GACTCATAAATT CTTTATTT	T	A			SILENT- NONCODING	transfere se	Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa.	1.30E-115	6
3272	cg43949162	51	CTCATAAATCTT TATTTGGCTAA CTTACTGATTGC ATTCATTACTAC CAAT	C	T			SILENT- NONCODING	transfere se	Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa.	1.30E-115	6
3273	cg43920566	1312	ATGCTAGCAGC AGATTTTTTTTT gap/TJATTGGTAC ATATTATCCTTCA AATC	gap	T			SILENT- NONCODING	transfere se	Human Gene Homologous to SWISSPROT-ID:P46975 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG - CAENORHABDITIS ELEGANS, 757 aa.	5.30E-103	3
3274	cg43920566	1845	ACAGGATGTTGC TTACCAGGACGG A/G/gapTTTTGG TATCTTAGTACT GAAGTTA	G	gap			SILENT- NONCODING	transfere se	Human Gene Homologous to SWISSPROT-ID:P46975 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG - CAENORHABDITIS ELEGANS, 757 aa.	5.30E-103	3
3275	cg43920566	2268	GGTTTTCTGTC CACAGGATATAA CT/gapTTTTTTT ATATAACAAGCA TAACAC	T	gap			SILENT- NONCODING	transfere se	Human Gene Homologous to SWISSPROT-ID:P46975 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG - CAENORHABDITIS ELEGANS, 757 aa.	5.30E-103	3
3276	cg43920566	2275	CCTGCCACAGGA TATAACTTTTTTT T/gapJATATAACA AGCATAAGACAC CACTG	T	gap			SILENT- NONCODING	transfere se	Human Gene Homologous to SWISSPROT-ID:P46975 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG - CAENORHABDITIS ELEGANS, 757 aa.	5.30E-103	3
3277	cg43928442	40	TTTTTTTTTTTT TTTTTTTTTTTTG /TTTTGCCTGAT GGCATTAGGTTT AT	G	T			SILENT- NONCODING	transfere se	Human Gene Similar to SPTREMBL- ID:O09034 GLUTATHIONE S- TRANSFERASE SUBUNIT 13 - RATTUS NORVEGICUS (RAT), 226 aa.	2.60E-87	7

3278	cg43954704	359	GTTGCTCCTGTC CTGGGGGGCTC TG[C/gap]CTCCA CCTCCCAGTCCA GGATGCT	C	gap			SILENT- NONCODING	transferra se	Human Gene Similar to SPTREMBL- ID:Q29121 UDP- GALNAC:POLYPEPTIDE ALFA-1,0 N- ACETYL GALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559.aa.	1.10E-68	2
3279	cg43954704	360	TTGCTCCTGTCC TGGGGGGCTCT GC[C/gap]TCCAC CTCCCAGTCCAG GATGCTG	C	gap			SILENT- NONCODING	transferra se	Human Gene Similar to SPTREMBL- ID:Q29121 UDP- GALNAC:POLYPEPTIDE ALFA-1,0 N- ACETYL GALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559.aa.	1.10E-68	2
3280	cg43268842	220	GAGGGGAGGG CCTCCGAGTTCC CA[AG]ACAAAAC ACAGGTACCTAA GGGCTT	A	G			SILENT- NONCODING	transferra se	Human Gene Similar to TREMBLNEW- ID:G2688866 CARNITINE ACETYL TRANSFERASE - MAGNAPORTHE GRISEA (RICE BLAST FUNGUS), 608 aa.	3.20E-64	22
3281	cg43917654	360	AAAAAATCTACT CTTAATGTATATT [A/gap]TTTCATAT TTGTTTAAACAAA GCAG	A	gap			SILENT- NONCODING	transferra se	Human Gene Similar to SWISSPROT- ID:P41819 DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-) (S- ADENOSYLMETHIONINE-8-N', N'- ADENOSYL(RRNA) DIMETHYLTRANSFERASE) (18S RRNA DIMETHYLASE) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 318 aa.	3.00E-52	5
3282	cg43917654	898	CTCCCTAAGAAC CATAAAAAAGA T[A/C]ATTTTATT GTAAATTCATTC CAGT	A	C			SILENT- NONCODING	transferra se	Human Gene Similar to SWISSPROT- ID:P41819 DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-) (S- ADENOSYLMETHIONINE-8-N', N'- ADENOSYL(RRNA) DIMETHYLTRANSFERASE) (18S RRNA DIMETHYLASE) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 318 aa.	3.00E-52	5

3283	cg43936623	112	CATCAACAGAGT C TGGGTTTAGGGT T[C]gap]CCCAGG AGAGCAAGGGA GATGGATG	gap			SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q29397 P87=TRANSPORTER-LIKE PROTEIN - BOS TAURUS (BOVINE), 742 aa.	0.00E+00	1
3284	cg43936623	292	TAAACAGTCAC G CACCTGGTACAG T[G/]TTACAAAA TGGGGAGAGTG ACCACA	T			SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q29397 P87=TRANSPORTER-LIKE PROTEIN - BOS TAURUS (BOVINE), 742 aa.	0.00E+00	1
3285	cg43936623	977	ACTGTGGGAGG C CAGGGTTGTGTG Tg[C]gap]ATCCG CTGAAATTACCC TTGGCTTA	gap			SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q29397 P87=TRANSPORTER-LIKE PROTEIN - BOS TAURUS (BOVINE), 742 aa.	0.00E+00	1
3286	cg43919796	4264	CACTGTATTTTG G GCGCATGTTGGT G[G]gap]CCCTCT GTGCCCTAGATA TATGCAC	gap			SILENT- NONCODI NG	transport	Human Gene SWISSNEW-ID:Q92973 IMPORTIN BETA-2 SUBUNIT (KARYOPHERIN BETA-2 SUBUNIT) (TRANSPORTIN) (M9 REGION INTERACTION PROTEIN) (MIP) - HOMO SAPIENS (HUMAN), 890 aa.jpcls:SWISSPROT-ID:Q92973 IMPORTIN BETA-2 SUBUNIT (KARYOPHERIN BETA-2 SUBUNIT) (TRANSPORTIN) (M9 REGION INTERACTION PROTEIN) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	5
3287	cg43998978	5306	TCCTTGGGGCTG gap CAGTTTGTGGT T[gap/A]GAGGGG CCTGGAGAAAT CATTTTC	A			SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16
3288	cg43998978	5412	CCAGGCACCTCAA G AAGCTGGGAACC A[G/C]GATCTCAG CGCCAGGTCCTAC CAGTT	C			SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16

3289	cg43988978	5413	CAGGCACTCAAA AGCTGGGAACCA G/GC/ATCTCAG CGCCAGGTCTAC CAGTTC	G	C				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16
3290	cg43988978	5426	GCTGGGAACCA GGATCTCAGCGC CA/GC/GTCTACC AGTCTCTGTTTT GGGCA	G	C				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16
3291	cg43988978	5427	CTGGGAACCCAG GATCTCAGCGCC AG/GC/CTCTACCA GTTCTCGTTTTG GGCCAG	G	C				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3292	cg43988978	5794	AGTCCTAGCAGA AAAATGTGTTAG G/G/gap/GCCTGG CCCAAAGCAGTG TGGTTG	G	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3293	cg43988978	5795	GTCCTAGCAGAA AAATGTGTTAGG G/G/gap/JCCTGGC CCAAAGCAGTGT TGGTTGC	G	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3294	cg43988978	5953	CTCCCAAGTATT ACCAGTGGGTAC C/A/gap/AAAAAA ATGTCCTCCCTGA GTCCTT	A	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3295	cg43988978	5960	GTATTACCAAGTG GGTACCAAAAAA A/A/gap/JGTCCC CTTGAGTCTTTT CCTTGT	A	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16

3296	cg43998978	6126	TTGAATATCAAT GATTTTTTTTTT[T[gap]TAAGTACT GTTCCGGGGAG AAAAAC	T	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3297	cg43998978	6127	TGAATATCAATG ATTTTTTTTTTT[T[gap]AAGTACTG TTCCGGGGAGAA AAACA	T	gap				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3298	cg43998978	6306	AGCAGCATCTTT TAAAGCCTGTC TT[C]TAAGGTGT CTCGTTAGAGCC CAAAG	T	C				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
3299	cg42684254	2485	CCATATATTTCT GAGTAGCATATA[T[G]AATTTTATG CTGGAATCTACT AGA	T	G				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P31645 SODIUM-DEPENDENT SEROTONIN TRANSPORTER (5HT TRANSPORTER) (5HTT) - HOMO SAPIENS (HUMAN), 630 aa.	0 (17q11.1)	17
3300	cg40351913	3767	TCTGGGGAGG GACACAGAGGA CAGT[C]TCCCG ATCGCCTCTGG TTGTGA	T	C				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0 (5p15.3)	5
3301	cg40351913	3786	GGACAGTTTCCC CATCGCCTTCTG GT[C]TGTGAAG ACAGCACAGAGA CGGCG	T	C				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0 (5p15.3)	5
3302	cg40351913	3789	CAGTTTCCCAT CGCCTTCTGTT GT[C]TGAAGACA GCACAGAGAGC GGCTTC	T	C				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0 (5p15.3)	5

3303	cg43935986	2512	GCCAGATAGCTG TTCCTGAGTTGC A/A/GGCACGAT GGAGATTGGAC ACTGTG	A	G				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0	6 (6p21.3)
3304	cg43935986	2553	GGACACTGTGTG CTTTTGGTGGG TG/A/GAGAGGT GGGTGGGGTG GGGTGTG	G	A				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0	6 (6p21.3)
3305	cg43935986	2697	TATTTAAATAT TTTCCITCTTAC G/A/TGAACTGTA TACATTCATATA GAAA	G	A				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0	6 (6p21.3)
3306	cg43934544	221	GGCCACAGGC CCCTGCTCCGG CCG[C/T]CGCTT GCAGACCGCG GCGCCGATG	C	T				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P48029 SODIUM- AND CHLORIDE- DEPENDENT CREATINE TRANSPORTER 1 (CT1) - HOMO SAPIENS (HUMAN), 635 aa.	0	X
3307	cg43935086	2211	TACTTTTAAATGA CTCTGGAATCTG gap/C/GTAGGCT CGAGCGGTCC CAAGGCG	gap	C				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q61102 ABC TRANSPORTER-7 - MUS MUSCULUS (MOUSE), 694 aa (fragment).	0	X
3308	cg43935086	28	TTTTTTTTTTTT TTTTTTTTTTTT /T/GGAATGTATG ATTTTTTTAATAA AA	G	T				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q61102 ABC TRANSPORTER-7 - MUS MUSCULUS (MOUSE), 694 aa (fragment).	0.00E+00	X
3309	cg43935086	30	TTTTTTTTTTTT TTTTTTTTTTTT G/T/GAATGTATG ATTTTTTTAATAA AAC	G	T				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q61102 ABC TRANSPORTER-7 - MUS MUSCULUS (MOUSE), 694 aa (fragment).	0.00E+00	X

3310	cg43934534	1405	GTCCCCGCAGG CCCACCACCCTC AC[G/C]CAGCCC CAGCCCTCCAGC CTCTGTC	G	C			SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P48029 SODIUM- AND CHLORIDE- DEPENDENT CREATINE TRANSPORTER 1 (CT1) - HOMO SAPIENS (HUMAN), 635 aa.	7.50E-294	
3311	cg43964039	1018	CTCTTCTCATGG TAATAGTGTCG C[C/A]TCAGTGCA AAGGAGACTAGA ACCG	C	A			SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
3312	cg43964039	494	ATTACTTCACAT TCAAAATAATGCI gap[G/A]TTTCAAG CCTGAGCATCAC GGCTG	gap	G			SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
3313	cg43964039	778	CCCTCAATCCAC AAGCATTTCAAA ATT[C/C]TTTTTC TAAAAACCAGCC ATTGA	T	C			SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
3314	cg43964039	864	TATTTACAAGTT GGCTTGTCAGAA TIA/TTACTATAA CTTAGTGTCTGT ATTGA	A	T			SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
3315	cg43992017	206	CCTGAGCTTCCT GCTTAGGGGCC GG[C/gap]CCCCA CCCACAGGGTCT CCCTGGAC	C	gap			SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q14728 TETRACYCLINE TRANSPORTER-LIKE PROTEIN MRNA - HOMO SAPIENS (HUMAN), 455 aa.	4.40E-241	
3316	cg44026704	172	CCTTCTGCTGGC CAGTCTGGGCAC CTT[A]GCAGGCC CCTGAGGGAGG GAGCTGT	T	A			SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q99808 EQUILIBRATIVE NUCLEOSIDE TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 456 aa.	1.50E-240	6

3317	cg43920728	85	CCATTTTCCACT AACAAAATAATTT [A/gap]GGATGAA GAATTCTGACTC AGTGTC	A	gap				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P22732 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER) - HOMO SAPIENS (HUMAN), 501 aa.	2.90E-237	1 (1p31)
3318	cg43317499	220	CTGCCCTCAGCCA CCTGAGTAGCTG G[C/G]AAGACAG AGCATAACCTTC GGTGGC	C	G				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q90406 TRANSMEMBRANE TRANSPORTER - DISCOPYGE OMMATA (ELECTRIC RAY), 724 aa.	1.20E-231	15
3319	cg39377146	4180	TGTCAGTCCGT TCCGAAGGCATT T[G/T]CCACTAGT TTTGGACTATG TAAAC	G	T				SILENT- NONCODI NG	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	1.60E-225	
3320	cg44003311	768	TCACGTCCGAGC TGCCAGGCAGT C[C/T]TTCTGCGC CCTCTGCTGGCC AGATG	C	T				SILENT- NONCODI NG	transport	Human Gene TREMBLNEW- ID:G2921449 ORGANIC CATION TRANSPORTER-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 424 aa.	1.50E-217	
3321	cg44011204	229	CACACACACACA CACACACACACA C[A/gap]CACACG TGCACACACACA TCCCCC	A	gap				SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.lpcis:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.lpcis:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	

3322	cg44011204	234	CACACACACACA CACACACACACA C[gap]A]GTGCAC ACACACATCCCC CCACAAC	gap	A			SILENT- NONCODI NG	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.lpcis:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.lpcis:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
3323	cg44011204	234	CACACACACACA CACACACACACA C[gap]A]GTGCAC ACACACATCCCC CCACAAC	gap	A			SILENT- NONCODI NG	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.lpcis:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.lpcis:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
3324	cg44011204	59	ATAGTTGACACT CAATTTTATTGCT [A/gap]AAAAAAAA TGTCCTCTGGAG TGACA	A gap	gap			SILENT- NONCODI NG	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.lpcis:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.lpcis:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	

3325	cg44011204	531	ATCTCTGTCCT GGAGGTGCTG GG[G/gap]CCCCT GGCTCCCCAGA GTGTGCAGG	G	gap			SILENT- NONCODI NG	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.lpcis:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.lpcis:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
3326	cg44011204	67	CACTCAATTTTAT TGCTAAAAAAA A/gapJTGTCCTCT GGAGTGACAGC AGGTAT	A	gap			SILENT- NONCODI NG	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.lpcis:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.lpcis:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
3327	cg43988801	1574	CAAAAGTTTGGC CACTTCCCTCTC A[A/G]AGACTAAC CCAGAAGGGAAT AAGAT	A	G			SILENT- NONCODI NG	transport	Human Gene TREMBLNEW- ID:E1283177 ABC TRANSPORTER - RATTUS NORVEGICUS (RAT), 565 aa.	9.80E-195	
3328	cg44025532	1782	CCTGCTGGCCA GGCAAGGGCC AGA[C/gap]CCCC CCCCAACCCCA GCTGCCATC	C	gap			SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P41234 ATP-BINDING CASSETTE TRANSPORTER 2 - MUS MUSCULUS (MOUSE), 1472 aa (fragment).	6.80E-174	
3329	cg44025532	1790	CCAGGCAAGGG GCCAGACCCCC CCC[C/gap]AACC CCCAGCTGCCAT CGCTCTCCC	C	gap			SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P41234 ATP-BINDING CASSETTE TRANSPORTER 2 - MUS MUSCULUS (MOUSE), 1472 aa (fragment).	6.80E-174	

3330	cg43924839	176	TGAAGAAATGTG TATCATCTAACA G[C/A]AAAGAAAT ATGAACCCAGATA ATGAA	C	A			SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P78382 CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR) - HOMO SAPIENS (HUMAN), 337 aa.	1.60E-172	6
3331	cg43924839	526	CCTTGTTACTTG AGTATTGTAGCC TTC/TACCATGAT TTTTTTTAAACACC GTAT	C	T			SILENT- NONCODI NG	transport	Human Gene SWISSPROT-ID:P78382 CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR) - HOMO SAPIENS (HUMAN), 337 aa.	1.60E-172	6
3332	cg42328251	238	ACACACACACAC ACACACACACAC A[gap/C]GACAAA ACCACAGGGCTA AGACACA	gap	C			SILENT- NONCODI NG	transport	Human Gene Homologous to SPTREMBL-ID:P97511 ZINC TRANSPORTER - MUS MUSCULUS (MOUSE), 341 aa.	6.40E-146	2
3333	cg43928832	363	TTTTTTTTTTTT TTTTTTTTTTTTA TJAGTATTAAAG AGATTTATTAAAT C	A	T			SILENT- NONCODI NG	transport	Human Gene Homologous to SWISSPROT-ID:Q15012 GOLGI 4- TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108) - HOMO SAPIENS (HUMAN), 233 aa.	2.00E-126	2
3334	cg44930322	977	CTTTTGTTTATTA GCACCAATTCTT C/TGCCACTAAG CTATTTGTTTTAT TAT	C	T			SILENT- NONCODI NG	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	4.80E-113	
3335	cg43924433	226	TCAATACCTTCA TTACATTTATAAA T/AACAAGATT ACACAGCACCCC ATCA	T	A			SILENT- NONCODI NG	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3336	cg43924433	251	TACAAGATTTAC ACAGCACCCCAT C[Agap]AAAAAA AAATTTAAACCC CITTACA	A	gap			SILENT- NONCODI NG	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9

3337	cg43924433	261	ACACAGCACCCCA ATCAAAAAAAAA A[Agap]TTAAAC CCTTTACAAATAT CTACA	A	gap			SILENT- NONCODI NG	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3338	cg43924433	261	CACAGCACCCCA TCAAAAAAAAA A[Agap]TTAAAC CCTTTACAAATAT CTACA	gap	A			SILENT- NONCODI NG	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3339	cg43924433	261	CACAGCACCCCA TCAAAAAAAAA A[Agap]TTAAAC CCTTTACAAATAT CTACA	gap	A			SILENT- NONCODI NG	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3340	cg43924433	334	TTCAAAGGGTG CTCTGTTAAAG T[G/C]GGCCCTA GTTAATGGTCCA TTTACT	G	C			SILENT- NONCODI NG	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3341	cg43924433	339	AGGGGTGCTCT GTTAAAGGTGG CC[C/gap]TAGTT AATGGTCCATT ACIGGIGC	C	gap			SILENT- NONCODI NG	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3342	cg43924433	569	TGCATCTCAGA GCAGTTAAGGCA G[G/T]AGTGTGAT GGATGAGAAAA CTTIG	G	T			SILENT- NONCODI NG	transport	Human Gene Homologous to SPTREMBL-ID:P70187 TETRACYCLINE TRANSPORTER - MUS MUSCULUS (MOUSE), 527 aa.	1.00E-108	9
3343	cg43961977	149	AACATTCCACCA AAAATCATGACT A[T/C]GCATCTAA CAGCTTCAAAAT ATAGA	T	C			SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:Q07837 NA+-INDEPENDENT NEUTRAL AND BASIC AMINO ACID TRANSPORT PROTEIN - HOMO SAPIENS (HUMAN), 685 aa.	5.90E-75	2

3344	cg2986272	1143	ACCTCAGCGAG GGCAACGCCGAG CTGT/GJCCGGA GCCCCCGGCC CGGAGCCCG	T	G				SILENT- NONCODI NG	transport	Human Gene Similar to SWISSPROT- ID:O08726 GALANIN RECEPTOR TYPE 2 (GAL2-R) (GALR2) - RATTUS NORVEGICUS (RAT), 372 aa.	3.60E-62	
3345	cg43319894	250	TGCTTCAGAGAT CCCTGCTGGCTC CIA/TJCGAGCAC CCTGGCCCGCA AAGAAGC	A	T				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3346	cg43319894	273	CCACGAGCACC CTGCCCCGCAAA GA/AGJGCTGGG GGACGTCGGAA GCGAGTCG	A	G				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3347	cg43319894	297	AAGCTGGGGGA CGTCGGAAGCG AGTIC/AJGAATTT GTGACATTTGCA CCAGCAC	C	A				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3348	cg43319894	315	AGCGAGTCGAAT TTGTGACATTTG CIA/GJCCAGCAC CCCCAGCCCG GAGCCTG	A	G				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3349	cg43319894	366	AGGAGCCTGTAG GGCCCCCGGCT GT/AGJGAGTCCA TCCTGGTAGCAG GTGAGG	A	G				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3350	cg43319894	378	GGCCCCCGGCT GTACAGTCCATC CT/GJGTAGCAG GTGAGGAGGAC ATCCGCT	G	T				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11

3351	cg43319894	381	CCCCGGCTGTAC AGTCCATCCTGG T/A/GGCAGGTG AGGAGGACATCC GCTGGG	A	G				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3352	cg43319894	387	CTGTACAGTCCA TCCTGGTAGCAG G/T/CJGAGGAGG ACATCCGCTGGG TGTGCG	T	C				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3353	cg43319894	411	GTGAGGAGGAC ATCCGCTGGGTG TG/C/TGAGGAC ATGGGGCTGAA GGACCCAG	C	T				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3354	cg43319894	834	TGAAACGGCTGT GGGAGGCTGGG CC/C/gapJTGGA CGCCCTCTCATA GCGTCCAG	C	gap				SILENT- NONCODI NG	transport	Human Gene Similar to SPTREMBL- ID:O09014 PEPTIDE/HISTIDINE TRANSPORTER - RATTUS NORVEGICUS (RAT), 572 aa.	9.80E-61	11
3355	cg43941204	1662	CACTTTCCATT CTGCGCCTTTTC T/C/GJTCACCCG GGTGGCGCTGG AAGTTAT	C	G				SILENT- NONCODI NG	transport	Human Gene Similar to SWISSPROT- ID:P09836 REGULATORY PROTEIN UHPG - ESCHERICHIA COLI, 439 aa.	8.40E-57	11
3356	cg43941204	1866	CCCTGTCCTGCC CGCATCCTACCC C/A/gapJTCGCCA CCTGAAGTGAGG CTAICCC	A	gap				SILENT- NONCODI NG	transport	Human Gene Similar to SWISSPROT- ID:P09836 REGULATORY PROTEIN UHPG - ESCHERICHIA COLI, 439 aa.	8.40E-57	11
3357	cg43941204	1955	GGTCCTAAGTCC TCTCAGCAGTGG G/T/CJGACTGCT GTTGCCAATACC TCAGAC	T	C				SILENT- NONCODI NG	transport	Human Gene Similar to SWISSPROT- ID:P09836 REGULATORY PROTEIN UHPG - ESCHERICHIA COLI, 439 aa.	8.40E-57	11

3358	cg43990999	1607	TATTGAATCTGG GTTCTTTTGTGAC [gap/T]TTTTTTTT TTCCCAATCCAA CAGCA	gap	T			SILENT- NONCODI NG	transport	Human Gene Similar to SWISSPROT- ID:P32802 ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 667 aa.	7.50E-55	10
3359	cg43269525	1024	TCTGTCGTGAAC TTCGACAATCT G[G/C]CATGACA ATGAGGGTGGG CATGATT	G	C			SILENT- NONCODI NG	ubiquitin	Human Gene SWISSNEW-ID:Q92462 UBIQUITIN-PROTEIN LIGASE PUB1 (EC 6.3.2.-) - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 767 aa.	6.50E-163	15
3360	cg43291895	1030	GTTGTTTCGTTTT GGCTTTTCTCC[C/T]TCCCCATGT CTGTTCTGGGTT TTCA	C	T			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3361	cg43291895	1075	TTTTCACGTGCT TCAGAGAAGAGG G[G/gap]CTGCCC CACCGCCACTCA CGTCACT	G	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	

3362	cg43291895	1182	AGGGGAGCTGA GCCCGACCTCTA CC[G/gap]GGGTC CCCCAGCTTCCG GACTGGCC	G	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3363	cg43291895	1185	GGAGCTGAGCC CGACTTCTACCG GG[G/gap]TCCCC CAGCTTCCGGAC TGGCCGCA	G	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3364	cg43291895	1230	GCCGCACCCCG GAGGAGCCACG GGG[G/gap]CGCT GCTGGGAACGT GGCGGGGGG	G	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3365	cg43291895	1262	TGGGAACGTGG GCGGGGGGCGG TTT[C/T]TGACA CTACCAGCCTGG GAGGCC	C	T			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	

3366	cg43291895	1304	GGGAGGCCCCAG GTGTAGCGGTCC GA[G/gap]GGGCC CGGTCCTGCCTG TCAGCTCC	G	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3367	cg43291895	1354	CAGGTCCTGGA GCCACGTCCAG CACATGAGTG GACGGATTACCC GTGGCCGA	A	T			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.50E-129	
3368	cg44003015	265	TTTTTTTTTTT TTTTTTTTTTT TTCCTTCAGGAG CATGTTATTGT GTT	G	T			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P52483 UBIQUITIN- CONJUGATING ENZYME E2-23 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - MUS MUSCULUS (MOUSE), 207 aa.	1.10E-109	
3369	cg44003015	318	AGATGATACATC AGGTGCTCTCTG A[G/gap]CTACAA AGGGTAAAAGGA AATCCTC	G	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P52483 UBIQUITIN- CONJUGATING ENZYME E2-23 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - MUS MUSCULUS (MOUSE), 207 aa.	1.10E-109	
3370	cg44005525	725	CAGCTCTCTTCT GTGACAGACAAA TTCATGTGAAGA ACTGTGAAACCC CAGTT	C	A			SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	

3371	cg44005525	735	CTGTGACAGACA AATCATGTAAGA A[C/T]TGTAAG CCAGTTTATGT AGCGT	C	T		SILENT- NONCODI NG	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH8 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
3372	cg44923887	1328	GGGCTGGGCTG GCTGCTCTGGAG GA[G/A]GGGGTC AGCAGGGGCCCC AGCGGACC	G	A		SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22
3373	cg44923887	2326	AAGCGAACGCCA GGCGGTGGCAC GT[G/A]TCAATTT CCACAGAGTCCT GCTTTG	G	A		SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22
3374	cg44923887	2367	TCCTGCTTTGCG GGGTGCTCTGAAT G[C/T]ACTGCAC GGGGTCTCTGCT CACACT	C	T		SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22

3375	cg44923887	2413	ACACTTGGCTGGA ACCAATCGTGGC AIGCJATTTTAGT CCACAGGTCGCT TTTCC	G	C			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22
3376	cg44923887	836	TGAACAATGTTA GGCTGCCGAAC CTG[A]CCCCATCA CTCCCCACTTCT GCACAG	G	A			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P51966 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4.00E-82	22
3377	cg43916797	310	AAGGCCAAAGGT TGAAGGGGTAG GG[A/T]GATGTAA AAGAGTTGGAA CAAAGC	A	T			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSNEW- ID:P51669 UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), 147 aa. pds:SWISSPROT-ID:P51669 UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS, 147 aa	5.20E-80	5

3378	cg43939935	1049	CAGTAAATATAA CTGTACAAAGGC ATT/ATTTAGAAT AACAAAAATATT TTAC	T	A			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.lpcds:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.	7.70E-79	12
3379	cg43939935	1050	AGTAAATATAAC TGACAAAGGCA TTT/ATTTAGAATA ACAAAAATATTT TACT	T	A			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.lpcds:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.	7.70E-79	12
3380	cg43939935	236	CAAGAGACAAGG TTGCAACCCGAA G[G/gap]TTAACA TTTATGTATTAT GACTGG	G	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.lpcds:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.	7.70E-79	12

3381	cg43094404	4004	TCCACAACTAAT ATAGACAACTTT ATC/TJGCGTGCG TAAGAGTTTAC ATGGCA	C	T			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SPTREMBL- ID:O08759 E6-AP UBIQUITIN PROTEIN LIGASE - MUS MUSCULUS (MOUSE), 885 aa.	3.20E-73	4
3382	cg43974851	1140	GCGGGCTCCTCT TCTCATCCATGT C/C/gapJTTCAG GTCTCAGCGTTT GCTCGCT	C	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 961 aa.	1.00E-70	1
3383	cg43974851	162	CAGAACACTTTA TGGTTTCAAATC C/T/gapJTTCAG TTTTTACCCCAA AGGAAA	T	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 961 aa.	1.00E-70	1
3384	cg43974851	174	TGGTTTCAAATC CTTTTTTTTTTTT T/gapJACCCCAAA GGAAATTTGAGA ATTCA	T	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 961 aa.	1.00E-70	1

3385	cg43947722	336	TACAATTAAAATA AAATAAGCATTI T/GTATGATTTT ACAAATATTGTT AT	T	G			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN- LIKE PROTEIN UBL1) (UBIQUITIN- RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 101 aa.lpcis:SWISSPROT-ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), 101 aa.	2.50E-50	
3386	cg43947722	769	GAGTGAAGTAAT ACATGCTAGAA CIA/TTCAGGGC CAATTGGAAAGT CATTAT	A	T			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN- LIKE PROTEIN UBL1) (UBIQUITIN- RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 101 aa.lpcis:SWISSPROT-ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), 101 aa.	2.50E-50	

3387	cg43947722	780	TCACATGCTAGA ACATCAGGGCCA AT/CJTGGAAAGT CATTATGAACAC TTGCA	T	C			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN- LIKE PROTEIN UBL1) (UBIQUITIN- RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 101 aa.lpcds:SWISSPROT-ID:Q93068 UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1) (UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) - HOMO SAPIENS (HUMAN), 101 aa.	2.50E-50	
3388	cg43948669	1717	GGGAAGCAGCG CCGGAGCGGGC GAGT/gap]TCAC GCTTCGGCCCC GCCGCTCTCC	T	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P55854 UBIQUITIN-LIKE PROTEIN SMT3A - HOMO SAPIENS (HUMAN), 103 aa.	5.10E-50	21
3389	cg43948669	1718	GGGAAGCAGCG CCGAGCGGGCG AGTT/gap]CACG CTTCGGCCCCG CCGCTCTCCC	T	gap			SILENT- NONCODI NG	ubiquitin	Human Gene Similar to SWISSPROT- ID:P55854 UBIQUITIN-LIKE PROTEIN SMT3A - HOMO SAPIENS (HUMAN), 103 aa.	5.10E-50	21
3390	cg42940644	112	CTTCTTGAAGGT GCAGGCCCTTGG AC/C/GJTGCCCA GACTCACAGTCC TGGCTGC	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14164 KIAA0151 PROTEIN - HOMO SAPIENS (HUMAN), 716 aa.	0.00E+00	1

3391	cg42940844	323	GTGACCCCTCAGA C AATCACAAGGGA G[C/T]GGAGAGA GCTGTGTTCAAC ATGAAA	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14164 KIAA0151 PROTEIN - HOMO SAPIENS (HUMAN), 716 aa.	0.00E+00	1
3392	cg42940844	327	CCCTCAGAAATC G ACAAAGGAGCG GA[G/A]JAGAGCT GTGTTCAACATG AAACGCT	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14164 KIAA0151 PROTEIN - HOMO SAPIENS (HUMAN), 716 aa.	0.00E+00	1
3393	cg43297012	2231	CTACGTTAACTT gap TGCCTAGTAGAG G[gap/C]CCTTCT TTGCACCTTGCTT CTCAATT	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P48382 DNA BINDING PROTEIN RFX5 - Homo sapiens (Human), 616 aa.	0.00E+00	1
3394	cg43917756	277	TTCCCCAAGCCA C CGCAGGCCATG GC[C/gap]TCAGC TCAGCAGGCTCT CCTCAGTG	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14157 HYPOTHETICAL PROTEIN KIAA0144 - Homo sapiens (Human), 983 aa.	0.00E+00	1
3395	cg43920218	5887	AGTCCTTAAAC G AGCAGGAAAGGT G[G/A]GCCTGTC CCCCCTTTGTGC AGCTAC	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3396	cg43920218	5758	CTGGCCCTCATT G CCTCCAAGTCCA C[G/T]GGAGGGT CCAGAAGAGGG AGTCAGA	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3397	cg43920218	8123	GACACTGCTGGC G GGGGCTCAGT GA[G/gap]CACTA CTCACAGATCCA CACCTGAC	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1

3398	cg43920218	6174	CCTGTTGGGTGG AGTCAGGCTGG GC[C/gap]TTGGT CTGCACCTGTAGC ACCTGTGT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3399	cg43920218	6229	TGAGTTCACATC ATGAATGTGGTG A[C/T]TCCAGAG TACCATCTCAGG CTTAA	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3400	cg43920218	6523	GTATAAATATAT GATATAGATTAT [A/T]TATGTTGTA ACGCCATATATT GAAG	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3401	cg43920218	6539	TAGATTATATAT GTTGTAACGCCA [T/C]ATATTGAAG GCCAACATAACT GGTG	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3402	cg43920218	6592	CAGGGTGGGTG ACAGAAATGAA AG[C/T]CTTTTG GTGATTGTTAAA GCAAGA	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3403	cg43920218	6609	AATGAAAGCCTT TTTGGTGATTGT T[A/T]AAGCAAGA TGTGTATAAAGA AATAA	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1
3404	cg43920218	6616	GCCTTTTGGTG ATTGTTAAAGCA A[G/A]ATGTGTAT AAAGAAATAAAT AGTTT	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75042 KIAA0454 PROTEIN - HOMO SAPIENS (HUMAN), 1882 aa (fragment).	0.00E+00	1

3405	cg43921252	154	CTCTCCACGGT GGGTGCCAGCA GG[C/gap]TCTCC CCTTCCAGTGA CCTCCCTC	C	gap				SILENT- NONCODING NG	UNCLAS- SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3406	cg43921252	607	ATGTCACAGGT CCCCGGGTGG GG[G/gap]CAGCA GCCAGGGCAGA AAAGCAGAA	G	gap				SILENT- NONCODING NG	UNCLAS- SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3407	cg43921266	915	TTATTTTCTTG GCTTCAAGCCCC [C/gap]TCCCATG ACGTGCAGGGC AGGGGT	C	gap				SILENT- NONCODING NG	UNCLAS- SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3408	cg43921266	924	TTTGGCTTCAAG CCCCCTCCCATG A[C/G]GTGCAGG GCAGGGGTGG GCATGAG	C	G				SILENT- NONCODING NG	UNCLAS- SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3409	cg43921266	102	GAATGGGGAG GCAAGGGCTCTT TA[gap/A]GCGTT TGCCAAAACCCAC TGCCACAC	gap	A				SILENT- NONCODING NG	UNCLAS- SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3410	cg43921266	984	ACGACGGAAGC CTCCACCCCCAC CC[C/gap]TGCCT GGCAGGTCCCA GATTACATG	C	gap				SILENT- NONCODING NG	UNCLAS- SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3411	cg43921266	118	GGCTCTTAGCG TTTGCCAAAACC A[gap/A]CTGCCA CACCCCTCCACC CCCTCTT	gap	A				SILENT- NONCODING NG	UNCLAS- SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1

3412	cg43921266	168	TGCCTTCCTCCT CCACGGTGGT GC[C/gap]AGCAG GCTCTCCCTTT CCAGTGAC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3413	cg43921266	482	TAGTGAATCAC AGCAGGCCAAG CC[C/gap]AGGGG CCCGGCTCAAG CTGTCCTCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3414	cg43921266	628	ATGTCACAGGGT CCCCGGGTGG GG[G/gap]CAGCA GCCAGGGCAGA AAAGCAGAA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3415	cg43921266	654	CAGCAGCCAGG GCAGAAAAGCAG AA[G/gap]CTAGC CTCTATAAAGC ACCCCTTT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3416	cg43921266	805	GAGATAGATGCT TTTTTTTTTTTT gap/T]GCTTGCTG TTTTCTTCAGTA TAAA	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3417	cg43921266	866	AAATAACTTCTCT TAGAAAAAAA gap/A]TACAGAAG AAAAAACCAAA GGGTT	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3418	cg43921266	911	AGGGTTATTTT CTTTGGCTTCAA G[C/gap]CCCCCTC CCATGACGTGCA GGGCAGG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1

3419	cg43921289	2069	CCACGTGAGTG GTAGCCGCCGC TGA[G/gap]GCCG AGCCTGCACCTGG GGCCACCCCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3420	cg43921289	2070	CACGTGAGTGGT AGCCGCCGCTG AG[G/gap]CCGAG CCTGCACCTGGG GCCACCCAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3421	cg43921289	2087	CCGCTGAGGCC GAGCTGCACTG GG[G/gap]CCACC CAGCCAGGCCT GGGGGCAGC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3422	cg43921289	2093	AGGCCGAGCCT GCAC TGGGGCC ACC[C/gap]AGCC AGGCC TGGGG CAGCCTCTCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
3423	cg43929087	21	CCCC TTTTTT TTTTTTT[A/TGA CTTCCTACATC AGTTTATTT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3424	cg43929087	209	ACAAAGGGACC TGGAACTCTGTAA G[G/C]TGATTCCA AAACGAAATAA GTAGA	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3425	cg43929087	22	CCCC TTTTTT TTTTTTT[A/GA CTTCCTACATC AGTTTATTTA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1

3426	cg43929067	23	CCCCCTTTTTTTT TTTTTTTTTGG/A CTTTCCTACATC AGTTTTATTAA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3427	cg43929067	24	CCCCCTTTTTTTT TTTTTTTTTGA/T CTTTCCTACATC AGTTTTATTAA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3428	cg43929067	25	CCCCCTTTTTTTT TTTTTTTTTGA/C TJTTCCTACATC AGTTTTATTAA A	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3429	cg43929067	54	CCTACATCAGTT TTATTTAAACAC [A/T]AACAAAGTAT TTCTCTTTCTGTA AGG	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
3430	cg43929790	189	AAGTACAGCAGC CAACATCTGGTC TTC/gapJAGAGCT GCTGGGAAAG GGCAGGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12839 (H326) - HOMO SAPIENS (HUMAN), 597 aa.	0	1
3431	cg43932517	138	CTTTCCTACTGG CGCCGGCTCCT GC[C/gap]AGAGG TCGGGGTGACA GCAGGATCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14746 LDLC PROTEIN - Homo sapiens (Human), 738 aa.	0	1
3432	cg43932517	80	GGTGTGTTTT TTTTTTTTTTTT T/ATGGGAGACA CTTCTTTATTTA GGA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14746 LDLC PROTEIN - Homo sapiens (Human), 738 aa.	0	1

3433	cg43945021	1881	TCCTCTGACTTT TACGGAGGGCTT G[C/gap]CAAAGT AGCCTATTGCAG CCAAAGT	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43308 KIAA0425 - HOMO SAPIENS (HUMAN), 1224 aa.	0	1
3434	cg43945021	1882	CCTCTGACTTTT ACGGAGGGCTT GC[C/gap]AAAGT AGCCTATTGCAG CCAAAGT	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43308 KIAA0425 - HOMO SAPIENS (HUMAN), 1224 aa.	0	1
3435	cg43944666	124	GCCCCCAGCAG GAGCACCACCAG GG[C/T]TAGCAA AGAATCCCAGAC CCCCGC	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O15228 DIHYDROXYACETONE PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.42) (DAP-AT) (GLYCERONE-PHOSPHATE O-ACYLTRANSFERASE) - Homo sapiens (Human), 680 aa.	0	1
3436	cg43947011	127	TAGCTCTTTT TTTTTTTTTTT[G /T]TGGGATAATC TATTTTAATGAAA CT	G	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIAA0253 - Homo sapiens (Human), 708 aa (fragment).	0	1
3437	cg43947011	265	CTGTGGGCTGG AGGTGGGATACC CA[C/gap]CCGCA GCACGCCACC CTAATGTGC	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIAA0253 - Homo sapiens (Human), 708 aa (fragment).	0	1
3438	cg43947011	267	GTGGGCTGGAG GTGGGATACCCA CC[C/gap]GCAGC ACGCCACCCCTA ATGTGCCA	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIAA0253 - Homo sapiens (Human), 708 aa (fragment).	0	1

3439	cg43947011	330	GAGAAAGGACA GTGGGAAGGAG ACA[G/gap]TAGG CTCAGCCCCAGAG ATGCCCCCTG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIA0253 - Homo sapiens (Human), 708 aa (fragment).	0	1
3440	cg43948542	4725	ATTAGTATCTTCT CAGATACAGACC [A/G]TTTTATGAT TTTTTAAAAAGTA AAA	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE-TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE-TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0	1
3441	cg43948542	4772	AAAAGTTCTAAA ATGAAGTCACAC A[A/G]GACAATTA TTCTTATGCCTA AGTTA	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE-TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE-TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0	1
3442	cg43850151	991	CACACAGTCAAC ACCTTGGTGACA G[G/gap]CATCTG CCCCCACTTCAA CCAGTAA	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa.	0	1
3443	cg43950151	2158	ACACGTGCCCTC GGGGAGCCCA CA[C/T]GGCACTT AGGGCTGGCAG CACCGCC	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa.	0	1

3444	cg43950151	273	CGTTTTTTTTTT TTTTTTTATGG[A/T]TTTCCAAC TA GGTTTATTTTAG TT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa.	0	1
3445	cg43951075	114	CCTTGAAAAC TT CTCATCCCTGA A[G/gap]GGTGGG GTGACCACCCCT CTGGGAC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49746 THROMBOSPONDIN 3 PRECURSOR - Homo sapiens (Human), 956 aa.	0	1
3446	cg43959426	4957	TATTCATCCAAA TCAAGCTAAAAT[G/T]TATTTAAGTT GATTCTGAGAGT ACA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15463 PTPL1-ASSOCIATED RHOGAP - HOMO SAPIENS (HUMAN), 1261 aa.	0	1
3447	cg43970200	270	AGTAGCTTTTCA GCATTCAGTTT G/A/T]GGCTCATG GGAAATGTTACT TAGCA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92845 SMAP - HOMO SAPIENS (HUMAN), 792 aa.	0	1
3448	cg43970200	319	CATCAAGATGTG GTTTGATGAGTG A/A/G]CAATGTCA GTATCAACTGTA CTTAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92845 SMAP - HOMO SAPIENS (HUMAN), 792 aa.	0	1
3449	cg43994728	1881	CAGGAATTTAA ACCAAGGATAAG A/G/T]ATGCCCTT GTCAAATCTTGG TTCCA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75041 KIAA0453 PROTEIN - HOMO SAPIENS (HUMAN), 1052 aa (fragment).	0	1
3450	cg43994728	2157	AACAGTTCAATG GGACTTTTTTTT [gap/T]CCTTCTCA ATCAACAGAGTT TACCA	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75041 KIAA0453 PROTEIN - HOMO SAPIENS (HUMAN), 1052 aa (fragment).	0	1

3451	cg44020180	1972	TTGTAGCAGAGA CACAGTGGCCTA G[C/gap]CAATCG GCAGTGCTATAC ACACAGT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0	1
3452	cg43925699	2081	TTGTTATAAGGC GCTGGGAGAGG AT[G/gap]GGCAG CTCCCACTGCC CAGAGCGG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q03989 MODULATOR RECOGNITION FACTOR I - HOMO SAPIENS (HUMAN), 614 aa (fragment).	0	2
3453	cg43925699	2083	GTTATAAGGCGC TGGGAGAGGAT GG[G/gap]CAGCT CCCACTGCCCA GAGCGGAG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q03989 MODULATOR RECOGNITION FACTOR I - HOMO SAPIENS (HUMAN), 614 aa (fragment).	0	2
3454	cg43926985	4868	CAGCATGTCCCA GTCACCTGCAGCA A[C/T]GCCTTG TTTGTTTCATTT TTTA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q00234 KIAA0235 - HOMO SAPIENS (HUMAN), 850 aa (fragment).	0	2
3455	cg43926985	5521	GTATAAATTAGA AAATGAAAAATG T[G/A]TGAATAAC ATTGTATGAAAT AAAC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q00234 KIAA0235 - HOMO SAPIENS (HUMAN), 850 aa (fragment).	0	2
3456	cg43961763	115	TTTTGGTCCAG TACTCCACAAA C[A/G]CTACAGAC AGTAACAAAATA ATICA	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P13521 SECRETOTRANIN II PRECURSOR (SGII) (CHROMOGGRANIN C) - Homo sapiens (Human), 617 aa.	0	2
3457	cg44033553	635	TCATGCCTGAGA CCAGAATGGAAT A[G/A]AACAATCC ATTGAATACAG CGATG	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42331 HYPOTHETICAL PROTEIN KIAA0053 - Homo sapiens (Human), 638 aa.	0	2

3458	cg44911887	144	CCGAGGCGCTCCT TGCTTCCCGCTC TGGCJCGAGGAG CCTTTCATCCGA AGCGCG	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99728 BRCA1-ASSOCIATED RING DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 777 aa.	0	2
3459	cg44911887	165	CTCTGCGAGGA GCCTTTCATCCG AA[G/gap]GCGGG ACGATGCCGGAT AATCGGCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99728 BRCA1-ASSOCIATED RING DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 777 aa.	0	2
3460	cg44911887	96	GAGCTTGGCCG GTTTCGAGTCGC TGA/GJCCTGCA GCTTCCCTGTGG TTTCCCG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99728 BRCA1-ASSOCIATED RING DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 777 aa.	0	2
3461	cg44927137	3131	ATTTGGGTGTC TACAAAAGCCTT TGA/GCAAATTAT CAGTAGTAGTT TTTT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15061 ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 688 aa (fragment).	0	2
3462	cg44927137	3449	TTTGTCTATAAT GGAGCTGTTTAT G/A/GCAAATTAA TACCATTCTCTT GTA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15061 ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	2
3463	cg43301812	1497	ATGGACAATGAG TGCTCCTCTGCA C/C/TCCCCCATA TCAATGGCAGTG GAACC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa.	0	3
3464	cg43308354	1161	CACCTAGTCCTC TGCTACCAACTC ATT/CJGTCATGAT GGGATGAGCC AGACAC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3

3465	cg43308354	1382	CAATGGTGTGTGT TAGACTCCCCTA TTT/gapJTTTTAAA ATGCTAATTAC ATTCIT	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3
3466	cg43308354	300	GACAGAACATC AAAGACCAACGT GIC/gapJACCTTG CTTCCATACCA GGCTGAG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3
3467	cg43308354	436	CTGTGGGGAGA GGGTAGGCAAT GGCJ/gapJTCCT GCAAACGGGCC CAGATCCGCC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3
3468	cg43308354	90	ATAATACAGCAA GATATTGTGGG GIG/JTTTCCTTT TTCTGTCAAGT AAGAA	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15050 KIAA0342 - HOMO SAPIENS (HUMAN), 1098 aa.	0	3
3469	cg43918935	3056	CTGTGTTTATCA TGTGTATATCGT CIC/JAGAAAGTA TTAAGGCTTAG GTAGA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment).	0	3
3470	cg43925942	4379	AAATAGTCCGA AACCAGGAATTC AIGAJTGATGTT TGTTTATACTGT TTGA	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3471	cg43925942	5380	GCTATAGTTGCG GGTGGAAACAGTC AAGJCCCTTTCTA GTAGTTTATGAT ATTGC	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3

3472	cg43925942	5427	TTGCCCTCTTTG TATCCCATTTTC T/CJACAGTTT TCCGCAGACTTC TTTC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3473	cg43925942	5713	ATGGTTTTCTCT CAGTCTCTAAG C/TJGGTCTATG TTATAGCTCTAG CAGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3474	cg43925942	5909	ATTATTGCACTT AATATTTGCCTG A/TJGCTTGATCA AAGGTCATTTGT GTAG	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3475	cg43925942	5984	GTAATTAATAAT ATTAAATCACA A/TJTAATAATTCTA TTATTGGAGAGC ATC	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3476	cg43925942	5967	ATTAAAAAATATT TAAATCACAATA A/TJAATTCATTA TTGGAGAGCATC TTT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
3477	cg43936625	38	TTTTTTTTTTTT TTTTTTTTTTTT /TTACTAAAGAA TAAAGATTTTAT T	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14688 KIAA0183 PROTEIN - HOMO SAPIENS (HUMAN), 1062 aa (fragment).	0	3
3478	cg43939697	3385	TAAATGTTTTTG GCCGGCGTGG TG[G/gap]CTCAT GCCTGTAATCTC AGTACATT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75766 TRIP PROTEIN - HOMO SAPIENS (HUMAN), 784 aa.	0	3

3479	cg43940975	130	TCCTTTTTTTTT TTTTTTTTCTA[G/T]GAGAAATTA GCTGTTCTTTATT GAC	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE-TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0	3
3480	cg43940975	131	CTTTTTTTTTTT TTTTTTTTCTAG[G/T]JAGAAATTTAG CTGTTCTTTATTG ACA	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE-TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0	3
3481	cg43957007	2507	AGTGATCCTTCT GCCTCAGCCTCC C/A/G]AGTAGCT GGGATTACAGGT GAGCAC	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92611 MYELOBLAST KIAA0212 - HOMO SAPIENS (HUMAN), 657 aa.	0	3
3482	cg43978396	6657	AAAAGGAGAGG GGTTAAGATGCA CC[G/A]JAGGCTG TAGCTGGGCTAC TTGATCT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31595 KIAA0620 PROTEIN - HOMO SAPIENS (HUMAN), 1985 aa (fragment).	0	3
3483	cg43978396	6750	AGCTTTTATATAT TAAAAAAGGTAT[C/T]ATGCACCAA CTGTGAATAGCT GCCG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31595 KIAA0620 PROTEIN - HOMO SAPIENS (HUMAN), 1985 aa (fragment).	0	3
3484	cg44021891	466	TGGTAATACTGA GGGGCTGGACA GA[G/gap]GCTCT TCTGAGCCTCAA GCGCCAGG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92560 BRCA1 ASSOCIATED PROTEIN 1 (MYELOBLAST KIAA0272) - HOMO SAPIENS (HUMAN), 729 aa.	0	3
3485	cg44021891	479	GGGCTGGACAG AGGCTCTTCTGA GC[C/gap]TCAAG CGCCAGGGACA GAGACCTAG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92560 BRCA1 ASSOCIATED PROTEIN 1 (MYELOBLAST KIAA0272) - HOMO SAPIENS (HUMAN), 729 aa.	0	3

3486	cg43917191	1115	CTATATGGAGTA AAATAAGTTAAA A/C/T/T/T/T/TCTAA TGAGAAATAGCTG ACAGG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74849 KIAA0826 PROTEIN - HOMO SAPIENS (HUMAN), 1236 aa (fragment).	0	4
3487	cg43917191	1120	TGGAGTAAAAATA AGTTAAACCTTTT [C/T]TAATGAGAA TAGCTGACAGGC AGCA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74849 KIAA0826 PROTEIN - HOMO SAPIENS (HUMAN), 1236 aa (fragment).	0	4
3488	cg43918628	3240	GTGTGTGTGTAT ATATATATATATA [T/gap]AATACATT CTATCTTACCCT AATCA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60272 KIAA0517 PROTEIN - HOMO SAPIENS (HUMAN), 792 aa (fragment).	0	4
3489	cg43918628	3241	TGTGTGTGTATA TATATATATATAT [A/gap]ATAGATTG TATCTTACCCTA ATCAT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60272 KIAA0517 PROTEIN - HOMO SAPIENS (HUMAN), 792 aa (fragment).	0	4
3490	cg43918628	387	ACAAAATCTAAA AAGAAAAACAAAG C[gap/A]AAAAAA AAAAAACCCCTT CAATTC	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60272 KIAA0517 PROTEIN - HOMO SAPIENS (HUMAN), 792 aa (fragment).	0	4
3491	cg43928426	5172	TGTACATATCTG GGCCTTTGGAG GC[C/gap]ACGTG TGGCATGGGAG GGGCTACCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75338 RGS12 - HOMO SAPIENS (HUMAN), 1376 aa.	0	4
3492	cg43930981	1361	CAAGCCAGGTCTG TCCCGTCTCTT G[G/gap]TGTGGC CACACCCTGTCC GGCATAT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0	4

3493	cg43930961	26	TTTTTTTTTTT TTATAGGCAAGG [C/T]TTTATGTTA TATTTATTTATTT TCC	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0	4
3494	cg43930961	629	AAAATCCAAGAC CAGCAGTTCCTC A[C/A]ATTGAGT ACTACTCAGATT GGCAG	C	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0	4
3495	cg43935402	14000	GACCACTCACGA TAAAGCAGATTT TT[gap]CTCTGC CTCTGCCACAAG GTTTCAG	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa.	0	4
3496	cg43979400	1082	CACACTTTCATC TCTGTTGCTGAA A[G/gap]CCTCTG AGCTTCAGCTAC TTAACTA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92628 HYPOTHETICAL PROTEIN KIAA0232 - Homo sapiens (Human), 1008 aa.	0	4
3497	cg43979400	2010	GCACATACCTGCT CTCCTGCGCTC TT[G/gap]CCTGTG GCACAATGCCAT GAGAGCC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92628 HYPOTHETICAL PROTEIN KIAA0232 - Homo sapiens (Human), 1008 aa.	0	4
3498	cg43979400	2080	CACAGACGCGA CTCACAAAGATGC GC[C/gap]GGCTC CCGGGGCTCAC CAAGGAGAA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92628 HYPOTHETICAL PROTEIN KIAA0232 - Homo sapiens (Human), 1008 aa.	0	4
3499	cg43994452	163	ACTGGCAGGGA CCTCCCCACAG CC[A/G]CCCCCA CAGGGTTCTCTG TTTCCCA	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4

3500	cg43994452	242	ACACATTACCCG ACTACCTGCTGG A/GC/JAGGAGGG TCATGAGGCAGC CTGTGG	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3501	cg43994452	50	TTTTTTTTTTTT TTTTTTTTTTTTG TTTCAGGTCCAC CAGAGGCTTTTA TTT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3502	cg43994452	572	TTCCAGACACCG GAACCTCCTAGT CTTC/JAGCCTGG CACACCCATGTC ACTCAG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3503	cg43994452	593	AGTCTAGCCTGG CACACCCATGTC A/C/TTCAGAAAG GTCAGGCTCAG GGTGG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3504	cg43994452	697	GCAGCCTCCCT TTGTCGGGGTCC AT/C/JGCAATCTA CACATGGTCGCA AGGIC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3505	cg43994452	772	GGGCACAGACG GCACTGGTGCAT GC/C/gapJTGTCG GGCTGGGGCCA CACTGGGGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0	4
3506	cg43260923	908	CACATAATTCCA ATTTTATTGAAT [G/A]TAGAGATTT TATGAAAACAAA TCCA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15023 KIAA0305 - HOMO SAPIENS (HUMAN), 1539 aa.	0	5

3507	cg43916866	104	TGTGTGCCAGGA CAACCGGCCGG AGC[<i>gap</i>]CACCG CAGCTCCCGATA CCGATGTT	C	<i>gap</i>		SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60337 KIAA0597 PROTEIN - HOMO SAPIENS (HUMAN), 971 aa (fragment).	0	5
3508	cg43916866	1412	CCTGTCGAGATC ACAGCAGGTCCA A[<i>AT</i>]ATAAAGTG ACAACTAGATTT AATAA	A	T		SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60337 KIAA0597 PROTEIN - HOMO SAPIENS (HUMAN), 971 aa (fragment).	0	5
3509	cg43916866	1413	CTGTCGAGATCA CAGCAGGTCCAA A[<i>AT</i>]TAAAGTGA CAACTAGATTTA ATAAA	A	T		SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60337 KIAA0597 PROTEIN - HOMO SAPIENS (HUMAN), 971 aa (fragment).	0	5
3510	cg43916866	176	AATTGCTTACCA CTTAGGGAAAA AT[<i>C</i>]TGTGAAG TATAAACAGCC AGAAC	T	C		SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60337 KIAA0597 PROTEIN - HOMO SAPIENS (HUMAN), 971 aa (fragment).	0	5
3511	cg43933355	236	CTGAGACTTAAT AAATGAGATAAA A[<i>G</i>]CAGTTTCT TACACCTAAGAA ACTGG	G	A		SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment).	0	5
3512	cg43933355	42	TTTTTTTTTTTT TTTTTTTTTTTTT A[<i>T</i>]TCGAACCAAG AGAACATTTTTTA T	T	A		SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment).	0	5
3513	cg43933355	403	CCAGGGGATGC TGGGCTTGTTAG CA[<i>C</i>]TTC AAGCT CTGGGACCTGAT TGGCCT	C	T		SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment).	0	5

3514	cg43934069	304	AGTAAAGATTTC TTTTGGTGATATA [C/gap]CAGAGTT AAGGGCAGTAGA AGAATA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92585 MYELOBLAST KIAA0200 - HOMO SAPIENS (HUMAN), 1016 aa.	0	5
3515	cg43934069	582	GTCTGAGCACCC TTTCTTCTGAGT [C/T]GTGGCTCCT GGAAGACGGGG CTGTG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92585 MYELOBLAST KIAA0200 - HOMO SAPIENS (HUMAN), 1016 aa.	0	5
3516	cg43942858	1107	CAAGCAAGGGC AGATCTGAGAGC CTC[G]TAATGCT AGCAGGTGCA GCTGGTG	C	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5
3517	cg43942958	1353	GGGAGGAAAGG CAGGAGGAGAT GAG[G/gap]CCAG CCCCACTGATGA CACCTTGGG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5
3518	cg43942958	1378	GCCAGCCCACTG GATGACACCTTG G[G/gap]CCAGGC CTCACAGCTGCA GGCATCA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5
3519	cg43942958	329	AGTGAGGGTATC CTTGCTCCCA G[C/gap]CCTGGG GCCCCCTGCGG TCACCTTT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5
3520	cg43942958	331	TGAGGGTATCCT TGTGGCTCCAGC C[C/gap]TGGGGC CCCCCTGCGGTCA CCTTGG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75163 KIAA0676 PROTEIN - HOMO SAPIENS (HUMAN), 1262 aa (fragment).	0	5

3521	cg43951735	319	ATAAATCTTCTCT TAGGCTAAACAA[C/gap]AAGACTCG GTCTATAATTCA GAGGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14776 PUTATIVE TRANSCRIPTION FACTOR CA150 - HOMO SAPIENS (HUMAN), 1098 aa.	0	5
3522	cg43951735	34	TTTTTTTTTTTT TTTTTTTTTTTT[A /TTATAAAAAGG GTTGGTTTATTG TAG	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14776 PUTATIVE TRANSCRIPTION FACTOR CA150 - HOMO SAPIENS (HUMAN), 1098 aa.	0	5
3523	cg43981461	5659	ATTAAGAAGTT CATAGATTTTAC A/C/TJGAATGTAA ATGTGTTATATG GAGAC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43314 KIAA0433 - HOMO SAPIENS (HUMAN), 1243 aa.	0	5
3524	cg43985488	443	CACGCCAGGCC CCAAGCAGGGT GAG[G/gap]CCTC CAACCCGGCCA GCTGAGCAGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q16643 DREBRIN E - Homo sapiens (Human), 649 aa.	0	5
3525	cg43985488	711	GAATGCAGGCAC GGCGGGCCGTC TG[G/gap]CCAGA GGCTGATGCAG GTGGGGGGC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q16643 DREBRIN E - Homo sapiens (Human), 649 aa.	0	5
3526	cg44026925	5089	CAATGAATCAAG ACTTCTACCCAA A[G/A]CAACATTT TTTTAAACTATAT TTAT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3527	cg44026925	5421	AATCAAAATTCAA AGATTTAATTC TT [G/C]CTATGAATT CTAAAGTTCGGC AAAC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5

3528	cg44026925	5450	TGAATTCCTAAAG TTCGGCAAACCA ATT/CJT/CATCATA AAATCCAAATAA TCTTG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3529	cg44026925	5504	CCTATTTATCTA GTGATTCATCTC C/A/GJATTCTGTT GAAAAAGCATAA TATAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3530	cg44026925	5525	CTCCAATTCTGT TGAAAAAGCATA AT/CJATAAATGT TGATGAGACTAG ACTCT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3531	cg44026925	5536	TTGAAAAAGCAT AATATAAATGTT G/A/GJTGAGACTA GACTCTAATGGA TAIGT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3532	cg44026925	5541	AAAGCATAATAT AAATGTTGATGA G/A/TJCTAGACTC TAATGGATAATGT TTATA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5
3533	cg43308181	5595	ATCATTTTCTTT TTTTTTTTTTTTT// gap CTGTTGTGG AAAAGCGTGAAT TTGT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92514 MYELOBLAST KIAA0240 - HOMO SAPIENS (HUMAN), 983 aa (fragment).	0	6
3534	cg43308181	5912	AAAATGTTTGTGA AAAAAAAATAAA A/gap CTATAACA AATTGCAGTTTA TTTTG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92514 MYELOBLAST KIAA0240 - HOMO SAPIENS (HUMAN), 983 aa (fragment).	0	6

3535	cg43924112	351	AAATCTGAGAC AAGACTAAACAA A[C/gap]AACAAA AAATCTCTAAC ACAAAT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa.	0	6
3536	cg43924112	5634	CGCCGCCCGCC CCGGCCCAAAA GTC[C/gap]GCCC GCGCTGTCCACA CAGTGGGCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa.	0	6
3537	cg43925091	168	TTTTTAAATCAA ACTCTGGGTTT T/AATTTCTGTAA AAGCTCCAGCTC TAC	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14999 HYPOTHETICAL PROTEIN KIAA0076 (HA0936) - Homo sapiens (Human), 1698 aa.	0	6
3538	cg43929503	327	TTTGGTTTATAG GAGAGATTTATT T/A/GAAGAAATA TTACAACATATAA AAA	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)- METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa.	0	6
3539	cg43929503	430	TAATAAAAAACTT TTAAAAATCCAGA A/TTGCACAAAG TACTGCACAATT TGAT	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)- METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa.	0	6
3540	cg43929503	5399	TGCTCTTTTCCA AATCTTTGAGCC G[G/C]CTGCGGA CATCGTCGGGCA GCGAGA	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)- METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa.	0	6

3541	cg43947531	101	CAAAATAACAA GTTTGTGAACA GICAJTTTCITTT CTAATATAATGA CTATG	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14244 MICROTUBULE ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 749 aa.	0	6
3542	cg43998751	2414	GGCTACAGTACC ATGCCTCTCAGC CIC[gap]CGTGTG TATAATATGAAG ACCAAAT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46139 DJ27K12.1 (GLUTAMATE-CYSTEINE LIGASE (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE), CATALYTIC (72.8KD) (GCS)) - HOMO SAPIENS (HUMAN), 637 aa.	0	6
3543	cg43998751	346	GCGGGGTGGAG CGGCACGCGCC TTC[G/T]GCAGGA GGCTGAGTGTC GTCTCGC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46139 DJ27K12.1 (GLUTAMATE-CYSTEINE LIGASE (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE), CATALYTIC (72.8KD) (GCS)) - HOMO SAPIENS (HUMAN), 637 aa.	0	6
3544	cg43998751	352	TGGAGCGGCAC GCGCCTTCGGC AGG[AC]GGCTG AGTGTCCTGCTC GCGCCCGG	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46139 DJ27K12.1 (GLUTAMATE-CYSTEINE LIGASE (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE), CATALYTIC (72.8KD) (GCS)) - HOMO SAPIENS (HUMAN), 637 aa.	0	6
3545	cg43998667	395	AACTGTTTATAA CAAAACACAAAAT A[gap]AAAAAAAA CAATGTTACTATT TACG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment).	0	6
3546	cg43998667	403	TATAACAAACAC AAAAATAAAAAA A[A/gap]CAATGTT ACTATTACGGC AAACAG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment).	0	6

3547	cg43944072	282	TTAGTGCGGTAC ATGCAGCCCTCG G[C/gap]ACGGAG GGTCAGTCCCC GCTGTTCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60719 CULLIN 1 - HOMO SAPIENS (HUMAN), 776 aa.	0	7
3548	cg44018111	266	ACTCCAGGACG GGGCCAGGCC CC[gap]CJTAAA AGGCACAATGGC AGGGCAGG	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O60568 PROCOLLAGEN-LYSINE 2- OXOGLUTARATE 5-DIOXYGENASE 3 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 3) (LH3) - Homo sapiens (Human), 738 aa.	0	7
3549	cg43316178	2924	GTCCACCACTCT ACCCACACAGGA GG[G/gap]CCGCC CGCCACCAAGC CTCACCTGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14163 KIAA0150 PROTEIN - HOMO SAPIENS (HUMAN), 944 aa (fragment).	0	8
3550	cg43274140	3669	GGTGGGAGAGG GGGAGTCTCAC GGG[G/gap]CCCC AGGCTTATTCAG AACTGGTGT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75151 KIAA0662 PROTEIN - HOMO SAPIENS (HUMAN), 677 aa (fragment).	0	9
3551	cg43274140	3831	CATGTACATTTC TAACAAAGTTTAT [C/T]GTGGCTATT AAAGTGTATTATT TCC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75151 KIAA0662 PROTEIN - HOMO SAPIENS (HUMAN), 677 aa (fragment).	0	9
3552	cg43916922	172	TTACCCAGGCC ACTGTTCCCTATG CIG/A]CACTGGC TTTGTAGGCATT CACATC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75181 KIAA0689 PROTEIN - HOMO SAPIENS (HUMAN), 847 aa (fragment).	0	9

3553	cg43947535	1017	GGCAGCACCCC TCCCAGAGGCA GCC[A/G]GGGAG GCCTCTCCACCA GGGCCTGC	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P21399 IRON-RESPONSIVE ELEMENT BINDING PROTEIN 1 (IRE-BP 1) (IRON REGULATORY PROTEIN 1) (RP1) (FERRITIN REPRESSOR PROTEIN) (ACONITATE HYDRATASE) (EC 4.2.1.3) (CITRATE HYDRO-LYASE) (ACONITASE) - Homo sapiens (Human), 889 aa.	0	9
3554	cg43958488	241	GTTGAGCACTGG ATTACGGTAGAG G[A/gap]GGGCTC CCAGGTCAGTCT GAGAGTT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31649 KIAA0674 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	0	9
3555	cg43958488	79	ATTTCAAAGTC ATTGACCTCTTG TTA/GTTCAGATTT AAGGCAAAGAAG AAGAT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31649 KIAA0674 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	0	9
3556	cg43970044	357	GGTCTCCACCTG AAACTTCTGCG TTC/TGGGATTGA CAGCCATCCATA AGAAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q75129 KIAA0634 PROTEIN - HOMO SAPIENS (HUMAN), 1321 aa (fragment).	0	9
3557	cg43978962	836	GAGGGTGCTGT GGTCACAGCTCG CG[G/gap]CCCCG GCCACCGAGGC CCAGTTCCC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92854 SEMAPHORIN - HOMO SAPIENS (HUMAN), 862 aa.	0	9
3558	cg43978962	842	GCTGTGGTCACA GCTCGCGGCCC CG[G/gap]CCACC GAGGCCAGTTC CCTTCCAG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92854 SEMAPHORIN - HOMO SAPIENS (HUMAN), 862 aa.	0	9

3559	cg43251586	1145	TGATCAACAGT TGACAGTTAGTT G[C/T]GAGGAAA GGGTCCAAAAG GCATGGA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76041 NEBULETTE - HOMO SAPIENS (HUMAN), 1014 aa.	0	10
3560	cg43923753	466	GTCACCTCCTGC AGCCATACCGTC A[G/gap]GCCAGC TTGGCCTAAAG CTGTTAT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment).	0	10
3561	cg43923753	467	TCACCTCCTGCA GCCATACCGTCA G[G/gap]CCAGCT TGGCCTAAAGC TGTTATC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment).	0	10
3562	cg43925680	124	ATGCCTTGTTTT TTTTTTTTTTT[A /T]TGGCTGTTAT GCTTTTAATGGA AGC	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13772 ARA70 - HOMO SAPIENS (HUMAN), 614 aa.	0	10
3563	cg43950416	42	CAGCAGCAGAG GGAGAGCTCGG GGC[G/T]TGAAG GGGAAACAGCG GAAGACCTA	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75166 KIAA0679 PROTEIN - HOMO SAPIENS (HUMAN), 767 aa (fragment).	0	10
3564	cg43950416	4189	AGGTAGGGTTCA GGGACTGATTGG T[C/gap]CCCATTT GCCCTCAGGTCA GTTGTT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75166 KIAA0679 PROTEIN - HOMO SAPIENS (HUMAN), 767 aa (fragment).	0	10
3565	cg43950416	4192	TAGGGTTCAGGG ACTGATTGGTCC C[C/gap]ATTTGC CCTCAGGTCAGT TGTTAA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75166 KIAA0679 PROTEIN - HOMO SAPIENS (HUMAN), 767 aa (fragment).	0	10

3566	cg43917151	113	TGCCAACTCCTG AGCTAGGACCTG G/GTAAACACAAA GTAAATAGGAC ACGAT	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBL-NEW- ACC:AAC98480 LYOSOMAL PEPSTATIN INSENSITIVE PROTEASE - HOMO SAPIENS (HUMAN), 563 aa.	0	11
3567	cg43983056	1243	CCACACACGTT AGACAATTTTT [C/T]TTTTTTC CAAGATTTTAGT AGTA	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O42480 RANBP7 - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1038 aa.	0	11
3568	cg43983056	1313	TACTTTCACCTC TTCAGTGTTAAA ATTCTAGAAAACC AAACAGTGCCAA CAGTA	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O42480 RANBP7 - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1038 aa.	0	11
3569	cg43983056	2744	CTCTAAGGTACC TCCCATCCCCC C/C[gap]ACCCCC AAAATCCCGCTG ATTCTT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O42480 RANBP7 - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1038 aa.	0	11
3570	cg44015570	435	TAAAAAGTAA GCCACATCTGCA A/C[gap]TTACAC AATCCAAATGG CTAGAGC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13136 LAR-INTERACTING PROTEIN 1B - HOMO SAPIENS (HUMAN), 1202 aa.	0	11
3571	cg43329920	303	GCAGGATGCTT AAGGAAGGCC CG[C/gap]CCAGT ATGAAAGCTGAG GATIGCCT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0	12
3572	cg43329920	305	AGGGATGCTTAA GGAAGCCCCG CC[C/gap]AGTAT GAAAGCTGAGGA TTGCCTCT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0	12

3573	cg43918566	2146	CCAGACTCTTCC TGGACTGGCTTG C[C/gap]TCCTCC CCACCTCCCCAC CCTGGAA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0	12
3574	cg43918566	2534	AGTCGTTTACC CTCTTCTATTGA AT/ATGCGCTTGG GATTTCCTTCTC CCTTT	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0	12
3575	cg43918566	2581	CTTCCCTGCC ACCCTGTCCCCT A[C/A]AATTGTG CTTCTGAGTTGA GGAGC	C	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0	12
3576	cg43918566	2668	CCTATCACCTCC AGCACAAATCCCA G[C/T]GAAAAAG GTGTGAAGCACC CACCAT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0	12
3577	cg43924515	390	ACATGCTTGGTC TTTCTGGCTTGG C[C/gap]AACTCC TTCTTGAAACT AAGGGCC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29728 (2'-5')OLIGOADENYLATE SYNTHETASE 2 (EC 2.7.7.-) ((2'-5')OLIGO(A) SYNTHETASE 2) (2-5A SYNTHETASE 2) (P69/P71) - Homo sapiens (Human), 726 aa.	0	12
3578	cg43932638	175	AGCTGCCGCTG CCACCAGAGCC GGC[G/gap]GGG CATCGCGCTGCT CATTCAATCCG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q43892 BICAUDAL-D - HOMO SAPIENS (HUMAN), 975 aa.	0	12
3579	cg43950437	295	GAGTAGCTGGG ATTACAGCGCA CG[gap/C]CAATA CGCCCGGCTAAT TTTTTATT	gap	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15021 ORF - HOMO SAPIENS (HUMAN), 1401 aa.	0	12

3580	cg44918447	227	AATCCAGCACT TTGGAAGGCTGA G[A/G]CAGGAGG ATCAGTTGAGGC CAGGAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa.	0	12
3581	cg44918447	239	TTGGAAGGCTGA GACAGGAGGAT CA[G/C]TTGAGG CCAGGAGTTCAA GACCAGC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa.	0	12
3582	cg44918447	278	AGTTCAAGACCA GCCTGGGCAAC ATT[G/G]GTGAGA GCCTGTCTCTAC AAAAAAT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa.	0	12
3583	cg44918447	475	TGAGACCTTGTC TCAAAAAA A[A/gap]AAACGC CTCCCCCTACC CCAGACA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa.	0	12
3584	cg43961443	242	AATTATTTCTTC GAGCCCGCTCT G[C/gap]GCTGCG CCGGCCTCCCC GCGCCCGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14393 GROWTH-ARREST-SPECIFIC PROTEIN - HOMO SAPIENS (HUMAN), 678 aa.	0	13
3585	cg43966200	530	CTCAATTGTTTAT ATATATTTTTTT [gap]ACAAAGTTTT AACCTTTTGGAA AAAC	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60349 KIAA0610 PROTEIN - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	13
3586	cg43966200	733	ATTTTATTCATT TTAAATCAAAGA G/AJACCATCCA TTTCCTAACAAA CAGG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60349 KIAA0610 PROTEIN - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	13

3587	cg43966200	817	CAGTCTTCCCT GTTTGAACAAG TT/CJTITTTGAG AATCTTAGTTTT AGTT	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60349 KIAA0610 PROTEIN - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	13
3588	cg43975253	415	AACAGTAGAGTT GTGCAATATGGA T[G/A]TTTCTTAC TACAAGAAAAAA ATTAT	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60898 FIM PROTEIN - HOMO SAPIENS (HUMAN), 1379 aa.	0	13
3589	cg43975253	52	TGGGTGATGCA GAAAGCCACAAA TT/GJTAAAAGG ACACTAAGGTTT TAATA	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60898 FIM PROTEIN - HOMO SAPIENS (HUMAN), 1379 aa.	0	13
3590	cg43975253	54	GGGTGATGCAG AAAGCCACAAAT TTT/GJAAAAGGA CACTAAGGTTTT AATAAG	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60898 FIM PROTEIN - HOMO SAPIENS (HUMAN), 1379 aa.	0	13
3591	cg43929104	2930	ACAAGAGGAAGT GCCTGCGGGT CCT/CJTITTTAG AAGCTTTGTGGG TTGATT	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3592	cg43929104	3069	GTCAGTATTCA GGTTCTACATT TT/gapJATCTGTA AAATGTGACTTT TTTTTT	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3593	cg43929104	3086	CTACATTTTATCT GTAAAATGTGAC T/gapJTTTTTTTT TTTTATCACACA GAA	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14

3594	cg43929104	3098	TGTAAATGTGA CTTTTTTTTTT T/gap]TATCACA CAGAAGTAAAT GTTGC	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3595	cg43929104	3099	GTAATGTGAC TTTTTTTTTTTTT T/gap]ATCACAAC AGAAGTAAATG TTGCT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3596	cg43929104	3099	TAAATGTGACT TTTTTTTTTTTTT gap/]TATCACAAC AGAAGTAAATG TTGCT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3597	cg43929104	367	AGCGAGCCGA GTTTGAGGCAGC GC[C/gap]TAGCG GTGAATCGGG CCCTCACCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3598	cg43929104	3568	CATTTGATTCT GAAAAGAAAGCT G[G/gap]CTTTGC CCATTTCTTATTA AAAAAA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
3599	cg43933104	1960	GCATACCTCTGC AATGTTGTTCTTT [gap/A]AAAAAG CATGGATTGCAT TTATAT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31841 KIAA0668 PROTEIN - HOMO SAPIENS (HUMAN), 1085 aa (fragment).	0	14

3600	cg43933104	1966	TCTGGCAATGTT GTTCTTTAAAAA [gap/A]GCATGGA TTGCATTTATATA GTGT	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31641 KIAA0666 PROTEIN - HOMO SAPIENS (HUMAN), 1085 aa (fragment).	0	14
3601	cg43948117	2921	ACCTGTCAAGTG TCAACCCATACC CT/C]GCAGAAG GCATGGGCTGC CACTCGG	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15040 KIAA0329 - HOMO SAPIENS (HUMAN), 1411 aa.	0	14
3602	cg43949523	136	AGCGTGGTGTT C AAAGGCTTTTAG C/C]gap]TCATCT CATATCAGTCTA GTCAGTG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15035 KIAA0321 - HOMO SAPIENS (HUMAN), 1542 aa (fragment).	0	14
3603	cg43968223	164	GGCATCTCTTAG C GCGGGCAGGAC GG[C/gap]CCCCC CAGGCTCAACTC AGGACAAC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment).	0	14
3604	cg43968223	218	AACGGGACTGA C GCGGGCCCATG GCC[C/gap]TCGG CCTGTGGCCACT GAGCTCCGC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment).	0	14
3605	cg43968223	388	TCCATGGCTCAG G CATCGTCCTTCT G[G/gap]CTTCCC AGCCCCGGGCC GAACGTC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment).	0	14
3606	cg43991855	247	GCCTCTAAGTTT A AGCCCTGCAACC A[A/gap]AGAGTT CCTCCAGGGAA GGAACGCT	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15037 KIAA0323 - HOMO SAPIENS (HUMAN), 724 aa (fragment).	0	14

3607	cg44018598	473	GGCAGTCTAAA TAGCAAGTGCTT C[C/gap]ACAAAA ATAAAAAAACG ATAATGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0	14
3608	cg44018598	592	CTATTCAGCTGG GTAATATTTTGAT [gap/T]GTTTATCA TGTGCACTTGCT TGCT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0	14
3609	cg44022133	4398	TATTATTAATGA TGTGGTCTATGG [A/gap]AAAAAAA TAAAAATCTGAC TTAGT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75158 KIAA0670 PROTEIN - HOMO SAPIENS (HUMAN), 1280 aa (fragment).	0	14
3610	cg43298473	3230	CAGCAGTTTGCA GTGGGGTAAGG AG[G/gap]CCAAG CCCATTTGTGTA ATCACCCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBL-NEW- ACC:AAD32135 CYTOSOLIC PHOSPHOLIPASE A2 BETA - HOMO SAPIENS (HUMAN), 1012 aa.	0	15
3611	cg43936094	85	CAACATTATTTT ATCATAAAAGTTI C/AJAGCAAATAA AACTATATACAA GATC	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBL-NEW- ACC:AAC62018 P53 TUMOR SUPPRESSOR-BINDING PROTEIN 1 - HOMO SAPIENS (HUMAN), 1972 aa.	0	15
3612	cg43149413	3078	TTGCCACGTA CCCAGGTCTGG CT[G/gap]GGGCC CAGGCCCGGAT GCAGAGGCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16
3613	cg43149413	3101	CTGGGGCCAG GCCCGGATGCA GAG[G/gap]CCTG CAGGGCCTCTGT CAATTGTAC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16

3614	cg43149413	3135	GCCTCTGTCAAT TGACGCGCCAC CIG/AJAGTGCCTT CAACACAGCTTG TCTCT	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16
3615	cg43149413	3148	GTACGCGCCAC CGAGTGCCTTCA AC/AJCAGCTTG TCTCTTGCCTGC CACTGT	A	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16
3616	cg43149413	3277	GTAAATATGTAC ATTTCTCAGGCT A[G/gap]GGCCAG CAGGGCTGCC CGAGTCTG	G	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15169 AXIN - HOMO SAPIENS (HUMAN), 900 aa (fragment).	0	16
3617	cg43928515	1062	GTGAAGTAGCTG AACAAAAAAGCTT A[A/gap]JAGAGAT TGCATGTCAATT TTTAAGC	A	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3618	cg43928515	16	TTTTTTTTTTTT TTT/CJTAAATTTA GGAAGATTTTAT TTTT	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3619	cg43928515	214	CACCGGTGTCC TCCCTCCACCT G[C/T]GTATGGG GTTTACTGTTATA GAATT	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3620	cg43928515	2886	AACATACAAAAC TTTGTTTTTTTTT T/gap/AAATATATA TACACAGTACAA GGCTG	T	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16

3621	cg43928515	3260	TGGGGAGGAAT GAGACTGGCCC CATC/TJGCTGCG GCAAAAGCAAAC TGGGCTT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3622	cg43928515	3265	AGGAATGAGACT GGCCCATCGCT G/C/TJGGCAAA GCAAACTGGGCT TGAGGC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
3623	cg43934724	428	AGAGGAATCTAG CGCGTCTGGCA GG[G/gap]CTGCG CTTCTTCACCTG CCCCCTAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15058 KIAA0350 - HOMO SAPIENS (HUMAN), 917 aa (fragment).	0	16
3624	cg43945577	2338	CCAAGAAACAGA AGACAAGGGCG AC[G/T]TGAGGA GGAAGGGGACA GTTCGAGT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
3625	cg43945577	2581	CACTCTGCTGAA CAGAAATTTATTT [C/T]TGAGTCAAA TATAATTTATTAT TAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
3626	cg43945577	2696	CGTTTGCAAGAA GAGTCCAGTTG A[C/T]GTGGTGT TGGTCCATGGC GGGGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
3627	cg43945577	2744	GGTACCCCTAGG GATTCATCTGTT TT[C/T]TTCACCT CCCTTTCATCT GAGATC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16

3628	cg43945577	2784	CATCTGAGATCC TGCTGGAAACCA C[G/A]GCAACCT GTATCCACTATT AGAGG	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
3629	cg43955093	1087	TCTCCTTTGTCA GGAATGCAAAA A[A/gap]TCACAC ACTCCTACCAGG TGTTTA	A	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3630	cg43955093	1257	GCTCAGTTTGG GTACACATCATT TT[<i>gap</i>]CTTGCA GTATTTCTAAAA GCTTIGC	T	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3631	cg43955093	1277	CATTTCTTGCA GTATTTCTAAAA G[C/gap]TTTGCC AGAGTCAAAAAT CCAAGTT	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3632	cg43955093	1288	AGTATTTCTAAAA GCTTTGCCAGAG T[C]CAAAAATCC AAGTTGGATT TAAG	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3633	cg43955093	1295	CTAAAAGCTTTG CCAGAGTCAAAA AT[C]CCAAGTT GGATTCTAAGCA GCCTT	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
3634	cg43955093	1450	CTCATGTACTA ACAGGCTGTAAC T[G/C]ATCAGCTG GATTAAGGAAA AAGCT	G	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16

3635	cg44014894	631	TTTCTACATCTG CAAGACAAAGTTT G[gap]CTTCAG CCATTATGTATA GATAGAT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC: AAC51331 CREB-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 2442 aa.	0	16
3636	cg43055918	353	ACATTCTCCCTT GAGGGAAGAAAA A[gap]GTGATT ATTAAATATGA GTAAAA	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC: P42694 HYPOTHETICAL PROTEIN KIAA0054 - Homo sapiens (Human), 1942 aa.	0	17
3637	cg43936393	383	AAACAAGTTTCA GTAAAAAGAAAA A[gap]A]CTAAAA CAACACTGAAG TAGAGTT	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC: AAD22032 THYROID HORMONE RECEPTOR-ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa.	0	17
3638	cg43936393	398	AAAAAGAAAAAC TAAACAAACAC TGT]AAGTAGAG TTTTGTAATACA ACTG	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC: AAD22032 THYROID HORMONE RECEPTOR-ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa.	0	17
3639	cg43936393	719	CTTAGGGAGGT GAGAACCTCCTT G[gap]CATATG CCCTACCTTAAT CTGAGCT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC: AAD22032 THYROID HORMONE RECEPTOR-ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa.	0	17
3640	cg43947963	156	AGCACAGAGACT GGGAGGGGTT GA[gap]C]CCCCA CTCCAGAACACC AATACCTC	gap	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC: Q14667 KIAA0100 (HUMAN COUNTERPART OF MOUSE E1 GENE) - HOMO SAPIENS (HUMAN), 2092 aa.	0	17
3641	cg43947963	86	ATATCCTACGGG GAAGGGTAGGG GA[C/gap]CCATG GCCAGCCCTGG CTCCTACTG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC: Q14667 KIAA0100 (HUMAN COUNTERPART OF MOUSE E1 GENE) - HOMO SAPIENS (HUMAN), 2092 aa.	0	17

3642	cg43949150	166	CTGTCTGGAGG GGCTGAGGCTTC GG[C/gap]CTCGG GAGGCTGAAGC AGGAGGCAG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75965 SPLICING FACTOR PRP8 - HOMO SAPIENS (HUMAN), 2335 aa.	0	17
3643	cg43949150	167	TGTCTGGAGGG GCTGAGGCTTCG GC[C/gap]TCGGG AGGCTGAAGCA GGAGGCAGG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75965 SPLICING FACTOR PRP8 - HOMO SAPIENS (HUMAN), 2335 aa.	0	17
3644	cg43964911	1457	TAGCTCACAGGT GAGGGGTTTA GG[C/G]CCCTC TAGGAGCGCC TGAGGCCA	C	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q12767 HYPOTHETICAL PROTEIN KIAA0195 - Homo sapiens (Human), 1356 aa.	0	17
3645	cg43980727	406	CCTCACTCCAGC ACACTCAGCCAG GTTGJGCTGGC AAGATGACACAT TTCTCTG	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P38432 P80-COILIN - Homo sapiens (Human), 576 aa.	0	17
3646	cg44023800	167	CCAGACAGACGA GGCCCGGGAAG GG[gap/C]AGCCC AGGGGACTGGG GTCTCTCCT	gap	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14521 GIANT LARVAE HOMOLOGUE - HOMO SAPIENS (HUMAN), 1015 aa.	0	17
3647	cg43957585	101	CCACAGACAGG CCTAGTATGGCT AC[G/A]GTACCGT ATATAAAAGACA ATTGCT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13433 ESTROGEN REGULATED LIV-1 PROTEIN - HOMO SAPIENS (HUMAN), 752 aa.	0	18
3648	cg43979984	189	TTAACTTTGGAC AACTTAAACTTA TTCTAGTGACAT TGCTGTCTAATA ATCA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92539 HYPOTHETICAL PROTEIN KIAA0249 - Homo sapiens (Human), 896 aa.	0	18

3649	cg44001787	1080	GCGCCTGCAGC ACGTTGCCTCCA GG[G/gap]CCCAG CCTCCAGAAAGC CTCAGAGC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15311 RLIP76 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa.	0	18
3650	cg44001787	185	TGCTGTCAATT GCAATGCCTGG GG[C/gap]CAAGC CAGGCCAGTGG ACTTGTGTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15311 RLIP76 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa.	0	18
3651	cg44001787	324	ATGGGCTTGTGG AAGGGAGGCAT GC[C/gap]GCCGC CAGCATGCATGC CAGGGGTC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15311 RLIP76 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa.	0	18
3652	cg44001787	719	AAAGTGAACGTA CTGAGACCGACA G[G/gap]ACAGCA AGAAAGGCATTG CACATT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15311 RLIP76 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa.	0	18
3653	cg42555863	2867	GGAGAGGAGGCC CCATGCCAGGCC TG[G/gap]CTGAG CCCGAGATTCCG TCCTCCCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14526 KIAA0290 - HOMO SAPIENS (HUMAN), 906 aa (fragment).	0	19
3654	cg42718880	95	GCAGTTTGGGG GTGGGGGACAA AGA[C/gap]CCCC CTCCAGCTCCTA AACTGGGTC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43360 F21856_2 - HOMO SAPIENS (HUMAN), 679 aa.	0	19
3655	cg43917942	2499	AGATAGCGAGAT CTAAATCTCTGC C[gap/A]AAAAAA AAAAAAAACCTT AAAAATT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19

3656	cg43917942	2500	AGATAGCGAGAT A CTAAATCTCTGC C[A/gap]AAAAAA AAAAAAACTTA AAAAATTA	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
3657	cg43917942	2514	AAATCTCTGCCA A AAAAAA A[A/gap]CTTAAAA ATTAAAAACACA AAGAGC	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
3658	cg43917942	2831	CTCCCGCCCTG G GCTCAGCTCCCG CG[G/gap]CCCCG CCCGTCCCCCT CCCAGGAC	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
3659	cg43927434	97	TCITTTTAAGGC G AAGCACCCGCA G[G/gap]TCAAGC CCCGCCCGTC CCCCAGCC	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92797 SYMPLEKIN - HOMO SAPIENS (HUMAN), 1142 aa.	0	19
3660	cg43975166	3601	CCGCTGCTGCTG C GGAAGACAGCA G[C/T]CTTGCG CGTCCACAATC CTGCGC	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00267 SUPT5H PROTEIN - HOMO SAPIENS (HUMAN), 1087 aa.	0	19
3661	cg43982840	541	ATTACTGAAGGA C AATAGAAAACTA T[C/A]TTACAAGT AGAACAGCCATA GACAA	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O15063 HYPOTHETICAL PROTEIN KIAA0355 - Homo sapiens (Human), 1070 aa.	0	19
3662	cg44022290	177	AGAGGGGGCCT gap CCCCCTGAGGC CCC[gap/C]ATTG GCCCCCTCCCA GGTATCCAAG	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14145 KIAA0132 PROTEIN - HOMO SAPIENS (HUMAN), 624 aa.	0	19

3663	cg43919691	157	AACGTCTAGGGG TGAGGGGCTGT GG[C/gap]CTCCA GTCGGCCCCAC AGCCTTTGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3664	cg43919691	158	ACGTCTAGGGGT GAGGGGCTGTG GC[C/gap]TCCAG TCGGCCCCACA GCCTTTGAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3665	cg43919691	349	ACTCGGCGGTG GCCCGGGGCTG CGC[C/gap]CAGG ATAGTGTATC AAATGTGAC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3666	cg43919691	350	CTCGGCGGTG CCCCGGGCTGC GCC[C/gap]AGGA TAGTGTATCA AATGTGACA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3667	cg43919691	456	TTGTCTCTCATG GCTTCTCTCGGA G[gap]CTACCCG AAGTTGGGCTG GATAACG	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3668	cg43919691	68	TTTTTTTTTTTT TTTTTTTTTTTTT TTCCGGGCACCA ACGTTGGTTTA ATG	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
3669	cg43921004	591	AGATGTCACAAA TTATAGCGGCAC C[C/gap]TTCAGAT TTAGGGTGAGTT TCTGA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60506 GRY-RBP - HOMO SAPIENS (HUMAN), 623 aa.	0	20

3670	cg43921598	2636	AAAGCACCCGTA GTAGCAAAAAACA T[A/gap]AAACAAA TAAAGTTCCCC CACATC	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43439 MTG8-LIKE PROTEIN (MTG8 RELATED PROTEIN) (EHT) - HOMO SAPIENS (HUMAN), 604 aa.	0	20
3671	cg43958732	4278	TCTAAATAAATTGT CTGTATTGTGCTT T/AJAATGTAAAA AAAAAAAAAAAA AAA	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45752 HYPOTHETICAL 112.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 1005 aa (fragment).	0	20
3672	cg43958732	4281	AAATAAATTGCT GTATTGTGCTTA AT/AJGTAAAA AAAAAAAAAAAA AAAAA	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45752 HYPOTHETICAL 112.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 1005 aa (fragment).	0	20
3673	cg43958732	4283	ATAAATTGCTGT ATTGTGCTTAAT GT/AJAAAAAAA AAAAAAAAAAAA AAAAA	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45752 HYPOTHETICAL 112.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 1005 aa (fragment).	0	20
3674	cg43317567	2185	TTCATCTCATT CCAAATTTGGTT C[G/C]AAAGCAC AGTACCTAAAA AGTCA	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60318 MCM3 IMPORT FACTOR (KIAA0572 PROTEIN) - HOMO SAPIENS (HUMAN), 1872 aa (fragment).	0	21
3675	cg44019279	4170	ATGCTTAATACG TGTCGGTCATAT A[C/T]AGTATTGA ATTTTACTGTAT AGTA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14149 HYPOTHETICAL PROTEIN KIAA0136 - Homo sapiens (Human), 950 aa (fragment).	0	21
3676	cg43936123	163	ACGCTAGCACAG GGCCTGCCGCA GG[G/gap]CCTGG ATCGGGCAAC GCAGGCGCC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60289 KIAA0542 PROTEIN - HOMO SAPIENS (HUMAN), 968 aa.	0	22

3677	cg43938220	185	AGTCTCACTCAG AATATTTAATTGG [C/T]TAAATGA GAAATGAATCT TTTT	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75132 KIAA0637 PROTEIN - HOMO SAPIENS (HUMAN), 1171 aa.	0	22
3678	cg43959772	3077	AGGGGTGCGTA GGTAATGGCGTC GG[G/T]ACCGCT CGGTCGGCTGTG GAGGGTA	G	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15081 KIAA0376 - HOMO SAPIENS (HUMAN), 885 aa (fragment).	0	22
3679	cg43959772	561	AATATTTACTAGA ACAACATTTAAAI C/A]GTATCGTCG GTCCGCAGAAG CCTGG	C	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15081 KIAA0376 - HOMO SAPIENS (HUMAN), 885 aa (fragment).	0	22
3680	cg43959772	882	AGGCAAGCCTCT AGATAGGCGGG GC[C/gap]AAGCC CTCCCCGTGCC ACCCTCTT	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15081 KIAA0376 - HOMO SAPIENS (HUMAN), 885 aa (fragment).	0	22
3681	cg43959772	886	AAGCCTCTAGAT AGGCGGGGCCA AG[C/gap]CCTCC CCGTGCCACC CTCTTTCCC	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15081 KIAA0376 - HOMO SAPIENS (HUMAN), 885 aa (fragment).	0	22
3682	cg43955358	2322	AAACAACCTTGA GCCTGTGCATAT A/A]gap]GGCATT TACATATGATGA CCTTGCA	A	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4- GLUCANTRANSFERASE) AMYLO-1,6- GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] - Homo sapiens (Human), 1515 aa.	0	1 (1p21)

3683	cg43955358	2360	TGATGACCTTGC ATCCTATAATAC A[A/gap]GTAATT GCATACCTTAATA TCTGTAA	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4- GLUCANOTRANSFERASE) AMYLO-1,6- GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] - Homo sapiens (Human), 1515 aa.	0	1 (1p21)
3684	cg43955358	77	CACAGAGGTAAC AATGACATTTGC C[C/T]ACTAGACA CAGTAGTTCAAG ACATA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4- GLUCANOTRANSFERASE) AMYLO-1,6- GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] - Homo sapiens (Human), 1515 aa.	0	1 (1p21)
3685	cg43925474	1066	CACAGATCAATA CCACCTTGACTT G[T/G]TGACCCA GAGAATTCTAAT TAGATT	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)
3686	cg43925474	1303	TCTCTCCCAATT AAAAAACAAGA G[T/gap]TTTTTG CTAGCTTGACAA TTTTAT	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)

3687	cg43925474	2277	CGGCTTTTATAA GAAAAAAAAAAAA A[A/gap]GACGAA TCTGTAATGAAG AAAAAAA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)
3688	cg43925474	489	CATACTTTAATAT TATGTTGGTCCA C/TJGGGGTATAC ACATTTTAACAAA AGA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)
3689	cg43925474	971	ATGGAAGAAAA CAAAACAAGCAT C/TJTTTCAAGA AGAAATGAATTG GATAT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	1 (1p32)
3690	cg43973809	2511	CCCCACCCCA GCCTGGGGGTC TGGT/GJCTGGG GCAGGGATTGCT CAGTGGAA	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47736 RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP) - Homo sapiens (Human), 663 aa.	0	1 (1p38.1)
3691	cg43973809	2559	GAAGCAGGACT GGGGGTCTGGC GTGT/CJCCCTC CCTGGGCCTCCA TCACCC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47736 RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP) - Homo sapiens (Human), 663 aa.	0	1 (1p38.1)
3692	cg43973809	3160	CCGAGAGTCCA GGCCTTGCCTCC CC[C/gap]GACCG CCATGGAGGGG GCAGCCCCGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47736 RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP) - Homo sapiens (Human), 663 aa.	0	1 (1p38.1)

3693	cg41573476	3166	AGAATAATACCTA TTATAAGTTAGG T(gap)/TGGACAAAT GATGTTGATTAT GTAAGG	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)
3694	cg41573476	610	CCCTCCTACTCA GGATAAGACTTT C(G)/AATTCTCC GGAGCTGAAAAA GGATC	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)
3695	cg41573476	611	CCTCCTACTCAG GATAAGACTTTC G(A)/C/ATTCTCCG GAGCTGAAAAAG GATCC	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)
3696	cg41573476	612	CTCCTACTCAGG ATAAGACTTTTCG A(A)/TTTCTCCGG AGCTGAAAAAGG ATCCT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)

3697	cg41573476	613	TCCTACTCAGGA TAAGACTTTTCGA ATTATCTCCGGA GCTGAAAAAGGA TCCTG	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47712 CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) LYSOPHOSPHOLIPASE (EC 3.1.1.5)] - Homo sapiens (Human), 749 aa.	0	1 (1q25)
3698	cg43117949	37	TCTGTCCACCAG CTGAGAAGGACA A[gap]/A]GGGCGG AAGGCAGCTGCA CAGAGCA	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10745 INTERPHOTORECEPTOR RETINOID- BINDING PROTEIN PRECURSOR (IRBP) (INTERSTITIAL RETINOL- BINDING PROTEIN) - Homo sapiens (Human), 1247 aa.	0	10 (10q11.2)
3699	cg43117949	4091	TATATATGTATAT ATATATGGCTTT CTTCAATAACCA CCTAAATTTTAAAC AAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10745 INTERPHOTORECEPTOR RETINOID- BINDING PROTEIN PRECURSOR (IRBP) (INTERSTITIAL RETINOL- BINDING PROTEIN) - Homo sapiens (Human), 1247 aa.	0	10 (10q11.2)
3700	cg43920702	134	GGCTCTTGTCAC CCACTCCTAACC C[gap]/C]TCTGCA GATTCCTCCGG GATGCTC	gap	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3701	cg43920702	338	GAAACTAGGATT TCCAAATCTGG A[gap]/A]GCAGGA CTGAAGTTATTT GGGGCAG	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3702	cg43920702	36	TTTTTTTTTTTT TTTTTTTTTTTTTAA TTTTTTTTTTTAAAC AAATGTATTCAT C	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)

3703	cg43920702	439	AGGGGCTGAGT GGTCCTAGGCTC CC[ap/C]GGGCT GGAGGTGGGAC CTGTGCTCC	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3704	cg43920702	464	GGGCTGGAGGT GGGACCTGTGCT CC[ap/C]TTGGG TTAAGGGTGAAA CCTCAGCT	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3705	cg43920702	812	TGGGCTCAGAGT TGGGGGACTAA GG[G/ap]CGGAG CCTGGGTCCCCA CAAGCGGT	gap	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00632 MENIN - HOMO SAPIENS (HUMAN), 610 aa.	0	11 (11q13)
3706	cg43269831	365	AAGAACTGTGGC CCCAGGATAAAA A[A/G]AATACAGT GAGAACAAAGAC CTCAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P15586 N-ACETYLGUCOSAMINE-6- SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6- SULFATASE) - Homo sapiens (Human), 552 aa.	0	12 (12q14)
3707	cg43950650	382	AGTAAAGGGCG TTCCAAGTCTTG Algap/TTTTTTTT TTTTTTTTTTTT AGCAG	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99700 ATAXIN-2 - HOMO SAPIENS (HUMAN), 1312 aa.	0	12 (12q24)
3708	cg43950650	402	CTTGATTTTTTT TTTTTTTTTTTTTg ap/TJAGCAGTAAT AGCAGCAAGAAT CACT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99700 ATAXIN-2 - HOMO SAPIENS (HUMAN), 1312 aa.	0	12 (12q24)

3709	cg43979800	1019	TCCTTCTTCCAG CCACCTGGAAAA A[C/T]GTTACAG AGAGTTATAGTG GTTAC	C	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3710	cg43979800	1116	AATTAATCTGCT AATATCTATTACC [G/A]CAGAAATAG TGTTAGAGGTAG TTTA	G	A				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3711	cg43979800	1147	ATAGTGTTAGAG GTAGTTATTAA [G/C]AGGCGTTT TAAATCATCCC ACTC	G	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)

3712	cg43979900	1152	GTTAGAGGTAGT TTATTAAAGAGG C[G/A]TTTTTAAA ATCATCCCACTG ATCAT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3713	cg43979900	157	AACCACTGAATC ACACAACATGGA C[C/A]AATCTCAA ATCATTATGCTG ATGGA	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3714	cg43979900	292	ATTCCTATCAAT GGCTGCCAACA TTT/CIGGGAGTG AAAGGAACGTGAC TGAGCA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)

3715	cg43979900	470	AAATAAAATTACA CCTCTATAATGT TTTC/GTTTTAAA AAATATTAGATA CATCA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3716	cg43979900	616	TAGCTAAGCCTA TGTTAGACTCTT A/C/TAAATTCCT AAATAGTAGAAT TAGTT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
3717	cg43973740	669	AGGTCCTGAAGG TGAGTGTCGGGA G/C/gapJTGCTGG GTAAACACATC ACAGGTA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q61123 MATERNAL EMBRYONIC MESSAGE 3 (MEM3) - MUS MUSCULUS (MOUSE), 754 aa.	0	16 (12q12)
3718	cg44928323	10345	TAAATTTGGTTT GATACTCAGAA A/TJAAACAAGATT TAATTTTTTAAAT TT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0	17 (17q11.2)
3719	cg44928323	11285	GACTTGTTAAAG AGGAAACCAGGA A/C/TTCAGTCAT GTTTTTGTCCTG GATAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0	17 (17q11.2)

3720	cg44928323	11963	ATGATAACTTAC TGTCCTTTCCAT C/C/TJGGGCCTA A/C/TJGGCAGT T/CCTTT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0	17 (17q11.2)
3721	cg44028807	2058	GGAGGAAGAAG CCCCGTTTCCAG GG[C/gap]ATCCG CAGCCCAGGGT AGGGAGAAA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14397 GLUCOKINASE REGULATORY PROTEIN (GLUCOKINASE REGULATOR) - Homo sapiens (Human), 625 aa.	0	2 (2p23.3)
3722	cg43960198	2178	CGGCCGGGCC GGGCTGAGGT CAG[C/gap]CTCA CTGCCTGCTTAT TGCCTCTTT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3723	cg43960198	2474	TGCAAGGCTGG CAGCCCCACC CCC[gap]CJACCC CCCAGGCCGCC TTGAGAAGCA	gap	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3724	cg43960198	2491	CCACCCCCACC CCCCAGGCCGC CTT[gap]GAGAA GCACAGTTTAAAC TCACTGCCG	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3725	cg43960198	2505	CCAGGCCGCCCTT GAGAAACACAGT TT[gap]AACTCAC TGCAGGCTCCT GAGCCTG	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)

3728	cg43960198	2700	GGCCCCATGCCT CTCCTCCCTCTC T[<i>gap</i>]/C]GGCAGG GCCCATCCTGG GCAGAGG	gap	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3727	cg43960198	2708	TGCCTCTCCTCC CTCTCTGGCAGG G[C]/ <i>gap</i>]CCCCATC CTGGGCAGAGG GGCCTGGG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3728	cg43960198	2711	CTCTCCTCCCTC TCTGGCAGGGC CC[C]/ <i>gap</i>]ATCCT GGGCAGAGGGG CCTGGGGCT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3729	cg43960198	2734	CCCATCCTGGGC AGAGGGGCCTG GG[G]/ <i>gap</i>]CTGGG CCCAGAGTCCAG CCGTCCAG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
3730	cg43956384	2427	GTACCTACTGGA GCCGCAGAAGG GA[A]/ <i>gap</i>]GTCCA CTCAGTCACATC CAGAAAAA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P13866 SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 664 aa.	0	22 (22q13.1)
3731	cg44025634	3380	TTGTGGGGGAA AACTATTATTTT [T]/GTGCAAAATGG AAAGATCAACAG ACTA	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P00450 CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE) - Homo sapiens (Human), 1065 aa.	0	3 (3q21)

3732	cg44025634	3873	TGGCAGATGTCA C CATGAGTAGAAT T[C/T]CTGCCCCAG CCTTAACTGCAT TCAGA	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P00450 CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE) - Homo sapiens (Human), 1065 aa.	0 3 (3q21)
3733	cg44025634	3985	GACACATGGTTG G TGAATACAATGA T[G/A]TATTCTT TATTTTCACATAC ACTC	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P00450 CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE) - Homo sapiens (Human), 1065 aa.	0 3 (3q21)
3734	cg44025634	4039	TAAAGAGGAAG gap AGTACACATCAA C[ga]/A/AAAAAT GGAAACAAGGCT TTGGCTG	A	gap		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P00450 CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE) - Homo sapiens (Human), 1065 aa.	0 3 (3q21)
3735	cg43955813	3033	TATATGTATGTAT G ATATGTATATGT G[ga]/AAAAACAG TTTGATAGTTG GAATA	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q03188 CENTROMERE PROTEIN C (CENP-C) (CENTROMERE AUTOANTIGEN C) - Homo sapiens (Human), 943 aa.	0 4 (4q12)
3736	cg43993542	322	CGGTTTCTGGG C CTGGGCTTTCTG C[C/gap]TTACTC ACTCCTTCTCCC TCCTTCT	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16471 PROLACTIN RECEPTOR PRECURSOR (PRL-R) - Homo sapiens (Human), 622 aa.	0 5 (5p13)
3737	cg43993542	449	CTGATGTGGCAG G ACTTTGCTCCCT G[G/A]CAAAACTA AAGAACTCTCCT ATTCA	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16471 PROLACTIN RECEPTOR PRECURSOR (PRL-R) - Homo sapiens (Human), 622 aa.	0 5 (5p13)
3738	cg43952287	161	TGTAAAAAAGCA G AACAGTGCCAAAT G[G/gap]CCCACTT TGGTAAAAACAC ACAGTGT	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P54136 ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19) (ARGININE--TRNA LIGASE) (ARGRS) - Homo sapiens (Human), 659 aa.	0 5 (5pter)

3739	cg43952287	92	TTTTTTTTTTTT TTTTTTTTTTTC /TCTGGTTGACA AATTTCTTTACT TA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P54136 ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19) (ARGININE-TRNA LIGASE) (ARGRS) - Homo sapiens (Human), 659 aa.	0 5 (5pter)
3740	cg43952287	93	TTTTTTTTTTTT TTTTTTTTTTTC /TJGGTTGACAA ATTTCTTTACTT AT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P54136 ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19) (ARGININE-TRNA LIGASE) (ARGRS) - Homo sapiens (Human), 659 aa.	0 5 (5pter)
3741	cg4395232	7346	GAGAGAAATTACA CTTTTTTTTTTTT gap/TJAAGTGCC GTGGAGGCCCTT GCTTCG	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54253 ATAXIN-1 (SPINOCEREBELLAR ATAXIA TYPE 1 PROTEIN) - Homo sapiens (Human), 816 aa.	0 6 (6p23)
3742	cg42907760	2137	CTGCCCTGCTCT GTGACAGAGCCT Ggap/GJAGACTT GGAGGTCCAGA GGCCCCCCC	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0 9 (9p12)
3743	cg42907760	2149	GTGACAGAGCCT GAGACTTGGAG GTgap/GJCCAGA GGCCCCCCCACC AACCAGCCCC	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0 9 (9p12)
3744	cg42907760	2174	CCAGAGGCCCC CCACCAACCAGC CCgap/GJAGCCA CTGTTGCTGGCT GTGTCGTT	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0 9 (9p12)
3745	cg42907760	2174	CCAGAGGCCCC CCACCAACCAGC CCgap/GJAGCCA CTGTTGCTGGCT GTGTCGTT	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0 9 (9p12)

3746	cg42907760	2272	CTGTTGCCACTT ACGGGGGCTGG AG[A/gap]AGGCC TGGATAAAGACA GAAGGCGG	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)
3747	cg42907760	2273	TGTTGCCACTTA CGGGGGCTGGA GA[A/gap]GGCCT GGATAAAGACAG AAGGCGGG	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)
3748	cg43958842	632	CCATTGGAATTT CAATCCAAGCAG C[A/G]TATTTTAC ACACACCTGAAG GAAAT	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P41252 ISOLEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS) (IRS) - Homo sapiens (Human), 1266 aa.	0	9 (9q21)
3749	cg42373006	59	TACACAAATGAA GTCCTTGGTGGA T[G/A]AATTC AAG TCAAAACAAATA ATAGA	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60267 KIAA0512 PROTEIN - HOMO SAPIENS (HUMAN), 632 aa.	0	X
3750	cg43921793	1986	GGATCTGCAGCA C GCTGGGCTGCC TC[C/gap]GATGG TGGAGAGCTGG ATGAAGGCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment).	0	X
3751	cg43921793	42	CGACTTTTTTTTT TTTTTTTTTTTTTT GTCAGACTTTTCA GCCTTTATTACAA A	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment).	0	X

3752	cg43921948	3315	AACAATGTGATT GGATTCCTTTAT GIG/CJCAAAATC GAGAGAAGCTG CCATCCA	G	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3753	cg43921948	3494	GAATGTTAGCCA TGACTTGGGCTT TTC/GJTGAAAGTT GGCTATAATTTCTCTAT	C	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3754	cg43921948	3989	TTGATGATGTGG AAATGCTGCAGG ATT/CJTAAATAAC TTGAAGAGCCTT TATAG	T	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3755	cg43921948	4592	TATGGTACTAAG GAAGTCCTGTTT TTT/gapJCAAAAAT GGAAGCCCACTT CTCAGA	T	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3756	cg43921948	4665	AAAAGTGAAGGG GAAACACACACA CJA/GJCAAAAAA CAAGTATTTGGC TTGTC	A	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X

3757	cg43921948	4673	GGGGAACACA CACACACAAAA AA[<u>gap</u>]/A]CAAGT ATTGGCTTGTC ACAGGAAT	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3758	cg43921948	4717	CAGGAATCTGAT TGCAATTAAGTGA A[<u>gap</u>]/GGATTA TTTAGAATATGTT AATGCA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3759	cg43921948	5894	CAGGTGATGTCT GGTCAACTGGCC T[<u>A</u>]/G]CCTTCAGC TAGAATCCTGTT AGGTC	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3760	cg43921948	5975	CTTGGTAATCTT CCATCCACTGCC C[<u>C</u>]/A]TGACCCTG TTCCCTGTCTAT AAATC	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X
3761	cg43921948	6017	CTATAAATCCCC AGTTTCCATGG T[<u>G</u>]/A]TATTCAGA GCTGAGTCCAGT CTCTC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0	X

3762	cg42886508	1928	TTCTCCAGTCAG AGTAGATGATGA G[G/gap]CCCCATG CCCCCTCAGCCCC ACGCCCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76007 TRIPLE LIM DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 615 aa.	0	X (Xp11.2 3)
3763	cg43927750	276	ACTGTATTGAG ATGTCTTACTTG GT[G/gap]GAGACCAAT TAAACTATGACA TAAAA	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13496 MYOTUBULARIN - Homo sapiens (Human), 603 aa.	0	X (Xq28)
3764	cg43927750	631	ATTGAAATGCAT AAACACAATACT TT[G/gap]CAAGAAT ACGCTCAACACA TGTACA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13496 MYOTUBULARIN - Homo sapiens (Human), 603 aa.	0	X (Xq28)
3765	cg43277486	593	TCGCCAAGCAGA CACAGAAATCCC C[A/G]GTGTGGG GAATGCAGCAGC TCTGCC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa.	0	XY
3766	cg43061097	4045	TGATGCATGTTG GCTGAGATGATC A[T/G]GGAGATG AGTGACACCCAGA GCTCAC	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD39482 OLIGOPHRENIN-1 LIKE PROTEIN - HOMO SAPIENS (HUMAN), 814 aa.	0	
3767	cg43061097	4046	GATGCATGTTGG CTGAGATGATCA T[G/T]GAGATGAG TGACACCCAGAGC TCACA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD39482 OLIGOPHRENIN-1 LIKE PROTEIN - HOMO SAPIENS (HUMAN), 814 aa.	0	
3768	cg43273039	4922	ATAAATTAAATTT TATTGTGTAATA A/TJAAATTATTAC ATAAAATGTGTTT TT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75763 SYNAPTONEURAL COMPLEX LATERAL ELEMENT PROTEIN - HOMO SAPIENS (HUMAN), 1530 aa.	0	

3769	cg43273039	4924	AAATTAATTTTAA TTGTGTAAAAAA[ATJATTATTACAT AAAAATGTGTTTTT GA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75763 SYNAPTONEMAL COMPLEX LATERAL ELEMENT PROTEIN - HOMO SAPIENS (HUMAN), 1530 aa.	0	
3770	cg43277456	2654	GACCGACAGTC GTGAGGATGGC AGA[G/gap]CTGC TGCATTCCCCCA CATGGGGAT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa.	0	
3771	cg43277456	2673	GGCAGAGCTGC TGCATTCCCCCA CAT/CJGGGGATT TCTGTGCTCTGCT TGGCGA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa.	0	
3772	cg43291710	555	GACAGTCTGAAG CATTAAAAAATTC [G/A]TAAAAAACA GTAACACTGACA AAAT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA34522 KIAA0802 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	0	
3773	cg43916588	1102	GGTCCATGGTGT TCCAGAGTCCCC TIG/AJAGTTTCAG GTTCCAGCTGATG TAGAT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75150 KIAA0661 PROTEIN - HOMO SAPIENS (HUMAN), 1001 aa.	0	
3774	cg43916588	352	GCACCCAGGAT GAAAGCAGGGTT AG[G/gap]TCCAG GGACCCAGTAGA GCCTTGGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75150 KIAA0661 PROTEIN - HOMO SAPIENS (HUMAN), 1001 aa.	0	
3775	cg43918446	1527	CTAAAACTGAT TTGCAAACTTGA A[C/A]GTCTAGAT GTGTGTAGGAAG ATTTT	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0	

3776	cg43918446	1559	ATGTGTGTAGGA AGATTTTAAAT T/CJAGGCAAT GGTCTCTAAAGA GACC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0
3777	cg43918446	1570	AAGATTTTAAAT TTAGGCAAAATG G/gapJTCTCTAAA GAGACCAATTT GCTTC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0
3778	cg43918446	1926	TGTTTTCCCA GGAACCTATTGAT G/A/CJCTGAGGA GACTTGAAAAGA GACCTA	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0
3779	cg43918446	1930	TTTCCCAGGAA CTATTGATGACT G/A/GJGGAGACT TGAAAAGAGACC TAAAGT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0
3780	cg43918446	2125	TCTCCATGTGGA GTAGGTCAAAGT CT/CJCGTCCTC CCTGGCCAGGT GGAAGC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0
3781	cg43918446	444	CAAAAATAACA ATCCCAACAAGAG T/C/AJATGTTACC CATTCTTAGCCA TTAAC	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0
3782	cg43918446	529	TGTACCCCAACTG GGACCAATACA A/A/gapJCATGAG ACACTAGGGTGG CTGTGCC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0

3783	cg43918446	601	AAGGAACCTTTAT CATGGGCTGAGA GTTATAGATAGA TAGCTTAGAACA ACATT	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0
3784	cg43918446	655	AAAGTGGGTGCT TCTACATGAGGA CTT/gapTTTTTTC CCCCCAAGTAGA AAAATA	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0
3785	cg43918446	661	GGTGCTTCTACA TGAGGACTTTTT TTT/gapCCCCC AAGTAGAAAAAT AATTAAA	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35446 F-SPONDIN PRECURSOR - Rattus norvegicus (Rat), 807 aa.	0
3786	cg43920875	2433	GTTCTGACTCCC AGTACGGTGTG T[G/T]GCGCCGC TAGGATATCCTT GTCAAG	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46199 TRANSLATION INITIATION FACTOR IF- 2, MITOCHONDRIAL PRECURSOR (IF- 2MT) (IF-2(MT)) - Homo sapiens (Human), 727 aa.	0
3787	cg43920875	2434	TTCTGACTCCCA GTACGGTGTGT G[G/T]GCGCCGCT AGGATATCCTTG TCAAGG	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46199 TRANSLATION INITIATION FACTOR IF- 2, MITOCHONDRIAL PRECURSOR (IF- 2MT) (IF-2(MT)) - Homo sapiens (Human), 727 aa.	0
3788	cg43923595	310	CCGGCAGTCCCT GCCCAGTCCCTC C[G/C]TCTGCTTC CTCCCACTCTTC CACAT	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99467 LYMPHOCYTE ANTIGEN 64 PRECURSOR (RP105) - HOMO SAPIENS (HUMAN), 661 aa.	0
3789	cg43932090	19	TTTTTTTTTTTT TTTTT[G/T]AAGG TTCTCAAGAAATTT TATTATAA	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment).	0

3780	cg43934688	2862	GTCTTCATATGT CAACTACAGAAA A[A/G]AAAAAAAAA ATAGAAAATTGAA GGATT	A	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
3791	cg43934688	2863	TCCTCATATGTC AACTACAGAAAA A[A/G]AAAAAAAAA TAGAAAATTGAAG GATT	A	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
3792	cg43934688	4242	ACTTTTATGTCA TCGTAAAAAGCTG A/gap]AAAAAATC CCTTTGTTTCTAT TTAT	A	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
3793	cg43934688	4248	TATGTCATCGTA AAAGCTGAAAAA A[A/gap]TCCCTTT GTTCTATTATA AAAA	A	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
3794	cg43935504	70	ATTTAGCACAG TTAAATTTTTTTT T/GTGTAAACAC AAACAAGATAA TTTA	T	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15044 KIAA0335 - HOMO SAPIENS (HUMAN), 1263 aa.	0	
3795	cg43936083	239	AAGTCAACAGGG AAAGAAGTGGGT A[C/gap]CCCTT TGCCAGAAGCTA ATTGTT	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa.	0	
3796	cg43936083	323	AAGATGTAGGCA GTGGCGGCAGG CC[C/gap]TGC GC CCACAGCTCCTC GCCTGTCC	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa.	0	

3797	cg43936083	335	GTGGCGGCAGG CCCTGGCGCCCA CAG[C/gap]TCCT CGCCTGTCTTT GACCACAGA	C	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa.	0	
3798	cg43936083	432	ATGATAGGGGAA CAATAGAGGGGA A[C/gap]CCAGCC TCAACCCCAAGTC AGAAGGT	C	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa.	0	
3799	cg43940146	185	AAACTCATTACT ATAAATTATTCTT [A/C]CAGTACTTT GCAAATTCAGAA TTTC	A	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15910 ENHANCER OF ZESTE HOMOLOG 2 (ENX-1) - Homo sapiens (Human), 746 aa.	0	
3800	cg43940485	662	CCTTTGGGTCAG TGTTGTTAATTAG G[G/gap]CTGAGA GCCTGGGTGAAA GGCAAGA	G	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60300 KIAA0553 PROTEIN - HOMO SAPIENS (HUMAN), 1095 aa (fragment).	0	
3801	cg43951590	167	CTGATAAAACAC ATACAAAAGTTA A[A/G]AGACAGCT CGATTTTCATCTT CCTCC	A	G			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14684 HYPOTHETICAL PROTEIN KIAA0179 - Homo sapiens (Human), 740 aa.	0	
3802	cg43951590	2663	TACAAAATCATA AAAAAGCCCCA TTT/AJTTCTTAAA GGTATAATTTATA GCGC	T	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14684 HYPOTHETICAL PROTEIN KIAA0179 - Homo sapiens (Human), 740 aa.	0	
3803	cg43960583	6448	CTGCTGTTTGCT TAAAAA A[A/gap]CACCCCT TGTCATGTATTTT CTGTAT	A	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q93073 HYPOTHETICAL PROTEIN KIAA0256 - Homo sapiens (Human), 635 aa.	0	

3804	cg43971555	235	TGAGCTTCAGGC GGTTGTCCCGAA G[G/gap]GTCAAG TGCCACGACAGG GTCTGGTC	G	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC00190 ALPHA MANNOSIDASE 6A8B - HOMO SAPIENS (HUMAN), 679 aa.	0	
3805	cg43971555	236	GAGCTTCAGGC GGTTGTCCCGAA GG[G/gap]TCAAG TGCCACGACAGG GTCTGGTC	G	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC00190 ALPHA MANNOSIDASE 6A8B - HOMO SAPIENS (HUMAN), 679 aa.	0	
3806	cg43975476	95	TATTATTTTCCTT TGGAAGAAGAAA [C/A]CAGAAAAAA AACTTCCTGATT GTAA	C	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75141 KIA0650 PROTEIN - HOMO SAPIENS (HUMAN), 848 aa (fragment).	0	
3807	cg43979857	123	ACGCAAGACAGA TGATGCAGGGG AA[C/T]GGGTGTC CACTCTTTCTTG TTCTCA	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60327 KIA0584 PROTEIN - HOMO SAPIENS (HUMAN), 738 aa (fragment).	0	
3808	cg43981392	25	TTTTTTTTTTTT TTTTTCTGCAAT/ CJTTGAGGAACA GTTCACTGATT ATT	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15297 WIP1 - HOMO SAPIENS (HUMAN), 605 aa.	0	
3809	cg43985672	614	AGTGGCTGGGA CAAGCTGGCGG GGG[C/gap]CAAG CACTGTTGAAGC AATAGGGTC	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15017 ORF - HOMO SAPIENS (HUMAN), 692 aa (fragment).	0	
3810	cg44001705	274	TGTTTCCATAC AAGACTGTCACG C[A/G]AAGGATCA ATTGTGCATGT GCCAG	A	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00539 NUCLEAR PROTEIN SA-1 - HOMO SAPIENS (HUMAN), 1258 aa.	0	

3811	cg44003843	6105	CAGAAATGTAAG TCAACTTAAGAA C/A/GJGTGAATGA ATGTAAAAACAT TCAGT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92545 MYELOBLAST KIAA0257 - HOMO SAPIENS (HUMAN), 1805 aa (fragment).	0	
3812	cg44003843	6131	GTGAATGAATGT AAAAACATTGAG TTC/TGAGACCAT ATGCATTTTCTG TGCTG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92545 MYELOBLAST KIAA0257 - HOMO SAPIENS (HUMAN), 1805 aa (fragment).	0	
3813	cg44009187	1459	ATGTCGGTCACG CGGCTAACTTGA C/C/gapJTGCGGG GTCTAAGGAAAG TCAACTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42858 HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN) (HD PROTEIN) - Homo sapiens (Human), 3144 aa.	0	
3814	cg44009187	18	TTTTTTTTTTTT TTTTG/TATGGT TTCCATTTTTTC CTTTAAT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42858 HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN) (HD PROTEIN) - Homo sapiens (Human), 3144 aa.	0	
3815	cg44022781	275	ATCTCTTGAGCT CTTCCCACTGA C/T/GJTGTCATTC ACAGGCATTCAA ACTGT	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14692 KIAA0187 PROTEIN - HOMO SAPIENS (HUMAN), 1282 aa.	0	
3816	cg44036048	65	TTTATTTTCAGTTT TGGCTCTTAAGC C/gapJACTTCCAT TGGGAAGAAGAA ACTCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45768 HYPOTHETICAL 94.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 851 aa (fragment).	0	
3817	cg44130923	5459	ATGTCCTATAAG TGGCGTGAAGTG A/A/JACGTTCTC TTTGGTGGTCAA CCCCG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q62383 SUPPRESSOR OF TY 6 (S. CEREVISIAE) HOMOLOG (SUPT6H) - MUS MUSCULUS (MOUSE), 1726 aa.	0	

3818	cg44921872	1595	GCAAAAAATTAG CCAGGCATGGT GGC/TATGCAC CTGTAGACCCAG CTACTTG	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O60879 DIAPHANOUS PROTEIN HOMOLOG 2 - Homo sapiens (Human), 1101 aa.	0	
3819	cg44921872	1848	AGGCTGATGCAG GAGGATCGCTTG A/A/GCCTGGGA GTTGAGGTTGC AGTGAG	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O60879 DIAPHANOUS PROTEIN HOMOLOG 2 - Homo sapiens (Human), 1101 aa.	0	
3820	cg44932392	194	AATTTATGTCCT TTAAGATACATT A/gap]AAAAAAA AAAAAAGACACA TCAAC	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0	
3821	cg44932392	208	TAAGATACATT AAAAAAA A[A/gap]GACACA TCAACTGCAAC GTGAAGG	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0	
3822	cg43942696	1416	TTCTGGGCCCTG TCTGCGGTTCCA C[A/G]TGTGATAC TGTGGGTGAGAC GGCAT	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPIN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3823	cg43942696	1438	CACATGTGATAC TGTGGGTGAGAC G[G/C]CATGGCC CATTCTGCACT TGGCCA	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPIN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8

3824	cg43942696	172	TCAAGACAGTGG TTACAAAAA A[A]gapjGTACTC TTCTGGCTACAC ACTTTAT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3825	cg43942696	260	CAATCACAATTT CCAGGATTAAAA AIC/TTCATCTATT CTTAAATCCTAC ACTGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3826	cg43942696	274	AGGATTAAAAAC CATCTATTCTTAA IAGTCTCTACACT GTTTATAGAGCAT CAAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3827	cg43942696	480	CAAAACAACCAA AAATTACCATGA CIC/TTCGGTACA GGAAAAACAGGA AGACTC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8
3828	cg43942696	69	AACAACACACATT TTGCTTTATTAG GIC/TGTTCATG GTAATATAACAC AGAGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16555 DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (COLLAPSEN RESPONSE MEDIATOR PROTEIN 2) (CRMP-2) (N2A3) - Homo sapiens (Human), 572 aa.	0	8

3829	cg43957189	387	CAGATGGGTGG GGCAGGGTGGG GTT[C/gap]CCCC CATCTGACCCTC TAGGGCTCT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q16610 EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) - Homo sapiens (Human), 540 aa.	1.0e-313	1
3830	cg43957189	392	GGTGGGGCAG GGTGGGGTTC CCC[C/gap]ATCT GACCCCTAGGG CTCTGGGGT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q16610 EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) - Homo sapiens (Human), 540 aa.	1.0e-313	1
3831	cg44002959	3908	CCTTGTTGGGG GACCAGGGCAG GGC[C/gap]TGGG ACAGGGAAGGG GGTGAGTTAG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92513 MYELOBLAST KIAA0239 - HOMO SAPIENS (HUMAN), 571 aa (fragment).	1.4e-316	5
3832	cg43958391	253	CCCCCGGAAC AGAAGGCAGTGA TG[C/gap]CAAAAT GCCAAGGAAGC AGCTTAAAA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14545 FLN29 - HOMO SAPIENS (HUMAN), 582 aa.	2.4e-316	12
3833	cg43958391	254	CCCCGGGAACA GAAGGCAGTGAT GC[C/gap]AAATG CCAAGGAAGCA GCTTAAAC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14545 FLN29 - HOMO SAPIENS (HUMAN), 582 aa.	2.4e-316	12
3834	cg43937128	170	CACAACTTGATG GTTTTTTCTTTT C/TTTTGCAAA GGACAATCTATA TGCT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa.	4.0e-317	X

3835	cg43937128	299	GGCTGGAGGAG GTATACAGGATA AC[A]gap]AAAAA AAAAAAATAGAA AAAAATAA	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa.	4.0e-317	X
3836	cg43937128	311	TATACAGGATAA CAAAAAA A[A]gap]TAGAAA AAAAATAAGAAAG TGGTTCC	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa.	4.0e-317	X
3837	cg43937128	311	ATACAGGATAAC AAAAA A[gap/A]TAGAAA AAAAATAAGAAAG TGGTTCC	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa.	4.0e-317	X
3838	cg43979183	1210	CCATGCCTGACA AGTTCTGAAGAG G[A]gap]AAAAA AAAAATTGTTTAA TCCAGT	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3839	cg43979183	1219	ACAAAGTTCTGAA GAGGAAAAA A[A]gap]ATTGTTT TAATCCAGTTTC TGCTG	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3840	cg43979183	1220	CAAGTTCTGAAG AGGAAAAA A[A]gap]TTGTTT AATCCAGTTTCT GTCTGC	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3841	cg43979183	1300	CCCTTTATGAA AGATAAAGCAGA A[C]G]AAAAAGTGA AATATATCTTCA GATTA	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	

3842	cg43979183	754	TCTCAATATACA CACAGATTAAAGA GTT[<i>gap</i>]TTTTTGC CTTGGCAAAAAT AAAACT	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3843	cg43979183	759	TATACACACACAGA TTAAGAGTTTTTT [<i>gap</i>]TGCCTTGG CAAAAATAAAAC TGAAGT	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3844	cg43979183	872	AAAGATTACAAT ACATTATTAACTT [A/C]CTTTTAAAC CACAGAGTAAAG TTAC	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3845	cg43979183	873	AAGATTACAATA CATTATTAACTTA [C/A]TTTTTAAAC ACAGAGTAAAGT TACT	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13485 DPC4 - HOMO SAPIENS (HUMAN), 552 aa.	4.1e-310	
3846	cg44002835	22	GTCGACTTTTTTT TTTTTTT[A/T]TA TAAAAAGGTCAC TTATTTTGCC	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13585 MELATONIN-RELATED RECEPTOR (H9) - Homo sapiens (Human), 613 aa.	5.0e-312	12
3847	cg44002835	406	GAGTCTGACAGT GTTCCGGCTGCT G[C/ <i>gap</i>]CTTTATA GTCTGTGTTCTC AAAGTT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13585 MELATONIN-RELATED RECEPTOR (H9) - Homo sapiens (Human), 613 aa.	5.0e-312	12
3848	cg43948793	394	GCCACACAAATC TGTGTGTGGCTA AIG[C]GATGAGG ATACAGAGAAAA GAAAA	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15051 HYPOTHETICAL PROTEIN KIAA0036 - Homo sapiens (Human), 598 aa.	5.5e-315	6

3849	cg42710561	1866	TGAGGAAATGTA TAAATACCACA T[A/G]GTATAAAA TTACATGTTAATA CAAT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92521 PIG-B - HOMO SAPIENS (HUMAN), 554 aa.	6.1e-311	15
3850	cg43938133	1324	CACCTCGGAAGT CCCAAGGGCAG TG[C/gap]GGATG ACCGATTGGCC ATGGAAGA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14195 DIHYDROXYRIMIDINASE RELATED PROTEIN-3 (DRP-3) (UNC-33-LIKE PHOSPHOPROTEIN) (ULIP PROTEIN) - Homo sapiens (Human), 570 aa.	6.6e-310	5
3851	cg43938133	1846	ACTTATTCAAAC CTGCAGTCAGAG A[C/T]AATGTTT CTCCTAAGCAAT TAAAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14195 DIHYDROXYRIMIDINASE RELATED PROTEIN-3 (DRP-3) (UNC-33-LIKE PHOSPHOPROTEIN) (ULIP PROTEIN) - Homo sapiens (Human), 570 aa.	6.6e-310	5
3852	cg43277973	62	TTTTCTTTTCAC AGTCGCGCTCTT gap[C/T]AATCTTG GACTGGAGGATA TACAG	gap	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P36269 GAMMA-GLUTAMYLTRANSFERASE 5 PRECURSOR (EC 2.3.2.2) (GAMMA- REL) - Homo sapiens (Human), 586 aa.	8.0e-314	22
3853	cg44015618	348	GGCAGGTTGATC TGGGAACGGC TG[G/A]CATGCTA GGGATGGTGGA GAAGTAG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q75148 KIAA0658 PROTEIN - HOMO SAPIENS (HUMAN), 589 aa (fragment).	8.7e-312	11
3854	cg44928804	2623	AATGAGAAAGGC CAGAGGCTGCAA A[A/gap]GACAGT CAAAGGACACGA GAGAAAG	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5- NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)

3855	cg44928804	3388	CCTCGGTTCTAT GCATATATGGAT T[Agap]GCTATAA AAAATGTCAATA AGATTG	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'- NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)
3856	cg44928804	3435	ATTGTACAAGGA AAATTAGAGAAA GGTTCACATTTA GGGTTTATTTTT ACAC	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'- NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)
3857	cg44928804	3493	TAAATAGGGTA AATCCTATTAGA A[Agap]ATTTTTTA AAGAACTTTTTT AAGTT	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'- NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)
3858	cg43956210	1844	ATCATGTAAAT AAGATATTAGAC T[Ggap]TTTTTTG AATAAAATATTT TATTG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA-GLUCOSAMINIDASE) (BETA-N- ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa.	3E-307	5 (5q13)
3859	cg43982721	1884	CTCTCCTAGACG CCCAGGACCGG CC[Ggap]CCCTG TGAGCCGTGCTG GCCCCACC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O14531 DIHYDROPYRIMIDINASE RELATED PROTEIN-4 (DRP-4) (ULIP4 PROTEIN) - Homo sapiens (Human), 572 aa.	1.6E-306	
3860	cg43982721	1937	AGGCCGCGGG CCCCAGGGCAC TCG[Cgap]CCCC CTCCTTAGCATT TCTTTTGT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O14531 DIHYDROPYRIMIDINASE RELATED PROTEIN-4 (DRP-4) (ULIP4 PROTEIN) - Homo sapiens (Human), 572 aa.	1.6E-306	

3861	cg43955051	136	AAATTATGGTAA CAATCAATTTCTTT TT/CJAAATGTCTA ACTTATTTAACC CCTT	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD10823 SQUALENE EPOXIDASE (EC 1.14.99.7) - HOMO SAPIENS (HUMAN), 574 aa.	1.9E-305	8
3862	cg43264444	216	GGAAGAGGGAA AAAGGTGCTTC TGT/CJTJTATTTT CACATCTGTAAT TTTAA	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene REMTREMBL- ACC:G513351 PROTEIN 1 - ARTIFICIAL SEQUENCE, 530 aa.	2.4E-305	11 (11q21)
3863	cg43991434	194	CATCTGCCAGT CCAGACCCTACC G/C/TJCCCCCTGC CCCAGGAGGTC CTTTAA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.7E-304	22
3864	cg43991434	427	ACAATCTGGTGT CTGCCCTGTCCAC A/C/TJGGTGTGG GGCCCAGGGTT GCCCTCT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.7E-304	22
3865	cg43991434	59	TTTTTTTTTTTT TTTTTTTTTTTTTG TJAAGCTGCCAC ACGACTTTATTT GTG	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.7E-304	22
3866	cg43991434	828	TCCCCACAACAG AGCAGGGCTGG GC/Cgap/AGCAG AAGACGTTAAAA CCCAAATC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.7E-304	22
3867	cg43962078	2297	TCTTTCTGTCCTT TTAAGTGACCTT G/TGAATTCCTT GATTTATTTATT GCA	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O43776 ASPARAGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.22) (ASPARAGINE- TRNA LIGASE) (ASNRS) - Homo sapiens (Human), 548 aa.	2.2E-304	18

3868	cg43982078	2507	ATAATCCTGAGG CATAGAAATTGA A[A/G]AATTGTGTA AAAATAGAAATTG CCTTA	A	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O43776 ASPARAGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.22) (ASPARAGINE-- TRNA LIGASE) (ASNRS) - Homo sapiens (Human), 548 aa.	2.2E-304	18
3869	cg43985349	3532	TGCCATGGTGGG GGCCGGGGCGG AC[G/A]CGTTCCCC ACCTTTGGGACC GGACGG	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBL-NEW- ACC:AAC69991 GLYPICAN-4 - HOMO SAPIENS (HUMAN), 556 aa.	2.7E-304	X
3870	cg43951838	334	CTTTCTGAGTGT GAACCTGGCTCG G[C/gap]CTGAAG CCTAGAGCTGGC TTGAAGA	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14194 DIHYDROPYRIMIDINASE RELATED PROTEIN-1 (DRP-1) (COLLAPIN RESPONSE MEDIATOR PROTEIN 1) (CRMP-1) - Homo sapiens (Human), 572 aa.	3.5E-304	4 (4p16.1)
3871	cg43951838	82	TTTTTTTTTTTT TTTTTTTTTTTTTG TTTGGGCAGTTC ATTTCTTTATTT TT	G	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14194 DIHYDROPYRIMIDINASE RELATED PROTEIN-1 (DRP-1) (COLLAPIN RESPONSE MEDIATOR PROTEIN 1) (CRMP-1) - Homo sapiens (Human), 572 aa.	3.5E-304	4 (4p16.1)
3872	cg43951838	84	TTTTTTTTTTTT TTTTTTTTTTGT GTTGGCAGTTCA TTTTCTTTATTT TTC	G	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14194 DIHYDROPYRIMIDINASE RELATED PROTEIN-1 (DRP-1) (COLLAPIN RESPONSE MEDIATOR PROTEIN 1) (CRMP-1) - Homo sapiens (Human), 572 aa.	3.5E-304	4 (4p16.1)
3873	cg43142595	591	CCTGGTGTGCT GAGATGGGCGC TG[C/gap]CTCCT CCCACCCACAGC GCGTCATC	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTRMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	

3874	cg43142595	592	CTGGTGCTGCTG AGATGGGCGCT GC[C/gap]TCCTC CCACCCACAGC GCGTCATCC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3875	cg43142595	703	CCCGCACCCAG ACCGTGCCGTCT GG[C/gap]AGGCA CTTCGGCCTCA GTGCCACG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3876	cg43142595	745	AGTGCCACGGC CCCCCCCCAG GCC[A/G]CTCAC ACTCTGGGG GCCACAGAG	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3877	cg43142595	753	GGCCCCCTCCC CAGGCCACTCAG AC[T/C]CCTGGG GGCCACACAG GTGCTGTC	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3878	cg43142595	910	GGCGGGGCCCT TGACACTGAGGC TG[gap/C]TCCCG CCCCACACGCA GCCTGGCGA	gap	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14927 N-ACETYLGLUCOSAMYL TRANSFERASE COMPONENT GPI1 - HOMO SAPIENS (HUMAN), 581 aa.	5.7E-304	
3879	cg43317253	3037	GGTCTGTTTC TAAAAA A[A/gap]CTGTTG TAGAAATTCTTAA TTTGGA	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P42568 AF-9 PROTEIN - Homo sapiens (Human), 568 aa.	2E-301	9

3880	cg43317253	3219	ATTAAATCTTTC TTTGGGGAAAAA A/TJCTTGGTTAT TCTGCCATAACA GAT	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P42568 AF-9 PROTEIN - Homo sapiens (Human), 568 aa.	2E-301	9
3881	cg43917155	2849	CATACTGTGTCT GTGAGTTTCTTC A/A/GJTACAAAT GGGCATTAGTA TAGTT	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAB87763 EMBRYONIC LUNG PROTEIN - HOMO SAPIENS (HUMAN), 568 aa.	2E-301	
3882	cg43917155	3090	GATCTCTTTGCT GAATTAATGAGT T/C/AJTAAACATG TGGACCCCAACTG CCGTG	C	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAB87763 EMBRYONIC LUNG PROTEIN - HOMO SAPIENS (HUMAN), 568 aa.	2E-301	
3883	cg43988371	4038	TCTGTGACTAA TCACTGAACATG A/C/TGAATGTTA AATTTTATGTC TGAA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA34487 KIAA0767 PROTEIN - HOMO SAPIENS (HUMAN), 573 aa (fragment).	4.1E-301	22
3884	cg44916847	322	ATGTCAACCTGC CCGACCCCTCTGG G/G/gapJTGAAC GGATGTGGACAC TGGAGGG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa.	4.3E-299	1
3885	cg44916847	496	TGTACATGTAAC ATGTGGCCATGC C/C/gapJAGGCAT CCCAGCATCTAT CCTGAAG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa.	4.3E-299	1
3886	cg44916847	507	CATGTGGCCATG CCCAGGCATCCC A/G/AJCATCTATC CTGAAGTCAGTG TAAAG	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa.	4.3E-299	1

3887	cg43286397	575	GACACTGAGAG GTTTCCATCTGC AGTTCGCAAG GGCTGCAGGTTG TGCCATG	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14134 ATAxia-Telangiectasia Group D- Associated Protein - Homo Sapiens (Human), 588 aa.	7E-299	11
3888	cg43923376	1791	TGAGCAGGAGTT TGAACAGACCTG A[G/gap]CCCCAG GCACCGAGGAG GGTGCTGG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P08865 BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N- ACETYL-BETA-GLUCOSAMINIDASE) (BETA-N-ACETHYHEXOSAMINIDASE) - Homo sapiens (Human), 529 aa.	9.2E-297	15
3889	cg43923376	1867	GGCTTCCACTGC ATCCTGGCCAGG G[G/gap]ACGGAG CCCCTTGCCCTC GTGCCCC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P08865 BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N- ACETYL-BETA-GLUCOSAMINIDASE) (BETA-N-ACETHYHEXOSAMINIDASE) - Homo sapiens (Human), 529 aa.	9.2E-297	15
3890	cg43280144	514	TCAGAAATTTAA GCCTCCCCACCT G[A/C]AAGATTAC ATATATAAACTC CCAC	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15320 MEA6 - Homo Sapiens (Human), 804 aa.	7.4E-295	
3891	cg43255486	1897	CTCCACCCATCC AGTGACTCTGG G[G/gap]CGCGGC CACAGGGGACG GGATGAGG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q14451 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 7 (GRB7 ADAPTER PROTEIN) (EPIDERMAL GROWTH FACTOR RECEPTOR GRB-7) (B47) - Homo sapiens (Human), 532 aa.	6.7E-294	17
3892	cg43998124	189	CCAACTCTGTGA ATTAGTATTAA G[A/G]TAACATC ACATATGTAAAC GCGAG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75174 KIAA0689 Protein - Homo Sapiens (Human), 547 aa (fragment).	4.7E-293	

3893	cg4398124	343	CTTGCAACAAA GAATTACTAATTT [A/C]AAGTGTA AATTTGCAAG GGAA	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75174 KIAA0889 PROTEIN - HOMO SAPIENS (HUMAN), 547 aa (fragment).	4.7E-293	
3894	cg43981656	1171	TGAATATTGTAA ATATTACAATTG G[ap]/GJTATTAG AAAGCCATGATG AATCCAG	gap	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3895	cg43981656	1269	ACCAGGCTTACC ATGTTCTAAATAA [C/T]TCAAGAAAA TATCTTTAAAAAA AAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3896	cg43981656	1294	TCAAGAAAAATAT CTTTAAAAA [gap/A]GGACTGC AATTTAACAGTA ATCTGT	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3897	cg43981656	1345	ATATCTTTAGCT GCCATTAAAAA A[G/A]AAAAAAGA ACAACCAAAAC AATGA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3898	cg43981656	809	TCAGGAAGAAA ATACTTTAAAGA C[A/G]TGCCAATT TGAAAAGGCATC AAAGT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3899	cg43981656	820	AATACTTTAAAG ACATGCCAATTT G[A/T]AAAGGCAT CAAAAGTAAAAA ATAAA	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10

3900	cg43981656	821	ATACCTTTAAAGA CATGCCAATTTG AATTAAGGCATC AAAGTAAAAAAA TAAAA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3901	cg43981656	833	CATGCCAATTTG AAAAGGCATCAA A[G]ATAAAAAA TAAAGCAAATG CTAAA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3902	cg43981656	841	TTGAAAAGGCAT CAAAGTAAAAAA A[gap]ATAAAAG CAAATGCTAAAA ACTACTT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
3903	cg43935280	272	AAAAATTTTTTT TTTTTTTTTTT[C /T]TCTGAGGAAG CCGAGAAACTTT AAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q62825 (RSEC6) - RATTUS NORVEGICUS (RAT), 755 aa (fragment).	3.8E-291	5
3904	cg43935280	444	ACCCAAGAGAG GCTGTGCGGCA GAG[C/gap]CCTG CACCACAGGC CTTGACAGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q62825 (RSEC6) - RATTUS NORVEGICUS (RAT), 755 aa (fragment).	3.8E-291	5
3905	cg43935280	446	CCAAGAGAGGCT GTGCGGCAGAG CC[C/gap]TGCAC CCACAGGCCTTT GACAGCAC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q62825 (RSEC6) - RATTUS NORVEGICUS (RAT), 755 aa (fragment).	3.8E-291	5
3906	cg43935280	530	TCACTCGACGCA CACCCTGGTGCAT C[A/G]CACTGGC ACCTAAAGACAG GCCGTG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q62825 (RSEC6) - RATTUS NORVEGICUS (RAT), 755 aa (fragment).	3.8E-291	5

3907	cg44003023	7606	AAGCAAGAGGA AAAACCTTTGGAC A[G/T]CGTAAAGA CTAGAATAGTCT TTTAA	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P40200 T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN) - Homo sapiens (Human), 569 aa.	9.9E-291	3
3908	cg44128920	1686	CGAGTCACGCTC AATTGAACCCCTG C[C/T]AGAGACG GGAAGAGGGGG GCTGTCG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
3909	cg44128920	1735	CGGCTGCTGCTT CTGGGCCACGG GG[A/G]GCCCA GGACCTATGCAC TTTATT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
3910	cg44128920	1749	GGGCCACGGGG AGCCCCAGGAC CTA[T/G]GCACCT TATTCTGACCC CGTGGCT	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
3911	cg44128920	1914	CATGTTTACAT CTTTCTTTCTGC [C/gap]GCTCGGC TCCGGCCATTT GTTTA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
3912	cg40886359	150	TCCCTCTCTGCA GAACCTCTCCTT T[A/gap]CCCCCCC ACCCCCCACCAC TGCCCCC	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18627 LYMPHOCYTE ACTIVATION GENE-3 PROTEIN PRECURSOR (LAG-3) (FDC PROTEIN) - Homo sapiens (Human), 525 aa.	1.6E-290 (12p13.3 2)	12
3913	cg42742569	3325	AAAAATGGATAC CAAAAGCACTAT T[A/T]GTCACCCA AGCTAAGTGGAA TAGCT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O15091 HYPOTHETICAL PROTEIN KIAA0391 - Homo sapiens (Human), 567 aa.	2.5E-290	

3914	cg43949262	81	GTAGAGGCACAC ATTGGACTCTGA C/GA/JATTCCCT TGCAGCAGACAT TTGTG	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa.	9E-290	
3915	cg43995003	1944	TTGCCATCAGTG ATCTCACTAAAA A/gap/AJTATACA GCTACTTCCAG CTAATCT	A	gap		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P10155 60 KD RO PROTEIN (60 KD RIBONUCLEOPROTEIN RO) (RORNP) (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) - Homo sapiens (Human), 538 aa.	1.9E-289	1
3916	cg43926814	360	AATAATCAAAG TAGAATTTTCTAT [C/gap]CCCCCCC ATTCTCCAGTA ATAAAA	gap	C		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA-62) - Homo sapiens (Human), 536 aa.	5E-289	14
3917	cg43926814	367	CAAAGTAGAATT TTCTATCCCCC C/C/gap/JATTCTC CAGTAATAAAAA GTAGTG	gap	C		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA-62) - Homo sapiens (Human), 536 aa.	5E-289	14
3918	cg43931799	255	CCTATGTGCGCG CGGGCCCTCCG GA/G/gap]GCTGA GGGGGAACAG CGCGGCCAG	gap	G		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA83001 KIAA1049 PROTEIN - HOMO SAPIENS (HUMAN), 550 aa (fragment).	7.6E-289	22
3919	cg43055270	2134	AAATATCAGAGT AAAACTTTCTAG A/A/gap]CAGTAC AAGGTTAAAGAG GTGAGGT	gap	A		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13884 BETA1-SYNTROPHIN - HOMO SAPIENS (HUMAN), 538 aa.	2.2E-288	8
3920	cg43055270	2305	GCCGAATAGTTG AGAAATGGACAT T/C/TJTACCTAC TCCTCCTAGCCC CCTAT	T	C		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13884 BETA1-SYNTROPHIN - HOMO SAPIENS (HUMAN), 538 aa.	2.2E-288	8

3921	cg43969619	2350	TCACACACATGT CATCAGGGCCCT C[gap/C]TGCACT CCACATGATGAG GTCAGAC	gap	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00973 BETA-1,4 N- ACETYL GALACTOSAMINYLTRANSFER ASE (EC 2.4.1.92) (N- ACETYLNEURAMINYL)- GALACTOSYLGLUCOSYL CERAMIDE) (GM2/GD2 SYNTHASE) (GALNAC-T) - Homo sapiens (Human), 533 aa.	2.5E-287	12
3922	cg43249886	1878	CCTCGCCCCCG CCCCCACC GGG TGA[A/G]AGTGTC GTCTCCGCTTCT CTCGGTG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q01101 ZINC FINGER PROTEIN IA-1 (INSULINOMA-ASSOCIATED PROTEIN 1) - Homo sapiens (Human), 510 aa.	1.4E-286	20
3923	cg43128343	1878	CACCTCTCTCCT CCACTCTGAGCC C[C/gap]CTGACC TTCACAACTCA ATAAACT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P27918 PROPERDIN PRECURSOR - Homo sapiens (Human), 469 aa.	2.2E-286	X (Xp11.4)
3924	cg43128343	1878	ACTTCTCTCCTC CACTCTGAGCCC C[C/gap]TGACCT TCCAAACCTCAA TAAACTA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P27918 PROPERDIN PRECURSOR - Homo sapiens (Human), 469 aa.	2.2E-286	X (Xp11.4)
3925	cg43128343	1921	CCTCTCCCCGCC GCTGCCATAACC C[C/gap]AATGTC TGGGCCCTGCG CAGCCCCC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P27918 PROPERDIN PRECURSOR - Homo sapiens (Human), 469 aa.	2.2E-286	X (Xp11.4)
3926	cg43968641	993	GTAATATAGGTG TGCACAAAAGG G[A/gap]AAACAC CCTATTTTCAATTT TCAATT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
3927	cg43968641	265	AAGTTAATTTCT TTTCTAATTTCTI T/GJCTCATACAC CTGAGTTATTTA AAAA	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8

3928	cg43968641	508	AGGACCACTGAA GAATAGCTCCAA TIG/TTGACACTA GACACAAAATAC CTTTG	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
3929	cg43968641	555	TTTGGGGGCAAA GACAGGGGCAA GC/T/CJGTGTC CGGTGGTGAAGT GAGAAAG	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
3930	cg43968641	825	TTTTGACTCATG AGGCAAGCTGT TIG/gapJCCACAA TCAGTGGCGACT CAAGTCA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
3931	cg43061073	119	AGCTATTTTAAAA CTAATGTAACCA[gap/TJTTTTTTTAA AAAAAGAAACTA TTTA	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14117 DIHYDROPYRIMIDINASE (EC 3.5.2.2) (DHPASE) (HYDANTOINASE) (DHP) - Homo sapiens (Human), 519 aa.	8.6E-285	8
3932	cg43968352	286	GTTACAATTTAA AAAAAGAATACA[ATT/CAGAAATAAT TAATAACTTAAGT GA	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60317 KIAA0571 PROTEIN - HOMO SAPIENS (HUMAN), 638 aa.	1.7E-284	11
3933	cg42709686	2604	GACAGTGATTAA TGGTCTGTTGG C/C/gapJAAGGCT TCTCCCTGTCGG TGAAGGA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P15848 ARYLSULFATASE B PRECURSOR (EC 3.1.6.12) (ASB) (N- ACETYLGALACTOSAMINE- 4- SULFATASE) (G4S) - Homo sapiens (Human), 533 aa.	4.3E-283	
3934	cg43943490	2217	TGCCTGGGGTCA TGAAAGGCAGAG C/C/gapJTGACGC ATGCAGTATGGC AGCCGGG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA10276 ARIADNE-2 PROTEIN (ARI2) - HOMO SAPIENS (HUMAN), 493 aa.	1.3E-281	3

3935	cg43946325	272	GATCCTAGCCTT GGGCCAGGGA TG[<i>gap</i>]CACAG GCTGAATGGAAG GGCTGGGA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15460 PROLYL 4-HYDROXYLASE ALPHA (II) SUBUNIT (II) - HOMO SAPIENS (HUMAN), 535 aa.	2.1E-281	5
3936	cg43946325	65	GCTCTTTTTTTT TTTTTTTTTTT TTAGGCTTCTGG TAGGGACATTTT ATT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15460 PROLYL 4-HYDROXYLASE ALPHA (II) SUBUNIT (II) - HOMO SAPIENS (HUMAN), 535 aa.	2.1E-281	5
3937	cg43946325	66	CTCTTTTTTTTT TTTTTTTTTTT TTAGGCTTCTGGT AGGGACATTTTA TTT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15460 PROLYL 4-HYDROXYLASE ALPHA (II) SUBUNIT (II) - HOMO SAPIENS (HUMAN), 535 aa.	2.1E-281	5
3938	cg44010409	223	CTCCAAATCCCA CCCCAGTCAAG TTC/TTGGGGAA GGTAGGGGTGTG AGCIGCT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14981 NUMA PROTEIN - HOMO SAPIENS (HUMAN), 2101 aa.	2.1E-281	11
3939	cg44010409	239	AGTGCAAGTCTG GGGAAGGTAGG GTG/TTGAGCTG CTGCTGAAGGCT GTCCCC	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14981 NUMA PROTEIN - HOMO SAPIENS (HUMAN), 2101 aa.	2.1E-281	11
3940	cg43931431	1146	CTTCTTGTGAAC CAGGGATACACA C/TATTCAGACAT TGGCAACACAGTA GTACA	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14154 HYPOTHETICAL PROTEIN KIAA0141 - Homo sapiens (Human), 515 aa.	7.2E-281	5
3941	cg43931431	320	ACATAAAATTGC AGTATGAACTGA TTG/TGACAAGAA CTCTGGGCCAG GAGTCA	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14154 HYPOTHETICAL PROTEIN KIAA0141 - Homo sapiens (Human), 515 aa.	7.2E-281	5

3942	cg43930921	329	CCGGAGCTCGC CTTGGTGCTGGG CA[C/gap]CAGTG GGCCCTGCCA GGCCTGTCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
3943	cg43930921	330	CGGAGCTCGCC TTGGTGCTGGG AC[C/gap]AGTGG GCCCTGCCAG GCCGTGCTCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
3944	cg43930921	340	CTTGGTGCTGGG CACCAGTGGC CC[C/gap]TGCCA GGCCTGTCTCT CCTTTTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
3945	cg43930921	344	GTGCTGGGCAC CAGTGGGCCCC TGC[C/gap]AGGC CTGTCTCTCTCT TTTTGAGCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
3946	cg44931278	33	TTTTTTTTTTT TTTTTTTTTTT TTACTACAAAAAT AAGCACTTTACT AA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15830 MUTY HOMOLOG - HOMO SAPIENS (HUMAN), 535 aa.	4.5E-280	1
3947	cg44931278	34	TTTTTTTTTTT TTTTTTTTTTT TTCTACAAAAATA AGCACTTTACTA AC	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15830 MUTY HOMOLOG - HOMO SAPIENS (HUMAN), 535 aa.	4.5E-280	1
3948	cg4398884	2376	GGCAATGCCCGT CCTCTGGCTTGG GTTCTTAATCTT CGGTGACACTG GCGTTG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51688 N-SULPHOGLUCOSAMINE SULPHOHYDROLASE PRECURSOR (EC 3.10.1.1) (SULFOGLUCOSAMINE SULFAMIDASE) (SULPHAMIDASE) - Homo sapiens (Human), 502 aa.	1.1E-279	17

3949	cg43998884	2628	CCATACTGGGGT GGGCTGGAGGA GG[gap]/CjCACAG GCCAGCTATTGT AAAAGCTT	gap	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51688 N-SULPHOGLUCOSAMINE SULPHOHYDROLASE PRECURSOR (EC 3.10.1.1) (SULFOGLUCOSAMINE SULFAMIDASE) (SULPHAMIDASE) - Homo sapiens (Human), 502 aa.	1.1E-279	17
3950	cg43958499	2184	GTCTGGCAATT TGATTTCTGAAC TTC/TJTTGTGCTAC CTCAGAGGCCA GCTTCC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75686 2'-5' OLIGOADENYLATE SYNTHETASE (P59OAS) - HOMO SAPIENS (HUMAN), 514 aa.	2.2E-279	12
3951	cg44001088	178	TCCACCACAGTA AAACATACAAAGT TTT/AJTTTGAAG AGAAAAGGTCAT ATGGA	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43428 RALBP1-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	2.2E-279	X
3952	cg44001088	179	CCACCACAGTAA AACATACAAAGT TTT/AJTTGCAAGA GAAAAGGTCATA TGGAT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43428 RALBP1-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	2.2E-279	X
3953	cg44031765	1170	ATTCACCTCAAG TCAGGTGAGACC CjA/GTTACATCAT GGGTCCCCCACTC ACAAG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa.	4.6E-279	22
3954	cg44022026	1864	TCCTTCTGGGGA AATAAATGAGTG TTC/gapJTGTTTCA GCAGCTAAAAA AAAAA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43292 HGAA1 - HOMO SAPIENS (HUMAN), 621 aa.	1.2E-278	8

3955	cg44002920	142	AGCACAGTTCAA AGTCATTAAATC C[G/A]GTACAAA GAAATGGCTCTC ACTTC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
3956	cg44002920	171	AAAAGAAATGGC TCTCACTTCCTG G[gap/G]ATTGGC ACCAGACATCCT ACCAGCT	gap	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
3957	cg44002920	176	AAATGGCTCTCA CTTCCTGGATTG G[gap/G]CACCAG ACATCCTACCAG CTGCAAT	gap	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
3958	cg43987191	1808	ACTCAAGACTTA TGGACAGGGAT G[G/gap]CAGGC CTCTCTCAGGAG CAGGGGC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P19235 ERYTHROPOIETIN RECEPTOR PRECURSOR (EPO-R) - Homo sapiens (Human), 508 aa.	8.5E-278 (19p13.3)	19

3959	cg43984386	281	ACGAGCTCTCGC CCACTCGCCGG AG[G/gap]AGACG GCCCTGGACTCC CAACCCCG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00401 N-WASP - HOMO SAPIENS (HUMAN), 505 aa.	5.9E-277	
3960	cg43983979	502	GATAGAAGGGA GCAGCATCAGAC AC[A/T]TTTTTC AGGCCCTGGTTT CATGTG	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3961	cg43983979	503	ATAGAAGGAGC AGCATCAGACAC A[T/A]TTTTTCAG GCCCTGGTTTCA TGTC	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3962	cg43983979	504	TAGAAGGAGCA GCATCAGACACA T[T/A]TTTCAGG CCCTGGTTTCAT GTGCC	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3963	cg43983979	505	AGAAGGAGCA GCATCAGACACA T[T/A]TTTCAGG CCCTGGTTTCAT GTGCC	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3964	cg43983979	582	TATCACTAAAC AATTTTTTTTTT T/gap]GTAAGGC TACTTTGTAGC TTTT	T	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3965	cg43983979	583	ATTCACATAACA ATTTTTTTTTTT T/gap]GTAAGGCT ACTTTGTAGCT TTTTG	T	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14

3966	cg439863979	702	CAATTCATTTCG TTGCCCTTTTGG GC[<i>gap</i>]CACTGT GGCCATGAACAG CCCTGCT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3967	cg439863979	712	CGTTGCCCTTTG AGGCCACTGTG GC[<i>gap</i>]ATGAA CAGCCCTGCTAC TATCTGTG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
3968	cg43988211	104	CAATTCAGAGG GGCCTGGCTGT GGC[<i>gap</i>]CAAAG CTGTGCCAAACG GTTGGGAT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD41476 TRANSCRIPTION FACTOR IIIC63 - HOMO SAPIENS (HUMAN), 519 aa.	6.2E-275	
3969	cg43988211	105	AATTCAGAGG GCCTGGCTGT GC[<i>gap</i>]AAAGC TGTGCCAAACG TTGGGATC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD41476 TRANSCRIPTION FACTOR IIIC63 - HOMO SAPIENS (HUMAN), 519 aa.	6.2E-275	
3970	cg43988211	182	TGAGACCATGGG CGAGGCTCCCC AC[G/A]CTATCTC CACCACCACAGT CATGAG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD41476 TRANSCRIPTION FACTOR IIIC63 - HOMO SAPIENS (HUMAN), 519 aa.	6.2E-275	
3971	cg43988211	302	CTCATCCTGAGA GGCATTGGGTG CC[<i>gap</i>]ACTCA CTGGCTGGATGC TGGGCTGG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD41476 TRANSCRIPTION FACTOR IIIC63 - HOMO SAPIENS (HUMAN), 519 aa.	6.2E-275	
3972	cg42935995	134	TGACCTGCACC ATAATTATGGTG A[G/A]TTCTAGG TTAGAAGATACC TTAGA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q12774 PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE) - Homo sapiens (Human), 519 aa.	1E-274	

3973	cg42835995	484	ACTGGGTTAGCT GGATTTTGTCTT TIG/gapJAGCTTT GAGAAAGGCCTA GTTCTCCA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q12774 PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE) - Homo sapiens (Human), 519 aa.	1E-274	
3974	cg43929467	1829	AAAAGACAAGGA CTGCTCTAGTGT TIG/CJAGGGATG TAGCTCAGCTTT TGGGCT	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12874 SPICESOME-ASSOCIATED PROTEIN SAP 61 - HOMO SAPIENS (HUMAN), 501 aa.	1.3E-274	1
3975	cg43929467	2628	CATCTCAAAAA AAAAAAAAGCGG GT/gapJGGGGG GAGTTGGGCTGT GTTGGA	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12874 SPICESOME-ASSOCIATED PROTEIN SAP 61 - HOMO SAPIENS (HUMAN), 501 aa.	1.3E-274	1
3976	cg43929467	2733	TTGCTAGGTCAG AATGAGAGACTG GT/AJGGGTCTGT CTACCTGTTTCT TCTAC	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12874 SPICESOME-ASSOCIATED PROTEIN SAP 61 - HOMO SAPIENS (HUMAN), 501 aa.	1.3E-274	1
3977	cg43947753	3093	TCATTGGGTAG CAACGTGGGTTT AIC/gapJCCAAA CACCTTTTATAC AAAAGA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13610 PERIODIC TRYPTOPHAN PROTEIN 1 HOMOLOG (KERATINOCYTE PROTEIN IEF SSP 9502) - Homo sapiens (Human), 501 aa.	7.1E-274	12
3978	cg43947753	3095	ATTGGGTAGCA ACGTGGGTTTAC CIC/gapJAAAAA CCTTTTATACAA AAGACA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13610 PERIODIC TRYPTOPHAN PROTEIN 1 HOMOLOG (KERATINOCYTE PROTEIN IEF SSP 9502) - Homo sapiens (Human), 501 aa.	7.1E-274	12

3979	cg43994885	55	TTTTTTTTTTTT TTTTTTTTTTTTTT CJTGTGTTGACA AATGTTGTTTATT G	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43147 KIAA0397 - HOMO SAPIENS (HUMAN), 488 aa.	1.2E-272	17
3980	cg43333012	406	TCAGCTCCCTCT TCCTGGATTAC A[A/G]AATTTCAT ACTTATCCACTA GAAA	A	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA- COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.5E-272	11 (11q23.3)
3981	cg43328330	1629	CTCTCGCCTTCC AGCAATTCCCG C[A/gap]GTGCTA CAAATGGGAAGT CAGAGAC	A	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16222 UDP-N-ACETYLGUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) (ANTIGEN X) (AGX) (AGX-1) (SPERM- ASSOCIATED ANTIGEN 2) - Homo sapiens (Human), 505 aa.	5.5E-271	1
3982	cg43970492	169	TCTATAAGATGT ATCTCCCCAAAG A[T/G]CACATTAA CTCCTCAAGTCA ACATC	T	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78395 PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA - HOMO SAPIENS (HUMAN), 509 aa.	3.6E-270	22
3983	cg43970492	201	AACTCCTCAAGT CAACATCTGCCT A[T/C]CCCCAACT TCCCCTTTTTC CTCA	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78395 PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA - HOMO SAPIENS (HUMAN), 509 aa.	3.6E-270	22
3984	cg43970492	391	AGCATTTGATAT GTGCACCCAGCT A[G/A]TTAGGCAT GAAACAGGGGC ACAGGA	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78395 PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA - HOMO SAPIENS (HUMAN), 509 aa.	3.6E-270	22
3985	cg43958878	1627	GAACGGGAAGTGC TGCCATGGGAG CG[C/gap]CCGCA GGGGGAGGAGT CCTTGCAGT	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9

3986	cg43958878	1641	CCATGGGAGCG CCCGCAGGGGG AGGAG/GTCCTT GCAGTTGGTGCC TACGGAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9
3987	cg43958878	1659	GGGGAGGAGTC CTTGAGTTGGT GC[C/gap]TACGG AGCCCGTGCCCT CCGGAGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9
3988	cg43926574	2586	AAATTAATTGG ATATTAATTGTA [A/T]AGACATCAT TTATTAATTTAA ACT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P43490 PRE-B CELL ENHANCING FACTOR PRECURSOR - Homo sapiens (Human), 491 aa.	1.1E-268	7
3989	cg43926574	3018	TATTAACCTGCC CTTACACAAAA T[C/T]ACACAAAA AGTTTCCTGATC TCGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P43490 PRE-B CELL ENHANCING FACTOR PRECURSOR - Homo sapiens (Human), 491 aa.	1.1E-268	7
3990	cg43927211	29	TTTTTTTTTTT TTTTTTTTTTTAA /T]GCCAGAGGTG AGATCTTTATTG ACT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15057 HYPOTHETICAL PROTEIN KIAA0041 - Homo sapiens (Human), 632 aa (fragment).	1.3E-268	3
3991	cg43951018	86	TTTTTTTTTTT TTTTTTTTTTTTT A]TTCCTCACTG CTTTATTTTGA A	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16851 UTP-GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE 2 (EC 2.7.7.9) (UDP- GLUCOSE PYROPHOSPHORYLASE 2) (UDPGP 2) (UGPASE 2) - Homo sapiens (Human), 507 aa.	1.8E-268	2

3992	cg43326821	251	GGCTAACCTTGC CGCGGGCCGAG CC[C/gap]TGCCT CGCCATGGACCA GGACTATG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q75869 R33374_1 - HOMO SAPIENS (HUMAN), 493 aa.	6.1E-268	
3993	cg43949042	268	GGAGAGGTGGG CTCTGGCAGCG GGT[G/T]TGAGG TGGCAGTGAGAA GCCAGGCC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q75907 ACAT RELATED GENE PRODUCT 1 - HOMO SAPIENS (HUMAN), 488 aa.	6.1E-268	
3994	cg44022853	30	TTTTTTTTTTT TTTTTTTTTTTTT AAGCAATTGTT TATGTTTAATT C	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12891 LYSOSOMAL HYALURONIDASE (PH-20 HOMOLOG) (LUCA-2) - HOMO SAPIENS (HUMAN), 473 aa.	2.1E-267	3
3995	cg43031103	742	CTTCAAAGTAGC CTGCTGGGAGC CTT[A]GATCATC AGAGGATGTTCA TCAGAG	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60240 PERILIPIN - HOMO SAPIENS (HUMAN), 522 aa.	6.3E-266	
3996	cg42919561	363	GGTGACTCTGGA GTTCTTGAGGG C[G/T]CCGTGCC CTGACTGTGGAT GTGAGC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q00515 LADININ - HOMO SAPIENS (HUMAN), 517 aa.	7.2E-265	
3997	cg43313186	2105	GTTTGTTTTCC CCTCAGCCCTGC C[A/C]CCGTGGG GAGTCTGGTTTT TCTCTT	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTROPHIN - HOMO SAPIENS (HUMAN), 505 aa.	8.3E-265	20 (20q11.2)
3998	cg43313186	2196	GCCTGTGAGCAC ACAGGCAGCCC GG[C/A]CCAAAAA AAAAAAAAAAAAA AAAAAA	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTROPHIN - HOMO SAPIENS (HUMAN), 505 aa.	8.3E-265	20 (20q11.2)

3999	cg43313186	2197	CCTGTGAGCACAC CAGGCAGCCCG GC[C/A]CAAAAA AAAAAAAAAAAA AAAAA	C	A				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTHROPHIN - HOMO SAPIENS (HUMAN), 505 aa.	8.3E-265	20 (20q11.2)
4000	cg43942622	1782	GGGAGCGGCAA GGCAGGGCAGG CGG[C/gap]CCCA GGAACCTGCCCA GTGCACAGG	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P11831 SERUM RESPONSE FACTOR (SRF) - Homo sapiens (Human), 508 aa.	5.1E-264	6
4001	cg43942622	297	CATAAAATATC ACCTCAACTCAT C[C/G]CTGACAC ACGCATGTCTC CCAAGG	C	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P11831 SERUM RESPONSE FACTOR (SRF) - Homo sapiens (Human), 508 aa.	5.1E-264	6
4002	cg43942622	41	TTTTTTTTTTT TTTTTTTTTTT[C TTTGTCACAAA AATGATACATTTA TT	C	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P11831 SERUM RESPONSE FACTOR (SRF) - Homo sapiens (Human), 508 aa.	5.1E-264	6
4003	cg43942622	562	GAAAGCCACCCA TAAGCCCCAGCT A[gap/G]TCTCCA GGAGAAAGCCC AGAAAGGT	gap	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P11831 SERUM RESPONSE FACTOR (SRF) - Homo sapiens (Human), 508 aa.	5.1E-264	6
4004	cg43934408	328	CACACAGGCC CTGCTCTGCCGC AG[G/gap]AAAT GGATTCCCAGGC CACAGAGC	G	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4005	cg43934408	369	CACAGAGCTGTC AGGCCTTTGACT TTT[C]GCAGAGAC CAAGCACCCAG AGGCT	T	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22

4006	cg43934408	715	ACCCCTTCCTA TGCCTCCAGG GTGAP/TJACTGT GTCTCAAAGAAC CTCTTCCC	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4007	cg43934408	729	GCCTCCAGGG TACTGTGTCTCA AA[G/gap]AACCT CTCCCTCCTGG GAACCATT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4008	cg43934408	729	CCTCCAGGGTA CTGTGTCTCAAA G[gap/G]AACCTC TTCCCTCCTGG AACCATT	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4009	cg43934408	745	TGCTCAAAGAA CCTCTTCCCTCC T[G/gap]GGAACC ATTTCCCACTCC TCTTCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4010	cg43934408	747	TCTCAAAGAACC TCTTCCCTCCTG G[G/gap]AACCAT TTCCCACTCCTC TTCTTT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15750 TAK1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 504 aa.	6.7E-263	22
4011	cg43980328	183	AAGACTCATGAA GTATAATCTCTC ATGCTCTCTTC TCTTCCCTCCTG CCAAG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4012	cg43980328	207	ATCTTCTTTCTCT TTCCCTGCCCCA [A/G]GCCCTAAGT TAGGGTTCCCAT CCAT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10

4013	cg43980328	273	GGTCAGGTGGC ATTGCTATCTCT G/A/GJGATTCCT GCCCATGAAAGC CACAA	A	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4014	cg43980328	385	AAACTGTGGTTT AAAAACAAACA A/A/CJCCAAACCAC TGTGAAATATTTA TTTT	A	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4015	cg43980328	455	TGATTAACCCAG TGCAGAAAAATA C/C/TJAGGTACAT TGGGTGAACGAT GAGCT	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4016	cg43980328	469	CAGAAAAATACC AAGTACATTGGG T/G/AJACGATGA GCTAGCTGTTCT AGTAT	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4017	cg43980328	523	CTTTTGTATCC AGTTAAGACCATI C/GJAGCATATAC AACATCATCACT AACT	C	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4018	cg43980328	535	CAGTTAAGACCA TCAGCATATACA A/C/TJATCATCAC TAACTCACAACAT GTAGC	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
4019	cg43980328	572	CTCAACAATGTA GCTGCAGGGTAA C/A/CJGTGGATA CCCTGTGTGCTC TACTG	A	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10

4020	cg43056973	129	GAGTGCCTCAGC AGCTTCTCCACA T[G/C]CTCTTCAG TCCCCAAAGTTG GAGAA	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20711 AROMATIC-L-AMINO-ACID DECARBOXYLASE (EC 4.1.1.28) (DOPA DECARBOXYLASE) (DDC) - Homo sapiens (Human), 480 aa.	5.2E-262	7 (7p11)
4021	cg43922182	2206	CCTCCTTTTTTCG GTTTCCCTCTTGT C[gap]/TJTTTTTT TTTATTTTTATTA CGAAG	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47974 TIS1D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.1E-261	2
4022	cg43922182	2216	CGGTTTCTCTCT GTCTTTTTTTTTT gap/TJATTTTTAT ACGAAGTTTCAT TCTT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47974 TIS1D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.1E-261	2
4023	cg44013054	271	TACACACACACA CACACACACACA C[Agap]CTTACA CACATGCACACA TCCTAAG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P15391 B-LYMPHOCYTE ANTIGEN CD19 PRECURSOR (B-LYMPHOCYTE SURFACE ANTIGEN B4) (LEU-12) (DIFFERENTIATION ANTIGEN CD19) - Homo sapiens (Human), 556 aa.	3.3E-261 (16p11.2)	16
4024	cg40296063	103	AGCCCTATGGGT GGGGATGGCAC CG[C/gap]CCTAC CGCCGAGAGAG TTGAAGCTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O94810 REGULATOR OF G-PROTEIN SIGNALING 11 (RGS11) - Homo sapiens (Human), 467 aa.	3.3E-261	
4025	cg43971058	1035	CATTAGTAACAT AACTCAACATCC TT[C]AATTGGT ATAGATGTGACA CAATT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60455 POLYADENYLATE BINDING PROTEIN- INTERACTING PROTEIN-1 - HOMO SAPIENS (HUMAN), 480 aa.	3.7E-261	
4026	cg27359628	100	TTCCCATGCCCC TCCCACGGTCAG C[AT]CCCCGATG GCCTGGGTGAG GGCTGA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALLING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.3E-260	

4027	cg27359828	123	GCACCCCGATG GCCTGGGTGAG GGCTTAJGATAG GCTGCTCTGACA CCATGGGG	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.3E-260	
4028	cg27359828	125	ACCCCGATGGC CTGGGTGAGGG CTGTAJGTAGGCT GCTCTGACACCA TGGGGAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.3E-260	
4029	cg27359828	76	ACAAGGGGAATA AAGTGGGACCCT TTTCJCCCATGCC CCTCCACCGTC AGCAC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.3E-260	
4030	cg43916882	242	AACAGTTATCTC AGAGGGTCAACC AIC/TJACAATGTC ATACAGAGACGC TGGTC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75475 LENS EPITHELIUM-DERIVED GROWTH FACTOR - HOMO SAPIENS (HUMAN), 530 aa.	2.3E-259	
4031	cg43980777	364	TCITTTGAGGCT TTACAATTACAAA TTCJGACAATGAT GTCAACCCATT ATCA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.2E-259	2
4032	cg43075307	103	GTATAGACCAAC ACTGTCCAACCA ATT/CJAGAACTTT CTGCCATGATGG CATAT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60623 DIPHTHAMIDE BIOSYNTHESIS PROTEIN-2 - HOMO SAPIENS (HUMAN), 489 aa.	1.3E-258	
4033	cg43075307	90	GAATAAGAGTCA AGTATAGACCAA CJA/GJCTGTCCAA CCAATAGAACTT TCTGC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60623 DIPHTHAMIDE BIOSYNTHESIS PROTEIN-2 - HOMO SAPIENS (HUMAN), 489 aa.	1.3E-258	

4034	cg43258841	140	GAAATACATTCT TTTCACATGATA A/T/CJGTTTTTCGC CCTTATTTATGG TCJTT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q14449 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.7E-258	
4035	cg43999171	48	TTTTTTTTTTTT TTTTTTTTTTTT[A /TJTACCAAACC CAACATTTATTG AGA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD21812 G9A - HOMO SAPIENS (HUMAN), 1001 aa.	3.8E-257	6
4036	cg43255855	1805	TAAGCTAAAAA CAGGCTGAAAAA G/G/AJAATTCCCA AAGAGAGTTAAC AAAAAC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43148 KIAA0398 - HOMO SAPIENS (HUMAN), 476 aa.	1E-256	18
4037	cg43918866	1419	CCTCAGCCTCCC AAGTAACTGGGA A/T/CJACAGGTAC CCACACCCACAC CCAGC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15519 CASPER - HOMO SAPIENS (HUMAN), 480 aa.	3.5E-256	2
4038	cg43963125	1099	TAGAGGAAACT GTAATATAAATG C/gap/AJTTTTTT TTTTTGCTTTTA AAGGA	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43717 PLACENTAL PROTEIN DIFF33 - HOMO SAPIENS (HUMAN), 473 aa.	3.5E-256	20
4039	cg43963125	403	GGTCTAGTACA GAATAGACAGTA A/A/TJCTTTGTT GAAAGAACTCTT TTATT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43717 PLACENTAL PROTEIN DIFF33 - HOMO SAPIENS (HUMAN), 473 aa.	3.5E-256	20
4040	cg43963125	563	TCAAGACTTTGC TCACTAGTCAGA C/C/TJGTAATTTT TAGAAGGAATAG GAGCA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43717 PLACENTAL PROTEIN DIFF33 - HOMO SAPIENS (HUMAN), 473 aa.	3.5E-256	20

4041	cg43949732	1699	TGAAGAACTGAA GGAGTCCTGCAT CT/gapJTTTTTTT TTTATCTGCTTCT GTTTA	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)
4042	cg43949732	1709	AAGGAGTCCTGC ATCTTTTTTTTTT T/gapJATCTGCTT CTGTTTAAAAAG CCAAC	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)
4043	cg43949732	1709	AGGAGTCCTGCA TCTTTTTTTTTTT gap/JATCTGCTT CTGTTTAAAAAG CCAAC	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)
4044	cg43949732	1828	GTTTGTAGTTCCTT ACAAACAGGGT [G/gap]GGGGG GGAAGGGCGTG CAAAACT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)

4045	cg43949732	1836	TCCTTACAAACA GGGTTGGGGG GG[G/gap]AAGGG CGTGCAAAACT AACATTGA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION UPREGULATED NUCLEAR PROTEIN) (TUNP) - Homo sapiens (Human), and Rattus norvegicus (Rat), 463 aa.	3.2E-255	9 (9q21.32)
4046	cg43274303	746	ATTGGGACCACC GGCTGGTGGTG CA[G/T]GTCCAGA ACATTCTGGGGG CTGCAG	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15175 PARANEOPlastic ANTIGEN - HOMO SAPIENS (HUMAN), 535 aa (fragment).	7.6E-254	17
4047	cg43943285	1459	ATTGACCCACAA AGTTTCAGAAAT TT[C/T]CTGAAAG TTTCCTCTTTT TCCTC	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04469 FIBRINOGEN GAMMA-B CHAIN PRECURSOR (FIBRINOGEN GAMMA) - Homo sapiens (Human), 453 aa.	4.2E-253	4
4048	cg43971614	736	CCTTATCAAAA AAAAATCTATTC [C/T]TTTATTCA GTTTTAAACATA CCA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	5.3E-253	5
4049	cg43040311	560	ATGGAATAGATT TTGCCAAACCTC A[C/T]TGCATATT TACAGTATTTAA GCAT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q00425 PUTATIVE RAS INHIBITOR - HOMO SAPIENS (HUMAN), 471 aa (fragment).	5.3E-253	20
4050	cg43040311	84	TTATGTGCAAAA TTCCATTAAAAA [A/gap]TCATTTAC AAAAGTACAACA CAGTA	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q00425 PUTATIVE RAS INHIBITOR - HOMO SAPIENS (HUMAN), 471 aa (fragment).	5.3E-253	20
4051	cg44034555	386	GAAGTGAGGGC CCAAAATAGGGA GT[G/T]TGGGTG ATGAGGGGTGA GTTCAAAAT	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13228 SELENIUM-BINDING PROTEIN 1 - Homo sapiens (Human), 472 aa.	3.8E-252	1

4052	cg43962954	103	CTGAGTGTACGG GGCCAGGGGA AG[G/gap]CTGGA GCCAAACCAAG TCTCTGGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4053	cg43962954	110	TCACGGGGCCCA GGGAAGGCTG GAG[C/gap]CAAA ACCAAGTCTCTG GGGCGGGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4054	cg43962954	111	CACGGGGCCAG GGGAAGGCTGG AGC[C/gap]AAAA CCAAGTCTCTGG GGGCGGGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4055	cg43962954	211	TAGAGACGGGA GAAGTCCAGTGT GCT[C/gap]TTCCAC CTCCCTCCAAGT CCCAAG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4056	cg43962954	328	AGGCCGGCGTG GTCAGGTCGGG GGC[G/A]GGAGG GCCGGGCTGG CTCTGTCTC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.8E-252	19
4057	cg43962954	213	CTGTCAACCTTT TATTGGAGTGG A[A/gap]CACATG AGGTTAGCTCG TGCCGGG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20

4058	cg43962064	305	ACACTGACGCCA CACTGAGCAGGA TG[<i>gap</i>]CACGGC CCGGGGCTCAC ACTGTCCA	G	<i>gap</i>			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4059	cg43962064	420	GGGACTGTGGC TCAGCTGACCCG TG[<i>gap</i>]CACAG CTGCACCTAAGA CATGGCCC	G	<i>gap</i>			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4060	cg43962064	461	GACATGGCCCTGA GCTAGCGCGGA AC[A/G]GCTCACA GTAGCGATACAT TCACAG	A	G			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4061	cg43962064	487	GCTCACAGTAGC GATACATTCACA G[G/ <i>gap</i>]ACACAG TTGGTGTCAGA AAAGGGG	G	<i>gap</i>			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4062	cg43962064	620	CAGCAGCTCATG CCCGGCATCCG CC[C/ <i>gap</i>]ATGCT GGGAGACTCCCT GAAAGGTG	C	<i>gap</i>			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4063	cg43962064	647	TGCTGGGAGACT CCCTGAAAGGTG G[G/ <i>gap</i>]CACCTG CCGTCATGAGG AGGTGTC	G	<i>gap</i>			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75354 CD39L2 - HOMO SAPIENS (HUMAN), 484 aa.	7E-251	20
4064	cg43924291	1180	ATATGCTTTAAG ACGCTTTCGTCC ATT[<i>gap</i>]TTCATAC CGCTCATTCTCA AGCGCC	T	<i>gap</i>			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43422 P52RIPK - HOMO SAPIENS (HUMAN), 492 aa.	3E-250	

4065	cg43924291	1182	ATGCTTTAAGAC GCTTCGTCCAT TTT/gap]CATACC GCTCATTCTCAA GCGCCAC	T	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43422 P52RIPK - HOMO SAPIENS (HUMAN), 492 aa.	3E-250	
4066	cg43924291	1182	TGCTTTAAGACG CTTCGTCCATT T/gap/]CATACC GCTCATTCTCAA GCGCCAC	gap	T			SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43422 P52RIPK - HOMO SAPIENS (HUMAN), 492 aa.	3E-250	
4067	cg42300443	318	TGGTGGAGCTTT GGAGCTGAGGC GG[G/gap]CAAGG CCTCTCAGATGG TCACGCTG	G	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P55249 ARACHIDONATE 12-LIPOXYGENASE, EPIDERMAL-TYPE (EC 1.13.11.31) (12- LOX) - Mus musculus (Mouse), 662 aa.	6.5E-249	
4068	cg44027341	2085	ATTGTACCTAAG TAAATTTCTTTA [A/G]GTCAGAAG CCCATTAATA GTTAC	A	G			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P00439 PHENYLALANINE-4-HYDROXYLASE (EC 1.14.16.1) (PAH) (PHE-4- MONOOXYGENASE) - Homo sapiens (Human), 452 aa.	1.6E-246	12
4069	cg43986564	127	CAAACTCAGTAG GAGTGCAAGG CT[G/A]TACCCCC GGAGCTAGACA GCCTGGG	G	A			SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa.	2.9E-245	3
4070	cg43986564	402	ACCTTGCCAAGT AGATGCATATGG A/gap/G]CATGGA ATGAATGGTGTG TGCIGTG	gap	G			SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa.	2.9E-245	3
4071	cg43986564	405	CTTGCCAAGTAG ATGCATATGGAC A/T/gap]GGAATG AATGGTGTCTGC TGTGGT	T	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa.	2.9E-245	3

4072	cg43980318	1501	TGAGAGGGAGG GGAAAAGACTTT CTT[<i>gap</i>]AAATAT TTCAATTTATGAC CTGCAAA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4073	cg43980318	1529	ATATTTTCATTAT GACCTGCAAATTI T/CJAAGAATAAA GACACTGAAGTA AGTT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4074	cg43980318	1561	AAGACACTGAAG TAAGTTTGAAGC C[<i>gap</i>]TCTACAG TTGTTTCCAGTC TTTTCAG	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4075	cg43980318	1700	CTCTCATGGTGC CACGTTTTTTTT [<i>gap</i>]TJCAATGTTT AGTAATAGTATA ATCCA	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4076	cg43980318	1700	CTCTCATGGTGC CACGTTTTTTTT [<i>gap</i>]TJCAATGTTT AGTAATAGTATA ATCCA	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
4077	cg43985612	131	CAGTAGCTGAAG GGCCTGAGCA GA[<i>gap</i>]CTGGT GCTGGAGGGG CCGGCATGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O43236 BRAIN PROTEIN H5 (PEANUT-LIKE PROTEIN 2) - Homo sapiens (Human), 478 aa.	6.9E-244	17
4078	cg43980589	1996	TTTATATCACTGT TTTTCACTGTTT T/CJTGTGGACAA ATAATGGTTGCT TTGC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00403 ZINC FINGER 5 PROTEIN - HOMO SAPIENS (HUMAN), 449 aa.	1.5E-243	18

4079	cg43920589	2080	ACCTACCCAAA GCTGTAGTCACA C[G/A]TCCTAAAG GCCAAGCAAACC CACC	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00403 ZINC FINGER 5 PROTEIN - HOMO SAPIENS (HUMAN), 449 aa.	1.5E-243	18
4080	cg43920589	2104	CGTCCTAAAGGC CAAGCAAAACCCA C[C/T]GGGATGG TGGGGGGTCTT GGAGCCA	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00403 ZINC FINGER 5 PROTEIN - HOMO SAPIENS (HUMAN), 449 aa.	1.5E-243	18
4081	cg43985156	167	GGTGACGGGCT CCGGGCTCCCG AGG[T/gap]GAAG AGCATCGGGG CTGAGGGATG	T	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75595 BCL-2-INTERACTING PROTEIN BECLIN - HOMO SAPIENS (HUMAN), 450 aa.	1.8E-243	17
4082	cg43985156	1811	CTTCTCTCTCG AAAAAACTAATT [T/A]AAATTGCT TTCTTTTTTTTA ACT	T	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75595 BCL-2-INTERACTING PROTEIN BECLIN - HOMO SAPIENS (HUMAN), 450 aa.	1.8E-243	17
4083	cg43315249	146	CATTTAACCTCC CAGGTTAAACAC C[T/C]TGTAATT ACCTTGAAGCTC TTTAC	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45712 HYPOTHETICAL 63.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 564 aa (fragment).	2.7E-242	17
4084	cg43315249	303	ACTTCAGAGAAA AATCCCAGATGA C[G/A]GCACTGG ACAGGTTATAAA GAGTTC	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45712 HYPOTHETICAL 63.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 564 aa (fragment).	2.7E-242	17
4085	cg43292372	786	AGCCCTTGGGAA GCCCATCTCAGG G[G/A]GATCCAG GAGCAGATGGC CAAAAA	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14740 SMAD7 PROTEIN - HOMO SAPIENS (HUMAN), 426 aa.	1.5E-241	

4086	cg44021361	109	TTATTGGAGG GCAGAGTCCAAC C/C/AJACCCAG GTCCTGAGGGTA GACTCA	C	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92685 NOT56-LIKE PROTEIN - Homo sapiens (Human), 438 aa.	6.3E-241	3
4087	cg43917689	1962	CAGGCCAAGA GCGCCTCACAAA GG[G/gap]CTGCT GCCTTGAACCTG GCCTGGGG	G	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92551 MYELOBLAST KIAA0263 - HOMO SAPIENS (HUMAN), 441 aa.	3.5E-240	3
4088	cg43976131	1814	GCGGAATGGA AGCAGTTTATGG AGT/CJTAAGTGG GGCTCTGCTATT TCCCCC	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92563 MYELOBLAST KIAA0275 - HOMO SAPIENS (HUMAN), 424 aa.	4.5E-240	
4089	cg43976131	1888	TTCCAGGGCAGA GTGAGGGGCAG AC[G/A]GGATGA GGCTCTTCTGTA AAGTCCA	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92563 MYELOBLAST KIAA0275 - HOMO SAPIENS (HUMAN), 424 aa.	4.5E-240	
4090	cg43976131	199	CGAGGCAGGGT CCCCAAGTGGA GGC[G/A]GGCG GGACGTGAGAG GATGGGGGC	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92563 MYELOBLAST KIAA0275 - HOMO SAPIENS (HUMAN), 424 aa.	4.5E-240	
4091	cg43928134	204	ATTCAAATGGAA ACAGACAATTTA A/C/AJAAAGAGAA GTAAAAAAATTTA TTGC	C	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA7335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa.	5.8E-240	8
4092	cg43928134	208	AAATGGAAACAG ACAATTTAACAA A/G/AJAGAAGTAA AAAAATTTATTGC AGTA	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA7335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa.	5.8E-240	8

4093	cg43928134	210	ATGGAACAGAC AATTTACAAAG A[G/A]AAGTAAA AAATTTATTGCA GTATT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA77335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa.	5.8E-240	8
4094	cg43928134	213	GAACAGACAAT TTAACAAAGAGA A[G/A]TAAAAAA TTTATTGCAGTAT TCGC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA77335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa.	5.8E-240	8
4095	cg43981846	1430	AATATGTGTTGT ATGCTCTTTTTCG [T/gap]TTTTTTTT TAAAAAAAAGAA TAAC	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD33924 LOMP PROTEIN - HOMO SAPIENS (HUMAN), 797 aa.	1.2E-239	13
4096	cg43981846	1439	TGTATGCTTTTT TGCTTTTTTTTTT /gap]AAAAAAAG AATAACTTTTTT GCC	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD33924 LOMP PROTEIN - HOMO SAPIENS (HUMAN), 797 aa.	1.2E-239	13
4097	cg43950854	1462	ACTGAAGAACCA TAAAGAAAAGAT G[A/gap]AAAAAA AAACTATCAAAG AAAGATG	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 - Mus musculus (Mouse), 445 aa.	3.2E-239	6
4098	cg43950854	1471	CCATAAAGAAAA GATGAAAAAAA A[A/gap]CTATCAA AGAAAGATGAAA TAATAA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 - Mus musculus (Mouse), 445 aa.	3.2E-239	6
4099	cg42750818	85	GCCAGGTTATAC CCTAGGACGGT GT[C/gap]CTTCC CTCCCTCCTAGG GTGGGAGG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99764 HYPOTHETICAL 48.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 437 aa (fragment).	2.9E-238	1

4100	cg43922856	1099	AGTTGAACGTGC CAAAGAGATACC ATC/JCAGTTGG ATTTCTAGGGT CAACA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2E-237	12 (12q22)
4101	cg43923262	1651	GCTAATGGCGAT CATCTTTGCCAC C/A/GJCCTGGGG AGAGCCTGCTTG GGAATG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15527 8-OXOGUANINE DNA GLYCOSYLASE 1 (EC 3.2.2.-) - HOMO SAPIENS (HUMAN), 424 aa.	4.8E-236	3
4102	cg41637661	54	TGGGCCGCCAG ACTCGGGAGAG GCTC/GJCGTCTT GTGCAAGGGTC CTGTGGGC	C	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O43913 ORIGIN RECOGNITION COMPLEX SUBUNIT 5 - Homo sapiens (Human), 435 aa.	6.1E-236	
4103	cg43932322	52	TCTTTTTTTTTT TTTTTTTTTTTTG /TATTTTTTTTTG TTTTTCCCAATT A	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O88941 GLYCOPROTEIN PROCESSING GLUCOSIDASE I - RATTUS NORVEGICUS (RAT), 834 aa.	6.5E-236	2
4104	cg43933215	299	GTCTCTCCCAGC CAAGTCAGGTGC C/C/TJAGCCAG ACCCTGCCCTGG CAAGGT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14849 MLN64 MRNA - HOMO SAPIENS (HUMAN), 445 aa.	1.6E-235	5
4105	cg43330158	1507	ACCTGAGCCACC CTCAGCAGGAG CT[G/gap]GGGTG GCCCTGAGCTC CAACGGCC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75462 CYTOKINE-LIKE FACTOR-1 PRECURSOR - HOMO SAPIENS (HUMAN), 422 aa.	2.1E-235	
4106	cg43957219	3538	GAGAGGAACATT CCATTTATTGTGA [G/T]TGGATTCC TCTGGAGGGCAT GTAC	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00345 HSP1-A - HOMO SAPIENS (HUMAN), 452 aa.	4.3E-235	X

4107	cg43955823	317	CTTATCTGTTCA AATATACCTGGA A[G/A]GGAATAC ACAGAGGGTTCA GCAGA	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05048 CLEAVAGE STIMULATION FACTOR, 50 KD SUBUNIT (CSTF 50 KD SUBUNIT) (CF-1 50 KD SUBUNIT) - Homo sapiens (Human), 431 aa.	5.5E-235	20
4108	cg43930174	1732	GTGGCAGGACT CGTGGGCCCTCT CC[G/A]GCCTGTT TCCCCTGCCACT CCAGCC	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14742 NUCLEOLAR PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	2.4E-234	12
4109	cg43930174	275	CCTGTGGACC GTTCTCCTAGC CC[G/T]GTGGTTT GGAACCAAGTGG CTTGGG	G	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14742 NUCLEOLAR PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	2.4E-234	12
4110	cg43948360	432	GCAAGGCAGCG GAGGGGCAGTG GGG[C/gap]CCCA GCATCCCCCTGAA GCCTCACCT	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O88746 TOM1 - MUS MUSCULUS (MOUSE), 492 aa.	5.1E-234	22
4111	cg43948360	435	AGGCAGCGGAG GGGCAGTGGGG CCC[C/gap]AGCA TCCCCTGAAGCC TCACCTGCA	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O88746 TOM1 - MUS MUSCULUS (MOUSE), 492 aa.	5.1E-234	22
4112	cg43962127	205	TCAGATCAGCAG ACCGAGTCGAAA T[G/C]TGATTCTT CAAAGCAAGTAT TGCTT	G	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7
4113	cg43962127	253	CTTACCCCTTGT CCTGAATGCAGT C[C/T]GTCATATG ACCACTAACTTG CATGT	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7

4114	cg43962127	270	ATG CAG TCC GTC ATATG ACCACTA A/C/T T T G C A T G T GACCA AAT G T T T GCAGA	C	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7
4115	cg43962127	317	CAGAGTGT T T T T TAGATATGCTCT C/G/A JGTGAGCC GTCATCCGTC A A TCCAAG	G	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7
4116	cg43962127	97	GTC T T A T T T T C C A GTAAAATATTCA C/A J A T A A T G T C A AAAGAATGAAAT GATA	C	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7
4117	cg43952917	525	TCTTACTTTGGC AAGAGAAAACAG A/G/A JGTATTTT GCTCCTCTCTA CCCAA	G	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q99611 SELENIDE:WATER DIKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 2) (SELENIUM DONOR PROTEIN 2) - Homo sapiens (Human), 448 aa.	1.5E-232	
4118	cg43940463	220	AAGAACCACCTC TAGCCTCCGCAG G/G/gap JCTCTT TGGGAACCCCTC CCTGCTT	G	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99771 JIP-1 - HOMO SAPIENS (HUMAN), 467 aa.	3.1E-232	
4119	cg43966506	2018	TCACCATGTTGG CCAGGCTGGTCT C/G/A JAACTCCTA ACCTCAGGCGAT CCACC	G	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92966 SNRNA ACTIVATING PROTEIN COMPLEX 50KD SUBUNIT - HOMO SAPIENS (HUMAN), 411 aa.	8.3E-232	9
4120	cg43966506	2914	AGGCTAGACCA TCAGATAGATTT A/C/T TCAAATAT TTTCTGGGAACC TTTAT	C	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92966 SNRNA ACTIVATING PROTEIN COMPLEX 50KD SUBUNIT - HOMO SAPIENS (HUMAN), 411 aa.	8.3E-232	9

4121	cg43983092	127	TAGCTAATTATT ACAAACTCATTT T/gap/AAAGACTA GAATTTTAAATC GAAGG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD29607 HYPOTHETICAL 53.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 448 aa.	1.7E-231	1
4122	cg43983092	922	TCCTGGTTTCCT TTTTGGCCCCG C[C/gap]ACAGAA AAGATGGATGTA GTAAGAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD29607 HYPOTHETICAL 53.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 448 aa.	1.7E-231	1
4123	cg43947107	420	GACCAAGCAGA GACTAGGCCTCA GG[C/gap]TAGCC CAGCAGGGCTTC CTGTGTCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75528 ADA3-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 432 aa.	2.8E-231	3
4124	cg43948144	1510	TAATATGTTTATT AGTTCTCTTTGG[A/gap]AAAAACT ACCACTGTGGTC TTAAA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74901 KIAA0878 PROTEIN - HOMO SAPIENS (HUMAN), 611 aa.	4.6E-231	5
4125	cg43948144	1541	ACTACCACTGTG GTCTTAAAGGG A[G/A]CAAAATAT ACCATAGGCTAA AACTA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74901 KIAA0878 PROTEIN - HOMO SAPIENS (HUMAN), 611 aa.	4.6E-231	5
4126	cg42676981	426	CCGAGACAGGT GTGCATGGTGG GTG[C/gap]CCCC TGCTGATGGTGT GAGGTCAGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08910 PROTEIN PHPS1-2 - Homo sapiens (Human), 425 aa.	5.9E-231	15
4127	cg42676981	544	CTGCTGGAGCGT GCCAGAGTCCG GA[G/gap]GCCTC ACTCCAGGTCCG CCTCCACC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08910 PROTEIN PHPS1-2 - Homo sapiens (Human), 425 aa.	5.9E-231	15

4128	cg42876981	545	TGCTGGAGCGT GCCAGAGTCCG GAG[gap]CCTC ACTCCAGGTCGG CCTCCACCT	G	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08910 PROTEIN PHPS1-2 - Homo sapiens (Human), 425 aa.	5.9E-231	15
4129	cg43968343	1175	TACATTGAGGAA AGTGAGATTCAC A[gap]GJCACAAA TACCAAGATGAC CAATGAA	gap	G			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4130	cg43968343	1420	CAGAGGGGACT CTCCGTACCCCT TC[A/G]GGAGGG TTTTGGGCAATA AAGCCAA	A	G			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4131	cg43968343	1453	TTTGGGCAATA AGCCAAATCTG T[A/G]CTTAAATA GGTGTGTCAT AAGAC	A	G			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4132	cg43968343	1488	GTGTGTCATCATA AGACAAATTTTA [A/G]CTCATTAT TAAAGGTCCTGA TGGA	A	G			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4133	cg43968343	1508	TTTAACTCATTT ATTAAAGGTCCTT G[A/T]GGACATT CCAAACTAGTAA CTTA	G	A			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)

4134	cg43968343	1750	TGCCTAACGCCA CGGGTCCACC GGT/CJGGGGGT CACAGCTGCTGG CTGGTGA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4135	cg43968343	546	GGAGGAAAGAG AAAGTGATCTTT ACT/AJTITTTTTC ATGGAACCCACCG GGGAT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4136	cg43968343	547	GAGGAAAGAGAA AGTGATCTTTAC TT/AJTITTTTTCAT GGAACCCACCGG GGATC	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4137	cg43968343	548	AGGAAAGAGAAA GTGATCTTTACT TT/AJTITTTTTCAT GGAACCCACCGG GGATCT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4138	cg43968343	551	AAAGAGAAAGTG ATCTTTACTTTTT TTCJTTCATGGAA CCACCGGGGAT CTTTT	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4139	cg43968343	705	AAATGGCATTAA AAATATCTACAG G/AJCAAGGACTA CCACGAAATACA ATATT	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)

4140	cg43968343	801	CACATGTCACAT TGATACACTATA C(A/T)TTTTTATAA TAAAAAATCGTA AATT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231	18 (18q21.3)
4141	cg43987280	142	CTTGACATGCAC ACATATATGGAT C(A/C)AAAAAGTAT GTACAACTAGAA AAACG	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55081 MICROFIBRILLAR-ASSOCIATED PROTEIN 1 - Homo sapiens (Human), 439 aa.	1.2E-230	15
4142	cg43987280	144	TGACATGCACAC ATATATGGATCA A(A/C)AAGTATGT ACAACTAGAAAA ACGGA	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55081 MICROFIBRILLAR-ASSOCIATED PROTEIN 1 - Homo sapiens (Human), 439 aa.	1.2E-230	15
4143	cg43987280	176	GTACAACTAGAA AAACGGACTCCA A(G/C)CAAAAATG GAAAACATGTTT CCATG	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55081 MICROFIBRILLAR-ASSOCIATED PROTEIN 1 - Homo sapiens (Human), 439 aa.	1.2E-230	15
4144	cg43274910	1083	GAGGTCACATGT AGCTGAGTGTGA A(A/gap)CCAAGA AAATACGAAGC TTCAAAA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27711 CGI-01 PROTEIN - HOMO SAPIENS (HUMAN), 642 aa.	3.2E-230	
4145	cg43274910	1125	GCTTCAAAAGTA CTGTGCGTTGTA TTTCTCTTCATT CTCTGGCAGGCT GGGAG	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27711 CGI-01 PROTEIN - HOMO SAPIENS (HUMAN), 642 aa.	3.2E-230	
4146	cg43274910	393	CACCTAGAAGAA TGCCCTGGAACAC AT(C/T)AACTTTC ATTACTAATGTTT TTGG	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27711 CGI-01 PROTEIN - HOMO SAPIENS (HUMAN), 642 aa.	3.2E-230	

4147	cg43274910	581	TCCATACACTCC CTCCACTGAGAA A[G/A]AGACAAAT GGCTTAGGCTAC AAGGT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27711 CGI-01 PROTEIN - HOMO SAPIENS (HUMAN), 642 aa.	3.2E-230	
4148	cg43918854	1838	CTGGCCAAGTCT GGCCAGCCTGG CC[C/gap]TGCAG GTCTCCCATGAA GGCCACCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228	22 (22q11.2)
4149	cg43918854	1990	GCAAGAAGGCCT CCTCAGCCCCG GG[G/gap]CTATG GCCCTGACCCCA GCTCTCCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228	22 (22q11.2)
4150	cg43918854	2000	TCCTCAGCCCCG GGGCTATGGCC CT[gap/T]GACCC CAGCTCTCCACT CTGCTGTT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228	22 (22q11.2)
4151	cg43918854	2039	CACCTCTGCTGT AGAGTGGCAGCT C[C/T]GAGCTGG TTGTGGCACAGT AGCTGG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228	22 (22q11.2)
4152	cg43918854	2062	CCGAGCTGGTTG TGGCACAGTAGC T[gap/T]GGGGAG ACCTCAGCAGG GCTGCTCA	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228	22 (22q11.2)
4153	cg43918854	2067	CTGGTTGTGGCA CAGTAGCTGGG GA[gap/T]GACCT CAGCAGGGCTG CTCAGTGCC	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228	22 (22q11.2)

4154	cg43969669	1576	GCTGTTGCTGTT GCTGTTGCTGTT G[G/gap]GCATCT TGCTGCTAATCC TGAGGCT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa.	8.8E-228	3
4155	cg43969669	1577	CTGTTGCTGTTG CTGTTGCTGTTG G[G/gap]CATCTT GCTGCTAATCCT GAGGCTG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa.	8.8E-228	3
4156	cg43969669	1614	TAATCCTGAGGC TGGTAGCAGAAT G[C/gap]ACATTG GAAGCTCCACC CCATAAT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa.	8.8E-228	3
4157	cg42896238	1684	TGCTTCAGCAA CCGGACCAGGA GG[G/gap]CCAGG GCCGGATGTGG GGACCCCTCT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q75800 BLU PROTEIN - HOMO SAPIENS (HUMAN), 440 aa.	1.4E-227	3
4158	cg43978295	248	TATCTTACCGCA ACACCAAAGAGG A[G/gap]GCTCAG CCTTCCCCAGTT CCCTGAG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4159	cg43978295	255	CCGCAACACCAA AGAGGAGGCTC AG[C/gap]CTTCC CCAGTTCCTGA GTTACAT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4160	cg43978295	256	CGCAACACCAAA GAGGAGGCTCA GC[C/gap]TTCCC CAGTTCCTGAG TTCACAT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6

4161	cg43978295	342	CAGGACCAATCA ATGTCCCGGA GG[G/gap]CAGAG AGGGTGGTGGG GCCACACTT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4162	cg43978295	395	CCATATGGAAG ACAGTATTCTCA G[A/T]TGAGGC AGGACTTTTTTG TGGGAG	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4163	cg43978295	87	CCTTTTTTTTT TTTTTTTTTTTTT AATAATATTCAT TATCCTTCATTAA A	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4164	cg43978295	89	TTTTTTTTTTTTT TTTTTTTTTTTTT TAAATATTCATTA TCCTTCATTAAAA A	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
4165	cg42913861	1886	ACCGGTGACCC GTTCCCGCGGG GG[G/gap]CTGGA AGAAAGCCGACCC GGGACTGC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4166	cg42913861	448	TGCTGCTATAAA AATAACTTTTTTT [gap]/TCAAAATGG CAGTTTCTGACT AATCAT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4167	cg42913861	680	GCCTCGGCCA AGGGCAACTTCT GG[A/G]CACACG CAGATCGGCAAG TGCTATG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)

4168	cg42913861	778	GGCGGGCAGGT GAGTGGGCAGG GGC[gap/C]ACGT CCACGGCCAGC CCTGATGGCT	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4169	cg42913861	802	GCACGTCCACG GCCAGCCCTGAT GGC/TJTGCGCC CACATGGGCAAC TTCTGCA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4170	cg42913861	933	CCATCCTCAGCA GTTCAAGAAATGC CTT/AJCCTCCCCG CCATTTCTCTCT GCGGT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3E-227	2 (2cen)
4171	cg44932825	112	CATGCCCTGGAG GTTAGTCTGGGG GGT/CJCGGCGG GATGGACACACA GACAGAC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43463 SU(VAR)3-9 HOMOLOG - HOMO SAPIENS (HUMAN), 412 aa.	9.8E-227	X
4172	cg43971224	248	ACCCCATAGACA CAGGCAGCATT A[G/C]TCATAATT TTTAAATTAACG TCAC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P15907 CMP-N-ACETYLNEURAMINATE-BETA- GALACTOSAMIDE-ALPHA-2,6- SIALYLTRANSFERASE (EC 2.4.99.1) (BETA-GALACTOSIDE ALPHA-2,6- SIALYLTRANSFERASE) (ALPHA 2,6- ST) (SIALYLTRANSFERASE 1) (B-CELL ANTIGEN CD75) (ST6GAL) - Homo sapiens (Human), 406 aa.	1.5E-225	3 (3q21)
4173	cg43918561	2555	CTAGACGCAGCC CGCAGGCAGCC CC[C/A]CACCCG CCGCCTCCTGCA CCGAGAG	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04177 TYROSINE 3-MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3- HYDROXYLASE) (TH) - Rattus norvegicus (Rat), 498 aa.	2.1E-224	11 (11p15.5)

4174	cg43952397	2935	TGGTCITTCAGT CAACGTGCTAGA ATT/ACCGATGAC TTATTAATCTCTA ATT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43144 KIAA0394 - HOMO SAPIENS (HUMAN), 412 aa.	9.4E-224	17
4175	cg43952397	8176	CAAGAAAGGCTG GGGCTGGCCCT GGG[G/gap]CTCA TCATGATGCTTT CCTGGATCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43144 KIAA0394 - HOMO SAPIENS (HUMAN), 412 aa.	9.4E-224	17
4176	cg43952397	7497	ATTCAAAGGGAC GCCAGCCATCCT T[G/A]GTGACAG GGGCCCCCAACTT AGCATC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43144 KIAA0394 - HOMO SAPIENS (HUMAN), 412 aa.	9.4E-224	17
4177	cg43986954	672	AATCATTTATTGG TCTTTACAGTGA T[C]GATGGAAGA ATGTACAGGTGT CCCC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC68871 METHYL-CPG BINDING PROTEIN MBD2 - HOMO SAPIENS (HUMAN), 411 aa.	9.4E-224	18
4178	cg43984330	86	AAAGAAACGGCC TTGTCCCCAAAG G[G/gap]TCTCCT CTTGAAGGAATG GGGGCAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P32121 BETA-ARRESTIN 2 - Homo sapiens (Human), 409 aa.	8.5E-223	17
4179	cg44916523	98	CCACCCTGCTTG GCCCAGGCTATG C[C/gap]TAGAAG CAAGTCAAAGGC AGGTAGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00467 HTRIP - HOMO SAPIENS (HUMAN), 469 aa.	3.4E-222	
4180	cg44916523	12	TTTTTTTTTTT[A] TATTTTATTTTAC ATGAAAATCTTC C	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00467 HTRIP - HOMO SAPIENS (HUMAN), 469 aa.	3.4E-222	
4181	cg44916523	13	TTTTTTTTTTT[A] TATTTTATTTTAC ATGAAAATCTTC CA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00467 HTRIP - HOMO SAPIENS (HUMAN), 469 aa.	3.4E-222	

4182	cg44032871	202	CAGCTTCCTGAG GAGGGGCCGGC CC[T/gap]CTCCT CTTGCCCTGTT GAAGCTTG	T	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O43566 REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) - Homo sapiens (Human), 441 aa (fragment).	1.1E-220	5
4183	cg44032871	253	GCACAGGCTGG GGAGGCTGGCA CTG[C/gap]CAAC GCCATCCCTCCA TGTTGGGCA	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O43566 REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) - Homo sapiens (Human), 441 aa (fragment).	1.1E-220	5
4184	cg44032871	254	CACAGGCTGGG GAGGCTGGCAC TGC[C/gap]AAGG CCATCCCTCCAT GTTGGGCAA	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O43566 REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) - Homo sapiens (Human), 441 aa (fragment).	1.1E-220	5
4185	cg43960557	159	GCAACACTGCTT TATTAGGCCGGG C[C/gap]AGCCAG GAGCAGACACAC GGCTCCT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa.	2.7E-220	22
4186	cg43960557	174	TAGCCCGGGCC AGCCAGGAGCA GAC[A/g]CACGG CTCCTCAGTACA CATTCCCC	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa.	2.7E-220	22
4187	cg43960557	2015	GTCGCGGATGG GCTGCAAGAGGT GG[G/gap]CGAAG CGCGCTCCAC GTCCTCCAT	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa.	2.7E-220	22

4188	cg42500526	489	CGCTCTCTAGAG CCAGGCACGAC CA(CA)TTGCTGA TTGGGGACAGG CTGTGCT	C	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99434 NEUROBLASTOMA - HOMO SAPIENS (HUMAN), 421 aa.	3E-220	1
4189	cg43313101	205	CITTGCTATT AAGTATTTTTT ap/TGCGCTCCTGT ACAAAATACATA AAAG	gap	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q62831 NEUROGLYCAN C PRECURSOR - RATTUS NORVEGICUS (RAT), 544 aa.	1.1E-219	3
4190	cg43994920	182	CAAGTGTCAGG CGACGTGGAAC CC(A)GIGGTGTC TTTTATGAATAAT CAAAAG	A	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15394 ORF, COMPLETE CDS - HOMO SAPIENS (HUMAN), 419 aa.	1.6E-219	3
4191	cg43041368	56	ATGAGAAAAGTA CTTTATTCGTGC AT(C)AATTTTC AGTCCATTCAA AATTA	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15504 CG1 - HOMO SAPIENS (HUMAN), 423 aa.	1.6E-219	7
4192	cg43934903	181	TTGAGGAACCTA CGGCCTGAACCT Tgap/AJAAAAAAA AATCTCTAAAGA CCTTAC	gap	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.1E-218	1
4193	cg43934903	190	CTACGGCCTGAA CCTTAAAAAAA A(gap/A)TCTCTAA AGACCTTACAGT CTGCIG	gap	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.1E-218	1
4194	cg43934903	398	AAAACCTATTAGA CCATATATTCTAT [A/G]TTTTTAAAG TGAATTATGCAT AAAA	A	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.1E-218	1

4195	cg43934903	464	ACATGATTGCAG TAACATTCTCAA G[gap]/AJAAAAAA AAACCCTAGTAT ACTTTAG	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.1E-218	1
4196	cg42891496	235	AAAGGCTGGCTC CCCTGGCCGAG GC[C/gap]TGGGA CTGATGCAAGAC AGCCAGCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00224 HYPOTHETICAL 46.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 409 aa.	1.3E-217	8
4197	cg43994694	985	TACCTCAGGCC TGCGGGTGGT CTG[A]GAGTTCC AAGGCATTGGG GAACCA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92554 MYELOBLAST KIAA0265 - HOMO SAPIENS (HUMAN), 401 aa (fragment).	2.1E-217	7
4198	cg43994694	1226	ACATCTGTAAGA CCACAAAAA A[A/gap]TGGGT TTACAGAATACG AAGACCA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92554 MYELOBLAST KIAA0265 - HOMO SAPIENS (HUMAN), 401 aa (fragment).	2.1E-217	7
4199	cg43261326	495	ACAGAAAAATTT AAAGTGAATGTG A[T/C]GTTGGAGA GAGTGGGAAGG AAAAGT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99984 MRNA EXPRESSED IN OSTEOBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 413 aa.	3.3E-217	1
4200	cg43917040	240	CTCATTATACAT TCCATGCCGTCA [G/gap]GTTAAAA CTCTGCTTTGAA TCGATG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75205 HYPOTHETICAL 44.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 403 aa.	8.4E-216	16
4201	cg43917040	241	TCATTATACATT CCATGCCGTGTCAG [G/gap]TTAAACT CTGCTTTGAATC GATGC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75205 HYPOTHETICAL 44.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 403 aa.	8.4E-216	16

4202	cg43917040	660	GCCTTCCAAACCT GCCTCCCGGAG GG[G/gap]CTTTC AGCTGGAGACC CCATTGGAG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75205 HYPOTHETICAL 44.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 403 aa.	8.4E-216	16
4203	cg43959148	375	GACATCCTTCCA GATGGTTCCCTG C[C/T]CCTAGGC CAACCTCCACAG TCATGT	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75955 FLOTILLIN-1 - HOMO SAPIENS (HUMAN), 427 aa.	1.4E-215	6
4204	cg43917498	199	GGCTCCAAGCAC GCCATATGAAGC A[C/T]GCCAATGT CACTTATGTGCC CTGAT	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4205	cg43917498	446	TCACGTGTAATA TCCTTTAGATTC [G/A]TCTTGTTAA CTCAGTTTTCAG TCAG	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4206	cg43917498	581	CAATGTAAAGAG AGCTCGAGTGTG G[gap/G]CCAAGG CATCGGACCTTA CACCTAA	gap	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4207	cg43917498	61	TATAATCTTTATT CTATAATCTCC[A/G]CCAGTGCTA GAATTTCTTCC CAA	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4208	cg43917498	676	TTCTTGCTAACC AGTCITTAAGGG[C/G]ACATAAGAA ACTCACGTTAA TTAT	C	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	

4209	cg43917498	703	CATAAGAACTC ACGTTAAATTATA TTCCTGACATA TTATTATCCATG AAA	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75968 HYPOTHETICAL 47.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 422 aa.	1.4E-215	
4210	cg43941592	1434	CGCCCTCCTCAC CGCCCTTCCTCG G[G]CJAGTCACTT CCACTGGTGGAC CACGG	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07988 PULMONARY SURFACTANT- ASSOCIATED PROTEIN B PRECURSOR (SP-B) (6 KD PROTEIN) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(PHE)) (18 KD PULMONARY- SURFACTANT PROTEIN) - Homo sapiens (Human), 381 aa.	2.1E-215	2 (2p12)
4211	cg43941592	2088	CCTGTGTAATAC AATGCTGCACC A[A]GJTGCTAATA AAGTCCTATTCT CTTTT	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07988 PULMONARY SURFACTANT- ASSOCIATED PROTEIN B PRECURSOR (SP-B) (6 KD PROTEIN) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(PHE)) (18 KD PULMONARY- SURFACTANT PROTEIN) - Homo sapiens (Human), 381 aa.	2.1E-215	2 (2p12)
4212	cg44006797	1111	CTGCTCTGCCCA TTTCCATTGGG G[gap]GJCCCACA GGCAGGGTCT GTGCTATC	gap	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE- ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4213	cg44006797	227	CGGCTTCCTCAC AAAGGAGGCAG GG[C]gap]CCCAT CACAGGGGTGTC CACCCCTG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE- ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	

4214	cg44006787	230	CTTCCTCACAAA GGAGGCAGGC CC[C/gap]ATCAC AGGGTGTCACAC CCCTGAAA	C	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE- ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4215	cg44006787	247	CAGGGCCCCAT CACAGGGTGTC CA[C/gap]CCCTG AAAGGCTCTCC AGCCTGGA	C	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE- ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4216	cg44006787	253	CCCATCACAGGGA TGTCACACCCCT G[A/G]AAGGCTC TCCAGCCTGGA AGAGCC	A	G			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE- ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4217	cg44006787	286	GAAGAGCCAGAA CAAAGTGCAATTG G[A/G]CCCACTC CCACCCCTCTCTG AGCTGC	A	G			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P78423 FRACTALKINE PRECURSOR (NEUROTACTIN) (CX3C MEMBRANE- ANCHORED CHEMOKINE) (SMALL INDUCIBLE CYTOKINE D1) - Homo sapiens (Human), 397 aa.	2.2E-215	
4218	cg43955639	1535	TTAGGACCTGAA CAGGGGTCCTG CC[A/G]GGCTGG GGACCCCTCTCTG GAAACCT	A	G			SILENT- NONCODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment).	2.8E-215	
4219	cg43950766	390	CATTAGTGAAC CTGCATTTCATG G[G/gap]GGGGG GGGGGGTACAC AGTATTTTA	G	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:AAAD44491 PTD004 - HOMO SAPIENS (HUMAN), 396 aa.	5.3E-214	22

4220	cg43950766	392	TTTAGTGAACCT GCATTTTCATGGG G[G/gap]GGGGG GGGTACACAGT ATTTTAAT	G	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:AAD44491 PTD004 - HOMO SAPIENS (HUMAN), 396 aa.	5.3E-214	22
4221	cg43947481	2202	ATCTTGCCATCC TCCCCTTCTGGT T[C/G]TCTGCACC CACCTGTCCCAC TGCAG	C	G			SILENT- NONCODING	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:AAD43978 CHROMATIN-SPECIFIC TRANSCRIPTION ELONGATION FACTOR FACT 140 KDA SUBUNIT - HOMO SAPIENS (HUMAN), 1047 aa.	8.6E-214	14
4222	cg43935715	913	GAATGTTGCCCT CCATTCTAAGGA ATTATGCAAAACA AATCTAAATGAT CTTCT	T	A			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q92597 NDRG1 PROTEIN (DIFFERENTIATION- RELATED GENE 1 PROTEIN) (DRG1) (REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN CAP43) - Homo sapiens (Human), 394 aa.	1.1E-213	8
4223	cg43935715	1088	TGCTGTAAAGC CAGGAGATTTTG TT[C/G]CCTGCTT TTGCTGCACATT AAGAG	T	C			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q92597 NDRG1 PROTEIN (DIFFERENTIATION- RELATED GENE 1 PROTEIN) (DRG1) (REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN CAP43) - Homo sapiens (Human), 394 aa.	1.1E-213	8
4224	cg43935715	823	CCTTACATCGAG TAACCCCAATTC C[G/A]CCCCCAC CCCAGTGCTCCT ACTCCG	G	A			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q92597 NDRG1 PROTEIN (DIFFERENTIATION- RELATED GENE 1 PROTEIN) (DRG1) (REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN CAP43) - Homo sapiens (Human), 394 aa.	1.1E-213	8

4225	cg44914050	2439	GTCACACAGCTA ATGAGTTCTAA C[G]AGGGAAC GGACTCAGGCTT GTCTGA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15392 DIMINUTO-LIKE PROTEIN - Homo sapiens (Human), 390 aa.	1.3E-213	1
4226	cg44914050	55	TTTTTTTTTTTT TTTTTTTTTTTT C[TTTTTCCAGG CCACTTTTATTTA A	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15392 DIMINUTO-LIKE PROTEIN - Homo sapiens (Human), 390 aa.	1.3E-213	1
4227	cg44914050	56	TTTTTTTTTTTT TTTTTTTTTTTT C[TTTTTCCAGG CACTTTTATTAA A	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15392 DIMINUTO-LIKE PROTEIN - Homo sapiens (Human), 390 aa.	1.3E-213	1
4228	cg43948829	117	CTCTCAAGAGAA AGAAGAGTTACT A[C]TTGCAGGAA CAGACATTTTTT AAA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2
4229	cg43948829	182	ACAGAAAACATT GTTATTACATA A[T]C/AATGTGGG GCTCTGTCTCTG CCGAC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2
4230	cg43948829	219	ATGTGGGGCTCT GTCTCTGCCGAC A[G]gapJGGGCTG GGTTCGGGCATT AGCTGTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2
4231	cg43948829	222	TGGGGCTCTGTC TCTGCCGACAGG G[G]gapJCTGGGT TCGGGCATTAGC TGTGCCG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2

4232	cg43948829	359	ACACGAGTCACC TCCAAAGAGCTG C[G/A]ACTGTTTG AGAATCTGCCAA GAGGA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43179 TUMOR-SUPPRESSING SUBCHROMOSOMAL TRANSFERABLE FRAGMENT 1 - HOMO SAPIENS (HUMAN), 387 aa.	2.9E-213	2
4233	cg43920203	55	TTATTGGCCAC AGAAGGGATGA GG[A/G]CGCGTG AAGGGCTAGG GATAAGAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75085 KIAA0477 PROTEIN - HOMO SAPIENS (HUMAN), 1132 aa.	3.2E-213	1
4234	cg43920203	57	ATTGGCCACAG AAGGGATGAGG AC[G/A]CGTGAA GGGGCTAGGGA TAAGAATG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75085 KIAA0477 PROTEIN - HOMO SAPIENS (HUMAN), 1132 aa.	3.2E-213	1
4235	cg43062448	124	TTAACAGTGTA GAAGGAAATCT C[A/C]GAAAAAGC AGATAGACAATG TAGAA	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213 (3q21.3)	3
4236	cg43062448	239	ACATGTGGAAC TAACTAGACCAT TT[C/T]AAGAAAG ACCAATTTCTAAT GCAA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213 (3q21.3)	3
4237	cg43062448	261	ATTTAAGAAAG ACCAATTTCTAAT [G/C]CAAATTTTC TGAGGTTTTCAG ATTT	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213 (3q21.3)	3
4238	cg43062448	262	TTTAAAGAAAGA CCAATTTCTAAT G[C/G]AAATTTTC TGAGGTTTTCAG ATTT	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213 (3q21.3)	3

4239	cg43985159	1351	AAGGCATGATAG TGCAAGAGGTAA GTTCTTTTGATT TATAGAACATTTA TAGA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15018 ORF - HOMO SAPIENS (HUMAN), 419 aa (fragment).	1.3E-212	10
4240	cg43950854	424	ATAGGCCAAATTC AGAGGTGATTTT ATCTCATTTTCA AATTATCATCAA GAGTG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O14524 HYPOTHETICAL PROTEIN KIAA0286 (HA6800) - Homo sapiens (Human), 429 aa (fragment).	2.6E-212	
4241	cg43989195	1616	CAAGTTTGTGTA TCAGAGCGGGA GTGTCGGGGG AGGAAAGAAAA CAAACAG	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15050 HYPOTHETICAL PROTEIN KIAA0112 (HA0609) - Homo sapiens (Human), 399 aa (fragment).	2.8E-211	8
4242	cg43989195	289	CGGTGCGCCGG ACCCACGCCGG AGGgap/CJCGAG CTACAGGCCCTG GCGCGGGAC	gap	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15050 HYPOTHETICAL PROTEIN KIAA0112 (HA0609) - Homo sapiens (Human), 399 aa (fragment).	2.8E-211	8
4243	cg43989944	1878	CCGCACTCACCT GGGGTTGGGG CA/GATGCCGC GCTGTGCTGCCT GICTTCG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60779 GROWTH ARREST SPECIFIC - MUS MUSCULUS (MOUSE), 489 aa.	1E-210	16
4244	cg43989944	2096	GGTGGGTGCAG CCAGCGTGCCG GAAACJGGGCA GGCAGCCTCCC GCTGCCAGT	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60779 GROWTH ARREST SPECIFIC - MUS MUSCULUS (MOUSE), 489 aa.	1E-210	16
4245	cg43989944	2849	TCTGGGTCTGTG TAGCTGGGGAG AGAGATGAGG CTGCAGAGATGG GGACCAG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60779 GROWTH ARREST SPECIFIC - MUS MUSCULUS (MOUSE), 489 aa.	1E-210	16

4246	cg43999944	3086	CTCCACAAATTT ATCCCATGAGCA A[G/T]AACCACTT TATAGCTGGCAT ATATT	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60779 GROWTH ARREST SPECIFIC - MUS MUSCULUS (MOUSE), 489 aa.	1E-210	16
4247	cg43984681	1347	TTGCGACACTCC CAAAGCGTAAG G[G/gap]CCGACC CAGGCATCTTGG CCCCCAG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O15382 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.42) (BCAT(M)) - Homo sapiens (Human), 392 aa.	1.3E-210	19 (19q13)
4248	cg43049444	168	ATCAGCTAGGCC AGGAGCCTCAG CG[G/C]TGCCCC TTCAGGCTCATC TGGCAAG	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10523 S-ARRESTIN (RETINAL S-ANTIGEN) (48 KD PROTEIN) (S-AG) (ROD PHOTORECEPTOR ARRESTIN) - Homo sapiens (Human), 405 aa.	2.7E-210	2
4249	cg43049444	294	GCCCTTCCCACC TGGTTGGTGACA A[A/gap]TCACAA GGTGGTAGAAGT TGCCAGG	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10523 S-ARRESTIN (RETINAL S-ANTIGEN) (48 KD PROTEIN) (S-AG) (ROD PHOTORECEPTOR ARRESTIN) - Homo sapiens (Human), 405 aa.	2.7E-210	2
4250	cg43049444	305	CTGGTTGGTGAC AAATCACAAAGT G[G/gap]TAGAAG TTGCCAGGGACA GATAACA	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10523 S-ARRESTIN (RETINAL S-ANTIGEN) (48 KD PROTEIN) (S-AG) (ROD PHOTORECEPTOR ARRESTIN) - Homo sapiens (Human), 405 aa.	2.7E-210	2
4251	cg44013820	17	TTTTTTTTTTTT TTT[A/T]AAGAAG GTAGATAAAATTT ATTGCCA	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15298 BASIC LEUCINE ZIPPER NUCLEAR FACTOR 1-LIKE (DJ206D15.4) (BASIC- LEUCINE ZIPPER NUCLEAR FACTOR JEM1) - HOMO SAPIENS (HUMAN), 400 aa.	3.5E-210	1
4252	cg44013820	18	TTTTTTTTTTTT TTTA[A/T]AGAAG GTAGATAAAATTT ATTGCCAC	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15298 BASIC LEUCINE ZIPPER NUCLEAR FACTOR 1-LIKE (DJ206D15.4) (BASIC- LEUCINE ZIPPER NUCLEAR FACTOR JEM1) - HOMO SAPIENS (HUMAN), 400 aa.	3.5E-210	1

4253	cg44013820	19	TTTTTTTTTTTT TTTAAATGGAAG GTAGATAAAATTT ATTGCCACT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15298 BASIC LEUCINE ZIPPER NUCLEAR FACTOR 1-LIKE (DJ206D15.4) (BASIC- LEUCINE ZIPPER NUCLEAR FACTOR JEM1) - HOMO SAPIENS (HUMAN), 400 aa.	3.5E-210	1
4254	cg44013820	955	TTAAATATATCTA TTTAGTTTTTTTT /CJTTCCTTACC CTGAGATATTTA TTA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15298 BASIC LEUCINE ZIPPER NUCLEAR FACTOR 1-LIKE (DJ206D15.4) (BASIC- LEUCINE ZIPPER NUCLEAR FACTOR JEM1) - HOMO SAPIENS (HUMAN), 400 aa.	3.5E-210	1
4255	cg43834875	455	CAGTCTCTGCAG GTACCAGATTCC C/C/T/GTTGTATC CAACTGCATACA TTTAC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75216 WUGSC:H_DJ1159004.1 PROTEIN - HOMO SAPIENS (HUMAN), 379 aa.	1.1E-208	
4256	cg43832174	188	AAGCGCTGCAAA ATCCCTGGCGGT G/C/gapJCCGCAA TCTAACGCTCTAC AATAACC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20
4257	cg43932174	190	GGCTGCAAAAT CCCTGGCGGTG CC/C/gapJGCAAT CTAACGCTCTACA ATAACCTC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20
4258	cg43932174	288	AGACGGCAAGTC GCCGCGGACGC CT/G/gapJGGGCT CTCAGCTGCTGA ACAATGAC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20
4259	cg43932174	291	CGGCAAGTCGC CGCGGACGCCT GGG[G/gap]CTCT CAGCTGCTGAAC AATGACATC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20

4260	cg43932174	82	TTTTTTTTTTTTT TTTTTTTTTTTTT T/GCAATCTGCA AAAGACTTTATTA CA	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20
4261	cg43995867	1354	TTGTTGTTTCTAA ATCTATATGAGA A/TJTGACAATAA GTATTTTATTAT AA	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4262	cg43995867	1361	TTCTAAATCTATA TGAGAAATTGACA A/gapJTAAGTATT TTTATTATAACTC AGCC	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4263	cg43995867	1364	TAAATCTATATGA GAATTGACAATA A/gapJGTATTTT ATTATAACTCAG CCCAT	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4264	cg43995867	1372	TATGAGAATTGA CAATAAGTATTTT T/gapJATTATAAC TCAGCCCATACA TATAT	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4265	cg43995867	1378	ATTGACAATAAG TATTTTATTATA A/gapJCTCAGCCC ATACATATATACT ATGT	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4266	cg43995867	1387	TAAGTATTTTAT TATAACTCAGCC C/gapJATACATAT ATACTATGTATG CAGTG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)

4267	cg43995867	53	CTCGTGCCCGTTA CGGCCATCACG GC[G/C]GCCGCA GTGGCGTCCTG GAGCCCTC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
4268	cg43293087	1916	GAATGGAGAAAG GGTAATAGGTTG GT[gap]/TJGCAGT GAATGGGCTGG GGTGGGGT	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P21128 PLACENTAL PROTEIN 11 PRECURSOR (EC 3.4.21.-) (PP11) - Homo sapiens (Human), 369 aa.	2.3E-206	12
4269	cg43293087	2234	TAACTCAATTAT GCATTTGTCCCC[C/gap]AACCCAC TGAGAACTAAAT GCTGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P21128 PLACENTAL PROTEIN 11 PRECURSOR (EC 3.4.21.-) (PP11) - Homo sapiens (Human), 369 aa.	2.3E-206	12
4270	cg43916807	313	AGGCCAGGCTG CAGGGCGGGC AGA[C/gap]CCTG GGCCCGGGTC TACGCTTTCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4271	cg43916807	315	GCCAGGCTGCA GGGCGGGCAG ACC[C/gap]TGGG CCCCGGGCTAC GCTTCTGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4272	cg43916807	551	AAGATCTCCACT TCGGTCTGCCAT T[gap]/A/AAAAAAA AAAAAAATCTTC CTTC	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4273	cg43916807	552	AAGATCTCCACT TCGGTCTGCCAT T[gap]/AAAAAAA AAAAATCTTTCT CTTC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10

4274	cg43916807	565	CGGTCTGCCATT AAAAAAAAAAAA A[<i>gap</i>]CTTTCT CTTCTTTTCTCT TAAAG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4275	cg43916807	565	GGTCTGCCATTA AAAAAAAAAAAA A[<i>gap</i>]ATCTTTCT CTTCTTTTCTCT TAAAG	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4276	cg43916807	805	GGGTGCAGCA GGCATGACACCA AG[<i>gap</i>]CAGAG CCCGCAGCAGG GGCCCCGGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14153 HYPOTHETICAL PROTEIN KIAA0140 - Homo sapiens (Human), 422 aa.	2.9E-206	10
4277	cg43948416	1041	ATTGTCCATCCC ATGAGGCAGGG CT[G <i>gap</i>]GGCCA TGCCAAGACAAT CTCAAGGA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.7E-206	11
4278	cg43948416	454	CCTTCCTGCCCT TGGAAATGGCGT G[C <i>gap</i>]CTGGGC AATAGGGACAGG CCACAGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.7E-206	11
4279	cg43948416	455	CTTCTGCCCTT GGAAATGGCGT GC[C <i>gap</i>]TGGGC AATAGGGACAGG CCACAGTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.7E-206	11
4280	cg43948416	758	CGCAGGAGGCC CCTGGAGCAGC CTG[G <i>gap</i>]CCTC AGCCCAGGGCA GGTGCCCCAGA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.7E-206	11

4281	cg43920365	1326	AATGGAGAAAGA AAGCCATTTTC C/A/G]TAAAAAGG GATGGTTCATCA TTGTG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4282	cg43920365	1468	ATCTAGACAGCC TAAATCTGATTT [A/G]GTCITTTATA AAAATAATATCTT GTG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4283	cg43920365	2051	TCTTATGGAAAT CTCTGTTATTAA G/A/C]TATTTCAA GATGAGACAACA CTGAA	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4284	cg43920365	2188	AAGATGGGAACC TTATTGGAATGT G/T/gap]TTTTTTT TTTCCATGATGT CCAATT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3
4285	cg43920365	2198	CCTTATTGGAAT GTGTTTTTTTTT T/gap]CCCATGAT GTCCAATTTTGT TGTGGG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus scrofa (Pig), 417 aa.	6E-206	3

4286	cg43920365	2198	CTTATTGGAATGT GTTTTTTTTTTTg ap/TJCCATGATGT CCAAATTTTGTG TGGG	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus.scrofa (Pig), 417 aa.	6E-206	3
4287	cg43920365	2198	CTTATTGGAATGT GTTTTTTTTTTTg ap/TJCCATGATGT CCAAATTTTGTG TGGG	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - Sus.scrofa (Pig), 417 aa.	6E-206	3
4288	cg43958860	1311	CTAATGTGATCA TATGAGGACCTT T[ap/C]ATATCTG TCITTTATTTAAC AAAAA	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48745 NOV PROTEIN HOMOLOG PRECURSOR (NOVH) - Homo sapiens (Human), 357 aa.	6E-206	8 (8q24.1)
4289	cg44002669	333	GAGAGGCCAGG GAGGGCTGGGC GGG[C/gap]CCCC CAGGCTGGGCC GAGCAGCGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa.	8.8E-205	
4290	cg44002669	338	GCCAGGGAGGG CTGGGCGGGCC CCC[C/gap]AGGC TGGGCCGAGCA GCGCAAGTAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa.	8.8E-205	
4291	cg44002669	348	GCTGGGCGGGC CCCCAGGCTG GGC[C/gap]GAGC AGCGCAAGTAGA GGAAGTCAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa.	8.8E-205	

4282	cg43278557	1618	AGGCAGACCCCTC CCAGAGGCCCG CC[C/gap]AGGTG GGCATGGTCCC CCATTTCT	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43581 SYNAPTOTAGMIN VII - HOMO SAPIENS (HUMAN), 418 aa (fragment).	1E-204	
4283	cg43948656	39	TTTTCTTTTT TTTTTTTTTTTTT AJTTAGAAGAA CAGAAATTATTC A	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB41267 HYPOTHETICAL 66.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 609 aa.	1.1E-204	X
4284	cg43302693	106	ATTCCAGCCACA CCCAGGCCGTG GG[C/gap]AGCCA CCCTCCGAGACA CCTGGGCC	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4285	cg43302693	137	CCCTCCGAGACA CCTGGGCCGGG GG[C/gap]AGGT CTCAGCAGAAGC GCCGTGGG	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4286	cg43302693	163	AGGTCTCAGCA GAAGCCCGTG GG[C/gap]AGCCA CCATCCGAGGCA CTTGGTGG	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4287	cg43302693	294	TCCTTCTCAGA GAACTGGGCATA G[C/gap]CAGAGC TGGGGTGAGAA GCCCTTC	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16

4298	cg43302693	295	CCTTCTCAGAG AACTGGGCATAG C[C/gap]AGAGCT GGGTGAGAAA GCCCTTCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4299	cg43302693	344	CAGCCCTGCTGCTG ACCGAGGCTCTG C[C/gap]AGTTCT CATACCCCTCC CCATCCC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4300	cg43302693	485	CTGCCCCACAGCG AAGCTGCCCATG G[G/gap]CCCCGGG GTCAAGCCACCA CCCACAT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4301	cg43302693	535	TGTCCAGGAGT CCGGCCAGCCC AC[C/T]ACATCCG CTCCCTAGCTCC GGCGAG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
4302	cg44000884	706	TGGAAGCTGGGT TAGTTCATGCTA G[G/A]TGGCTGT AGCACTGACCTC ATGTAT	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43567 RING ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 381 aa.	4.8E-204	3
4303	cg44000884	939	TCAAAAAGTCCTG TTTCAGTAATTG [A/C]TTAAACTGT AGAATACTAAAA AATA	A	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43567 RING ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 381 aa.	4.8E-204	3

4304	cg43950996	1036	TGTAATTCCAAG AGGAGGGTGGG GA[gap]GCGAG GCCATAGTCTCC GAGTCCCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4305	cg43950996	1044	CAAGAGGAGGG TGGGAGGCGA GGC[C/gap]ATAG TCTCCGAGTCCC AGGACGATG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4306	cg43950996	1060	AGCGAGGCCA TAGTCTCCGAGT CC[C/A]AGGACG ATGGCTGACAAT ACACCAA	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4307	cg43950996	819	AGGTGAACGCCA GTCCAGAAAGAA G[G/gap]TGCTGG AGCCCTGCTCT GTCTCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4308	cg43950996	861	CTGTCTCTCCA TCACGGTGCTCC C[C/gap]TAGGGC CTCCCCAGGCCT CCTGGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4309	cg43950996	866	CTCTCCATCAG GTGCTCCCCTAG G[G/gap]CCTCCC CAGGCCTCCTTG GCTCAGT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4310	cg43950996	873	TCACGGTGCTCC CCTAGGGCCTCC C[C/A]AGGCCTC CTGGCTCAGTC CAGGTG	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1

4311	cg43950996	895	CCCCAGGCCTC CTTGGCTCAGTC CA[G/A]GTGTCTG CAGGAGGAAGG TGTGTC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1
4312	cg44021565	115	GTTTCATTATTG CTTTAAGAGTTA C/TATACCATGA GACACACAGTTG TGGT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
4313	cg44021565	191	CGCAGTGCTCAC GGGAGGCAAGT GG[G/A]CAGGG ACGGTCCAGATC GATGGCC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
4314	cg44021565	220	GGGACGGTCCA GATCGATGGCCA CC[C/A]ACTGAG CCGCTGCTACGT GGCCCCC	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
4315	cg43942842	1577	TGCATCTTCAGT TAATGTAACAGG A/T/A/AAAAAGGC AATGGATTTTATT TTAT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49903 SELENIDE, WATER DIKINASE 1 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 1) (SELENIUM DONOR PROTEIN 1) - Homo sapiens (Human), 383 aa.	1.9E-203	17
4316	cg43959472	122	TTTTTTTTTTTT TTTTTTTTTTTTT GJGGCATCAGAA ATGCTGTTTATT CT	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.4E-203	15
4317	cg43959472	123	TTTTTTTTTTTT TTTTTTTTTTTTG /TGCATCAGAAA TGCTGTTTATTTC TC	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.4E-203	15